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Attorney's Docket No.: 2345.2051-004

SUSCEPTIBILITY GENE FOR MYOCARDIAL INFARCTION, STROKE,
AND PAOD; METHODS OF TREATMENT

RELATED APPLICATIONS

This application is a continuation-in-part of International Application No.
PCT/US03/32556, which designated the United States and was filed on October 16,
5 2003, published in English, which claims the benefit of U.S. Provisional Application
No. 60/419,433, filed on October 17, 2002 and U.S. Provisional Application No.
60/449,331, filed on February 21, 2003. The entire teachings of the above
applications are incorporated herein by reference.

10 BACKGROUND OF THE INVENTION

Myocardial infarction (MI) and Acute Coronary Syndrome (ACS), *e.g.*, unstable
angina, non-ST-elevation myocardial infarction (NSTEMI) or ST-elevation
myocardial infarction (STEMI), are the leading causes of hospital admissions in
15 industrialized countries. Cardiovascular disease continues to be the principle cause of
death in the United States, Europe and Japan. The costs of the disease are high both
in terms of morbidity and mortality, as well as in terms of the financial burden on
health care systems.

Myocardial infarction generally occurs when there is an abrupt decrease in
20 coronary blood flow following a thrombotic occlusion of a coronary artery previously
damaged by atherosclerosis. In most cases, infarction occurs when an atherosclerotic
plaque fissures, ruptures or ulcerates and when conditions favor thrombogenesis. In
rare cases, infarction may be due to coronary artery occlusion caused by coronary

emboli, congenital abnormalities, coronary spasm, and a wide variety of systemic, particularly inflammatory diseases. Medical risk factors for MI include cigarette smoking, diabetes, hypertension and serum total cholesterol levels > 200 mg/dL, elevated serum LDL cholesterol, and low serum HDL cholesterol. Event rates in
5 individuals without a prior history of cardiovascular disease are about 1%. In individuals who have had a first MI or ACS, the risk of a repeat MI within the next year is 10-14%, despite maximal medical management including angioplasty and stent placement.

Atherosclerosis can affect vascular beds in many large and medium arteries.
10 Myocardial infarction and unstable angina (acute coronary syndrome (ACS)) stem from coronary artery atherosclerosis, while ischemic stroke most frequently is a consequence of carotid or cerebral artery atherosclerosis. Limb ischemia caused by peripheral arterial occlusive disease (PAOD) may occur as a consequence of iliac, femoral and popliteal artery atherosclerosis. The atherosclerotic diseases remain
15 common despite the wide-spread use of medications that inhibit thrombosis (aspirin) or treat medical risk factors such as elevated cholesterol levels in blood (statins), diabetes, or hypertension (diuretics and anti-hypertensives).

Atherosclerotic disease is initiated by the accumulation of lipids within the artery wall, and in particular, the accumulation of low-density lipoprotein (LDL)
20 cholesterol. The trapped LDL becomes oxidized and internalized by macrophages. This causes the formation of atherosclerotic lesions containing accumulations of cholesterol-engorged macrophages, referred to as “foam cells”. As disease progresses, smooth muscle cells proliferate and grow into the artery wall forming a “fibrous cap” of extracellular matrix enclosing a lipid-rich, necrotic core. Present in
25 the arterial walls of most people throughout their lifetimes, fibrous atherosclerotic plaques are relatively stable. Such fibrous lesions cause extensive remodeling of the arterial wall, outwardly displacing the external, elastic membrane, without reduction in luminal diameter or serious impact on delivery of oxygen to the heart.

Accordingly, patients can develop large, fibrous atherosclerotic lesions without
30 luminal narrowing until late in the disease process. However, the coronary arterial lumen can become gradually narrowed over time and in some cases compromise

blood flow to the heart, especially under high demand states such as exercise. This can result in reversible ischemia causing chest pain relieved by rest called stable angina.

In contrast to the relative stability of fibrous atherosclerotic lesions, the culprit
5 lesions associated with myocardial infarction and unstable angina (each of which are part of the acute coronary syndrome) are characterized by a thin fibrous cap, a large lipid core, and infiltration of inflammatory cells such as T-lymphocytes and monocyte/macrophages. Non-invasive imaging techniques have shown that most MI's occur at sites with low- or intermediate- grade stenoses, indicating that coronary
10 artery occlusion is due most frequently to rupture of culprit lesions with consequent formation of a thrombus or blood clot and not solely due to luminal narrowing by stenosis. Plaque rupture may be due to erosion or uneven thinning of the fibrous cap, usually at the margins of the lesion where macrophages enter, accumulate, and become activated by a local inflammatory process. Thinning of the fibrous cap may
15 result from degradation of the extracellular matrix by proteases released from activated macrophages. These changes producing plaque instability and risk of MI may be augmented by production of tissue-factor procoagulant and other factors increasing the likelihood of thrombosis.

In acute coronary syndrome, the culprit lesion showing rupture or erosion with
20 local thrombosis typically is treated by angioplasty or by balloon dilation and placement of a stent to maintain luminal patency. Patients experiencing ACS are at high risk for a second coronary event due to the multi-vessel nature of coronary artery disease with event rates approaching 10-14% within 12 months after the first incident.

The emerging view of MI is as an inflammatory disease of the arterial vessel
25 wall on preexisting chronic atherosclerotic lesions, sometimes triggering rupture of culprit lesions and leading to local thrombosis and subsequent myocardial infarction. The process that triggers and sustains arterial wall inflammation leading to plaque instability is unknown, however, it results in the release into the circulation of tumor necrosis factor alpha and interleukin-6. These and other cytokines or biological
30 mediators released from the damaged vessel wall stimulate an inflammatory response in the liver causing elevation in several non-specific general inflammatory markers

including C-reactive protein. Although not specific to atherosclerosis, elevated C-reactive protein (CRP) and serum amyloid A appear to predict risk for MI, perhaps as surrogates for vessel wall inflammation.

Although classical risk factors such as smoking, hyperlipidemia, hypertension,
5 and diabetes are associated with many cases of coronary heart disease (CHD) and MI, many patients do not have involvement of these risk factors. In fact, many patients who exhibit one or more of these risk factors do not develop MI. Family history has long been recognized as one of the major risk factors. Although some of the familial clustering of MI reflects the genetic contribution to the other conventional risk
10 factors, a large number of studies have suggested that there are significant genetic susceptibility factors, beyond those of the known risk factors (Friedlander Y, *et al.*, *Br. Heart J.* 1985; 53:382-7, Shea S. *et al.*, *J. Am. Coll. Cardiol.* 1984; 4:793-801, and Hopkins P.N., *et al.*, *Am. J. Cardiol.* 1988; 62:703-7). Major genetic susceptibility factors have only been identified for the rare Mendelian forms of
15 hyperlipidemia such as a familial hypercholesterolemia.

Genetic risk is conferred by subtle differences in genes among individuals in a population. Genes differ between individuals most frequently due to single nucleotide polymorphisms (SNP), although other variations are also important. SNP are located on average every 1000 base pairs in the human genome. Accordingly, a
20 typical human gene containing 250,000 base pairs may contain 250 different SNP. Only a minor number of SNP are located in exons and alter the amino acid sequence of the protein encoded by the gene. Most SNP have no effect on gene function, while others may alter transcription, splicing, translation, or stability of the mRNA encoded by the gene. Additional genetic polymorphism in the human genome is caused by
25 insertion, deletion, translocation, or inversion of either short or long stretches of DNA. Genetic polymorphisms conferring disease risk may therefore directly alter the amino acid sequence of proteins, may increase the amount of protein produced from the gene, or may decrease the amount of protein produced by the gene.

As genetic polymorphisms conferring risk of disease are uncovered, genetic
30 testing for such risk factors is becoming important for clinical medicine. Examples are apolipoprotein E testing to identify genetic carriers of the apoE4 polymorphism in

dementia patients for the differential diagnosis of Alzheimer's disease, and of Factor V Leiden testing for predisposition to deep venous thrombosis. More importantly, in the treatment of cancer, diagnosis of genetic variants in tumor cells is used for the selection of the most appropriate treatment regime for the individual patient. In
5 breast cancer, genetic variation in estrogen receptor expression or heregulin type 2 (Her2) receptor tyrosine kinase expression determine if anti-estrogenic drugs (tamoxifen) or anti-Her2 antibody (Herceptin) will be incorporated into the treatment plan. In chronic myeloid leukemia (CML) diagnosis of the Philadelphia chromosome genetic translocation fusing the genes encoding the Bcr and Abl receptor tyrosine
10 kinases indicates that Gleevec (STI571), a specific inhibitor of the Bcr-Abl kinase should be used for treatment of the cancer. For CML patients with such a genetic alteration, inhibition of the Bcr-Abl kinase leads to rapid elimination of the tumor cells and remission from leukemia.

Many general inflammatory markers predict risk of coronary heart disease,
15 although these markers are not specific to atherosclerosis. For example, Stein (Stein, S., *Am J Cardiol* , 87 (suppl):21A-26A (2001)) discusses the use of any one of the following serum inflammatory markers as surrogates for predicting risk of coronary heart disease including C-reactive protein (CRP), serum amyloid A, fibrinogen, interleukin-6, tissue necrosis factor-alpha, soluble vascular cell adhesion molecules
20 (sVCAM), soluble intervascular adhesion molecules (sICAM), E-selectin, matrix metalloprotease type-1, matrix metalloprotease type-2, matrix metalloprotease type-3, and matrix metalloprotease type-9. Elevation in one more of these serum inflammatory markers is not specific to coronary heart disease but also occurs with age or in association with cerebrovascular disease, peripheral vascular disease, non-
25 insulin dependent diabetes, osteoarthritis, bacterial infection, and sepsis.

Serum C-reactive protein (CRP) is viewed as a convenient and sensitive marker of systemic inflammation. Generally CRP is measured in serum samples using commercially available enzyme-linked immunosorbent assays (EIA). Consistent across multiple published studies is the finding of a correlation between increased risk
30 for coronary artery disease with increased serum CRP. For example, in the Women's Health Study, CRP was measured in 27,939 apparently healthy American women.

The cut-off points for quintiles of serum CRP in women were: less than or equal to 0.49, more than 0.49 to 1.08, more than 1.08 to 2.09, more than 2.09 to 4.19, and more than 4.19 mg CRP per liter, see Ridker, P.M. *et al.*, *New England. J. Med.*, 347: 1557-1565 (2001). In comparison to the lowest quintile, and even when adjusting for
5 age, every quintile more than 0.49 mg CRP per liter was associated with increased risk for coronary heart disease with the highest relative risk of 4.5 seen for those women in the highest quintile of serum CRP (more than 4.19 mg CRP per liter). A similar correlation between increased serum CRP and increased risk for coronary heart disease in women has been reported (Ridker, P.M *et al.*, *New Engl. J. Med.*,
10 342:836-843 (2000) and Bermudez, E.A. *et al.*, *Arterioscler. Thromb. Vasc. Biol.*, 22: 1668-1673 (2002)). Men also show a correlation between increased serum inflammatory markers such as CR and increased risk for coronary heart disease has been reported (Doggen, C.J.M. *et al.*, *J. Internal Med.*, 248:406-414 (2000) and Ridker, P.M. *et al.*, *New England. J. Med.*, 336: 973-979 (1997)). Quintiles for serum
15 CRP as reported by Doggen *et al.*, were less than 0.65, more than 0.65 to 1.18, more than 1.18 to 2.07, more than 2.07 to 4.23, and more than 4.23 mg CRP per liter. Unlike women, elevated serum CRP correlates with increased relative risk for coronary heart disease only in the 4th and 5th quintiles of CRP (relative risk of 1.7x and 1.9x, respectively).

20 Serum CRP in women also has been measured in conjunction with lipid markers such as levels of serum low density lipoprotein-cholesterol (LDL-C). In the study by Ridker, P.M. *et al.* (2002), serum CRP and LDL-C are minimally correlated, screening for both serum markers provided better prognostic indication than either alone. Thus, women with serum CRP above median values (more than 1.52 mg CRP
25 per liter) and also serum LDL-C above median values (more than 123.7 mg LDL-C per deciliter) were at highest risk for coronary heart disease.

Elevated CRP or other serum inflammatory markers is also prognostic for increased risk of a second myocardial infarct in patients with a previous myocardial infarct (Retterstol, L. *et al.*, *Atheroscler.*, 160: 433-440 (2002)).

30 Since CRP is produced in the liver, there is no *a priori* mechanistic explanation for why elevation in CRP and other serum inflammatory markers should be

prognostic for coronary artery disease. As discussed by Doggen, C.J.M., *et al.*, one or more of the following factors were speculated to account for the correlation observed: (1) intrinsic inflammation and tissue damage within arterial lesions, (2) prior infection by *Helicobacter pylori* or by *Chlamydia pneumoniae*, (3) release of peptide cytokines including interleukin-6, or (4) activation of the complement system.

The end products of the leukotriene pathway are potent inflammatory lipid mediators derived from arachidonic acid. They can potentially contribute to development of atherosclerosis and destabilization of atherosclerotic plaques through lipid oxidation and/or proinflammatory effects. LTC₄, LTD₄, and LTE₄, are known to induce vasoconstriction. Allen *et al.*, *Circulation*, 97:2406-2413 (1998) described a novel mechanism in which atherosclerosis is associated with the appearance of a leukotriene receptor(s) capable of inducing hyperactivity of human epicardial coronary arteries in response to LTC₄ and LTD₄. LTB₄, on the other hand, is a strong proinflammatory agent. Increased production of these end products, of the leukotriene pathway, could therefore serve as a risk factor for MI and atherosclerosis, whereas both inflammation and vasoconstriction/vasospasm have a well established role in the pathogenesis of MI and atherosclerosis. It has also been shown that a heterozygous deficiency of the 5-LO enzyme in a knockout mouse model decreases atherosclerotic lesion size in LDLR^{-/-} mice by about 95%. (Mehrabian *et al.*, *Circulation Research*. 91:120 (2002)). However, such genetic evidence for leukotriene involvement in MI or atherosclerosis in humans has not been reported. Mehrabian *et al.* did report a very small genetic association study looking for correlation between promoter polymorphisms of 5-LO and carotid intimal thickening in normal individuals. However, their data paradoxically suggest that a lower amount of leukotriene production correlates with carotid atherosclerosis.

SUMMARY OF THE INVENTION

As described herein, a gene on chromosome 13q12 has been identified as playing a major role in myocardial infarction (MI). This gene, herein after referred to as the MI gene, comprises nucleic acid that encodes 5-lipoxygenase activating protein

(ALOX5AP or FLAP,) herein after referred to as FLAP. The gene has also been shown to play a role in stroke and PAOD.

The invention pertains to methods of treatment (prophylactic and/or therapeutic) for certain diseases and conditions (*e.g.*, MI, ACS, atherosclerosis, stroke, PAOD) associated with FLAP or with other members of the leukotriene pathway (*e.g.*, biosynthetic enzymes such as FLAP, arachidonate 4-lipoxygenase (5-LO), leukotriene C4 synthetase (LTC4S), leukotriene A4 hydrolase (LTA4H), leukotriene B4 12-hydroxydehydrogenase (LTB4DH)); receptors and/or binding agents of the enzymes; and receptors for the leukotrienes LTA4, LTB4, LTC4, LTD4, LTE4, Cys LT1, Cys LT2, including leukotriene B4 receptor 1 (BLT1), leukotriene B4 receptor 2 (BLT2), cysteinyl leukotriene receptor 1 (CysLTR1), cysteinyl leukotriene receptor 2 (CysLTR2). The methods include the following: methods of treatment for myocardial infarction or susceptibility to myocardial infarction; methods of treatment for transient ischemic attack, transient monocular blindness or stroke, or susceptibility to stroke; methods of treatment for claudication, PAOD or susceptibility to PAOD; methods of treatment for acute coronary syndrome (*e.g.*, unstable angina, non-ST-elevation myocardial infarction (NSTEMI) or ST-elevation myocardial infarction (STEMI)); methods for reducing risk of MI, stroke or PAOD in persons with asymptomatic ankle/brachial index less than 0.9; methods for decreasing risk of a second myocardial infarction or stroke; methods of treatment for atherosclerosis, such as for patients requiring treatment (*e.g.*, angioplasty, stents, revascularization procedure) to restore blood flow in arteries (*e.g.*, coronary, carotid, and/or femoral arteries); methods of treatment for asymptomatic ankle/brachial index of less than 0.9; and/or methods for decreasing leukotriene synthesis (*e.g.*, for treatment of myocardial infarction, stroke or PAOD).

In the methods of the invention, a leukotriene synthesis inhibitor is administered to an individual in a therapeutically effective amount. The leukotriene synthesis inhibitor can be an agent that inhibits or antagonizes a member of the leukotriene synthesis pathway (*e.g.*, FLAP, 5-LO, LTC4S, LTA4H, and LTB4DH). For example, the leukotriene synthesis inhibitor can be an agent that inhibits or antagonizes FLAP polypeptide activity (*e.g.*, a FLAP inhibitor) and/or FLAP nucleic acid expression, as

described herein (*e.g.*, a FLAP nucleic acid antagonist). In another embodiment, the leukotriene synthesis inhibitor is an agent that inhibits or antagonizes polypeptide activity and/or nucleic acid expression of another member of the leukotriene biosynthetic pathway (*e.g.*, LTC4S, LTA4H, LTB4DH). In preferred embodiments, the agent alters activity and/or nucleic acid expression of FLAP or of 5-LO.

Preferred agents include those set forth in the Agent Table herein. In another embodiment, preferred agents can be: 1-((4-chlorophenyl)methyl)-3-((1,1-dimethylethyl)thio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)-1H-Indole-2-propanoic acid otherwise known as MK-0591, (R)-(+)-alpha-cyclopentyl-4-(2-quinolinylmethoxy)-Benzeneacetic acid otherwise known as BAY-x-1005, 3-(3-(1,1-dimethylethylthio-5-(quinoline-2-ylmethoxy)-1-(4-chloromethylphenyl)indole-2-yl)-2,2-dimethylpropionaldehyde oxime-0-2-acetic acid otherwise known as A-81834, optically pure enantiomers, salts, chemical derivatives, and analogues; or can be zileuton, atreleuton, 6-((3-fluoro-5-(tetrahydro-4-methoxy-2H-pyran-4-yl)phenoxy)methyl)-1-methyl-2(1H)-quinolinone otherwise known as ZD-2138, 1-((4-chlorophenyl)methyl)-3-((1,1-dimethylethyl)thio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)-1H-Indole-2-propanoic acid otherwise known as MK-886, 4-(3-(4-(2-Methyl-imidazol-1-yl)-phenylsulfanyl)-phenyl)-tetrahydro-pyran-4-carboxylic acid amide otherwise known as CJ-13610, their optically pure enantiomers, salts, chemical derivatives, and analogues. In another embodiment, the agent alters metabolism or activity of a leukotriene (*e.g.*, LTA4, LTB4, LTC4, LTD4, LTE4, Cys LT1, Cys LT2), such as leukotriene antagonists or antibodies to leukotrienes, as well as agents which alter activity of a leukotriene receptor (*e.g.*, BLT1, BLT2, CysLTR1, and CysLTR2).

In certain embodiments of the invention, the individual is an individual who has at least one risk factor, such as an at-risk haplotype for myocardial infarction, stroke or PAOD; an at-risk haplotype in the FLAP gene; a polymorphism in a FLAP nucleic acid; an at-risk polymorphism in the 5-LO gene promoter, diabetes; hypertension; hypercholesterolemia; elevated triglycerides; elevated lp(a); obesity; ankle/brachial index (ABI) less than 0.9; a past or current smoker; transient ischemic attack; transient monocular blindness; carotid endarterectomy; asymptomatic carotid stenosis;

claudication; limb ischemia leading to gangrene, ulceration or amputation; a vascular or peripheral artery revascularization graft; an elevated inflammatory marker (e.g., a marker such as C-reactive protein (CRP), serum amyloid A, fibrinogen, a leukotriene, a leukotriene metabolite, interleukin-6, tissue necrosis factor-alpha, a soluble vascular cell adhesion molecule (sVCAM), a soluble intervascular adhesion molecule (sICAM), E-selectin, matrix metalloprotease type-1, matrix metalloprotease type-2, matrix metalloprotease type-3, matrix metalloprotease type-9, myeloperoxidase (MPO), and N-tyrosine); increased LDL cholesterol and/or decreased HDL cholesterol; increased leukotriene synthesis; and/or at least one previous myocardial infarction, ACS, stable angina, previous transient ischemic attack, transient monocular blindness, or stroke, asymptomatic carotid stenosis or carotid endarterectomy, atherosclerosis, requires treatment for restoration of coronary artery blood flow (e.g., angioplasty, stent, revascularization procedure).

The invention additionally pertains to methods of assessing an individual for an increased risk of MI, ACS, atherosclerosis, stroke, or PAOD, by assessing a level of a leukotriene metabolite (e.g., LTE4, LTD4, LTB4) in the individual (e.g., in a sample of blood, serum, plasma or urine). An increased level of leukotriene metabolite is indicative of an increased risk. The invention also encompasses methods of assessing an individual for an increased risk of MI, ACS, atherosclerosis, stroke, transient ischemic attack, transient monocular blindness, asymptomatic carotid stenosis, PAOD, claudication, or limb ischemia, by stimulating production of a leukotriene or a leukotriene metabolite in a test sample from the individual (e.g., a sample comprising neutrophils), using a calcium ionophore, and comparing the level of the leukotriene or leukotriene metabolite with a control level. A level of production of the leukotriene or leukotriene metabolite that is significantly greater than the control level, is indicative of increased risk.

The invention further pertains to methods of assessing response to treatment with a leukotriene synthesis inhibitor, by assessing a level of a leukotriene or leukotriene metabolite in the individual before treatment, and comparing the level to a level of the leukotriene or leukotriene metabolite assessed during or after treatment. A level that is significantly lower during or after treatment, than before treatment, is

indicative of efficacy of the treatment with the leukotriene synthesis inhibitor. The invention additionally pertains to methods of assessing response to treatment with a leukotriene synthesis inhibitor, by stimulating production of a leukotriene or a leukotriene metabolite in a first test sample from the individual (e.g., a sample
5 comprising neutrophils) before treatment, using a calcium ionophore, and comparing the level of the leukotriene or leukotriene metabolite with a level of production of the leukotriene or leukotriene in a second test sample from the individual, during or after treatment. A level of production of the leukotriene or leukotriene metabolite in the second test sample that is significantly lower than the level in the first test sample, is
10 indicative of efficacy of the treatment. Similarly, the invention encompasses methods of assessing response to treatment with a leukotriene synthesis inhibitor, by assessing a level of an inflammatory marker in the individual before treatment, and during or after treatment. A level of the inflammatory marker during or after treatment, that is significantly lower than the level of inflammatory marker before
15 treatment, is indicative of efficacy of the treatment.

The invention also pertains to use of leukotriene synthesis inhibitors for the manufacture of a medicament for the treatment of MI, ACS, stroke, PAOD, and/or atherosclerosis, as described herein, as well as for the manufacture of a medicament for the reduction of leukotriene synthesis.

20

BRIEF DESCRIPTION OF THE DRAWINGS

The foregoing and other objects, features and advantages of the invention will be apparent from the following more particular description of preferred embodiments
25 of the invention. The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee.

FIG. 1 shows the multipoint non-parametric LOD scores of a linkage scan of 160 female patients in large extended pedigrees and genotyped using a 1000
30 framework map on chromosome 13. A LOD score suggestive of linkage of 2.5

was found at marker D13S289. The marker map for chromosome 13 that was used in the linkage analysis is shown in Table 1.

FIG. 2 shows LOD score results for the families after adding 14 additional markers to the candidate region. The inclusion of additional microsatellite markers increased the information on sharing by descent from 0.7 to 0.8, around the markers that gave the highest LOD scores. The marker map used in the second step of linkage analysis is shown in Table 2.

FIG. 3.1 shows the results from a haplotype association case-control analysis of 437 female MI patients versus 721 controls using combinations 4 and 5 microsatellite markers to define the test haplotypes. The p -value of the association is plotted on the y-axis and position of markers on the x-axis. Only haplotypes that show association with a p -value $< 10^{-5}$ are shown in the figure. The most significant microsatellite marker haplotype association is found using markers DG13S1103, DG13S166, DG13S1287, DG13S1061 and DG13S301, with alleles 4, 0, 2, 14 and 3, respectively (p -value of 1.02×10^{-7}). Carrier frequency of the haplotype is 7.3% in female MI patients and 0.3% in controls. The segment that is common to all the haplotypes shown in the figure includes only one gene, FLAP.

FIG. 3.2 shows the alleles of the markers defining the most significant microsatellite marker haplotypes. The segment defined with a black square is common to all the of most significantly associated haplotypes. The FLAP nucleic acid is located between makers DG13S166 and D13S1238. Two marker haplotype involving alleles 0 and -2 for markers DG13S166 and D13S1238, respectively, is found in excess in patients. Carrier frequency of this haploype is 27% in patients and 15.4% in controls (p -value 1×10^{-3}). Therefore, association analysis confirms that the most tightly MI-associated gene within the linkage peak is FLAP.

FIG. 4 shows the markers and genes around the FLAP (ALOX5AP) gene.

FIG. 5 shows the relative location of key SNPs and exons of the ALOX5AP/FLAP gene (exons shown in vertical rectangles). Haplotype length varies between 33 to 68 kb.

FIG. 6.1-6.82 show the genomic sequence of the FLAP gene (SEQ ID NO: 1).

FIG. 7 shows the amino acid sequence of FLAP (SEQ ID NO:2) and the mRNA of FLAP (SEQ ID NO: 3).

FIG. 8.1-8.40 show the sequences of the FLAP nucleic acid flanking the SNPs that were identified by sequencing samples from patients (SEQ ID NOs: 398-535).

5 FIG. 9 shows a significant positive correlation between serum LTE4 levels and serum CRP levels.

FIG. 10 depicts LTB4 production of ionomycin stimulated neutrophils from MI patients (n=41) and controls (n=35). The log-transformed (mean + SD) values measured at 15 and 30 minutes of stimulated cells are shown. (a) LTB4 production in 10 MI patients and controls. The difference in the mean values between patients and the controls is tested using a two-sample t-test of the log-transformed values. (b) LTB4 production in MI male carriers (red bars) and non-carriers (white bars) of HapA. Mean values of controls (blue bars) are included for comparison. Of note, males with the HapA produce highest amounts of LTB4 ($p < 0.005$ compared to controls). (c).

15 Schematic representation of the 5-LO pathway with leukotriene bioactive products.

FIG. 11 shows a genome wide linkage scan using 1,000 microsatellite markers for all (black) (n=713), female (red), (n=140), male (blue) (n=575), and early onset MI patients (green) (n=194). The LOD score is expressed on the y axis and the distance from the pter in Kosambi cM on the x axis.

20 FIG. 12 shows a schematic view of the chromosome 13 linkage region showing the FLAP gene. (a) The linkage scan for female MI patients and the one LOD drop region that includes the FLAP gene; (b) Microsatellite association for all MI patients: single marker association (black dots) and two, three, four and five marker haplotype association (black, blue, green and red horizontal lines, respectively). The blue and the 25 red arrows indicate the location of the most significant haplotype association across the FLAP gene in males and females, respectively. (c) The FLAP gene structure, with exons shown as colored cylinders, and the location of all the SNPs typed in the region (green vertical lines). The green vertical lines indicate the position of the microsatellites (shown in b) and SNPs (shown in c) used in the analysis.

30 FIG. 13 shows linkage scan using framework microsatellite markers on chromosome 13 for male patients with ischemic stroke or TIA (n=342 in 164 families

at 6 meioses). The LOD score is expressed on the y axis and the distance from the pter in Kosambi cM on the x axis.

FIG. 14 shows a pairwise linkage disequilibrium (LD) between SNPs in a 60 Kb region encompassing FLAP. The markers are plotted equidistantly. Two measures of LD are shown: D' in the upper left triangle and P values in the lower right triangle. Colored lines indicate the positions of the exons of *FLAP* and the green stars indicate the location of the markers of the at-risk haplotype A4. Scales for the LD strength are provided for both measures to the right.

10 DETAILED DESCRIPTION OF THE INVENTION

Extensive genealogical information has been combined with powerful gene sharing methods to map a gene on chromosome 13q12 that is associated with myocardial infarction. A genome wide search for susceptibility genes for MI, using a framework map of 1000 microsatellite markers, revealed a locus suggestive of linkage on 13q12. Sixty families with 159 female MI patients that clustered within and including 6 meiotic events were used in linkage analysis. At first, only female MI patients were used in the linkage analysis in an effort to enrich for patients with stronger genetic factors contributing to their risk for MI. The epidemiological study of a population-based sample of Icelandic MI patients had previously suggested that the genetic factors for MI might be stronger for females than males, as the relative risk for siblings of female MI patients was significantly higher than the relative risk for siblings of male probands (1.59 (CI 1.47 - 1.73) vs. 1.35 (CI 1.28 - 1.42)) (unpublished data). The highest LOD score (2.5) was found at marker D13S289. The LOD score results for the families remained the same after adding 14 microsatellite markers to the candidate region. The inclusion of the additional markers increased the information on sharing by descent from 0.7 to 0.8, around the markers that gave the highest LOD scores. This linkage analysis mapped a gene contributing to MI to chromosome 13q12.

The candidate MI locus on chromosome 13q12 was then finely mapped with microsatellite markers. Patients with myocardial infarction and controls were initially genotyped with microsatellite markers with an average spacing between markers of

less than 100Kb over the 12Mb candidate region. Initial haplotype association analysis that included all genotyped microsatellite markers across the MI candidate locus, resulted in several extended haplotypes composed of 4 and 5 microsatellite markers that were significantly associated with female MI (see, *e.g.*, Tables 4 and 5 below). A region common to all these extended haplotypes, is defined by markers DG13S166 and D13S1238. This region includes only one gene, the FLAP nucleic acid sequence. The two marker haplotype involving alleles 0 and -2 for markers DG13S166 and D13S1238, respectively, was found in excess in patients. Specific variants of the gene were then sought that were associated with MI.

10 In order to screen for SNPs in the FLAP gene, the whole gene was sequenced, both exons and introns. Initially, 9 SNPs identified within the gene were genotyped in patients and controls. Additional microsatellite markers close to or within the FLAP gene were also genotyped in all patients and controls. Five publicly known SNPs that are located within a 200Kb distance 5' to the FLAP gene were also genotyped in
15 patients and controls. Haplotype association analysis in this case-control study including these additional markers showed several different variants of the same haplotype that were all significantly associated with female MI (see, *e.g.*, Table 6). Table 7 shows two haplotypes that are representative of these female MI risk haplotypes which are referred to herein as the female MI "at risk" haplotypes. The
20 relative risk for male MI patients that had the female MI-"at risk" haplotype was increased (see, *e.g.*, Table 7), indicating that the female MI-"at risk" haplotype also increased the risk of having an MI in males. These results further strengthened the hypothesis that the FLAP gene was an MI susceptibility gene.

25 *SNP haplotype association to MI, and subsequently to stroke and PAOD*

 In an effort to identify haplotypes involving only SNP markers that associate with MI, additional SNPs were identified by sequencing the FLAP gene and the region flanking the gene. Currently, a total of 45 SNPs in 1343 patients and 624 unrelated controls have been genotyped. Two correlated series of SNP haplotypes
30 have been observed in excess in patients, denoted as A and B in Table 9. The length of the haplotypes varies between 33 and 69 Kb, and the haplotypes cover one or two

blocks of linkage disequilibrium. Both series of haplotypes contain the common allele 2 of the SNP SG13S25. All haplotypes in the A series contain the SNP DG00AAHID, while all haplotypes in the B series contain the SNP DG00AAHII. In the B series, the haplotypes B4, B5, and B6 have a relative risk (RR) greater than 2 and with allelic frequencies above 10%. The haplotypes in the A series have slightly lower RR and lower p-values, but higher frequency (15-16%). The haplotypes in series B and A are strongly correlated, *i.e.*, the haplotypes in B define a subset of the haplotypes in A. Hence, haplotypes in series B are more specific than A. However, haplotypes in series A are more sensitive, *i.e.* they capture more individuals with the putative mutation, as is observed in the population attributable risk which is less for B than for A. Furthermore, these haplotypes show similar risk ratios and allelic frequencies for early-onset patients (defined as onset of first MI before the age of 55) and for both genders. In addition, analyzing various groups of patients with known risk factors, such as hypertension, high cholesterol, smoking and diabetes, do not reveal any significant correlation with these haplotypes, suggesting that the haplotypes in the FLAP gene represent an independent genetic susceptibility factor for MI.

Because stroke and PAOD are diseases that are closely related to MI (all occur on the basis of atherosclerosis the SNP haplotype in the FLAP gene that confers risk to MI was assessed to determine whether it also conferred risk of stroke and/or PAOD. Table 14 shows that haplotype A4 increases the risk of having a stroke to a similar extent as it increases the risk of having an MI. Although not as significantly, haplotype A4 also confers risk of developing PAOD.

The FLAP nucleic acid encodes a 5-lipoxygenase activating protein, which, in combination with 5-lipoxygenase (5-LO), is required for leukotriene synthesis. FLAP acts coordinately with 5-LO to catalyze the first step in the synthesis of leukotrienes from arachidonic acid. It catalyzes the conversion of arachidonic acid to 5(S)-hydroperoxy-6-trans-8,11,14-cis-eicosatetraenoic acid (5-HPETE), and further to the allylic epoxide 5 (S)-trans7,9 trans 11,14-cis-eicosatetraenoic acid (leukotriene A4, LTA4).

The leukotrienes are a family of highly potent biological mediators of inflammatory processes produced primarily by bone marrow derived leukocytes such as monocytes, macrophages, and neutrophils. Both FLAP and 5-LO are detected within atherosclerosis lesions, indicating that the vessel itself can be a source of leukotrienes. It is demonstrated herein that the MI-risk FLAP haplotype is associated with higher serum leukotriene levels. Increased production of leukotriene in individuals with pre-existing atherosclerosis lesions may lead to plaque instability or friability of the fibrous cap leading to local thrombotic events. If this occurs in coronary artery arteries it leads to MI or unstable angina. If it occurs in the cerebrovasculature it leads to stroke or transient ischemic attack. If it occurs in large arteries to the limbs, it causes or exacerbates limb ischemia in persons with peripheral arterial occlusive disease (PAOD). Therefore, those with genetically influenced predisposition to produce higher leukotriene levels have higher risk for events due to pre-existing atherosclerosis such as MI.

Inhibitors of FLAP function impede translocation of 5-LO from the cytoplasm to the cell membrane and inhibit activation of 5-LO and thereby decrease leukotriene synthesis.

As a result of these discoveries, methods are now available for the treatment of myocardial infarction (MI) and acute coronary syndrome (ACS), as well as stroke and PAOD, through the use of leukotriene inhibitors, such as agents that inhibit leukotriene biosynthesis or antagonize signaling through leukotriene receptors. The term, "treatment" as used herein, refers not only to ameliorating symptoms associated with the disease or condition, but also preventing or delaying the onset of the disease or condition; preventing or delaying the occurrence of a second episode of the disease or condition; and/or also lessening the severity or frequency of symptoms of the disease or condition. In the case of atherosclerosis, "treatment" also refers to a minimization or reversal of the development of plaques. Methods are additionally available for assessing an individual's risk for MI, ACS, stroke or PAOD. In a preferred embodiment, the individual to be treated is an individual who is susceptible (at increased risk) for MI, ACS, stroke or PAOD, such as an individual who is in one of the representative target populations described herein.

REPRESENTATIVE TARGET POPULATIONS

In one embodiment of the invention, an individual who is at risk for MI, ACS, stroke or PAOD is an individual who has an at-risk haplotype in FLAP, as described
5 herein. In one embodiment, a haplotype associated with a susceptibility to myocardial infarction, ACS, stroke or PAOD comprises markers DG00AAFIU, SG13S25, DG00AAJFF, DG00AAHII, SG13S32 and SG13S35 at the 13q12 locus. In another embodiment, a haplotype associated with a susceptibility to myocardial infarction, ACS, stroke or PAOD comprises markers DG00AAFIU, SG13S25, DG00AAHII,
10 SG13S30 and SG13S42 at the 13q12 locus. In a third embodiment, a haplotype associated with a susceptibility to myocardial infarction, ACS, stroke or PAOD comprises markers SG13S25, DG00AAHII, SG13S30 and SG13S42 at the 13q12 locus. In a fourth embodiment, a haplotype associated with a susceptibility to myocardial infarction, ACS, stroke or PAOD comprises markers DG00AAFIU,
15 SG13S25, DG00AAHID, B_SNP_310657 and SG13S32 at the 13q12 locus. In a fifth embodiment, a haplotype associated with a susceptibility to myocardial infarction, ACS, stroke or PAOD comprises markers SG13S25, DG00AAHID, B_SNP_310657 and SG13S32 at the 13q12 locus. Additional haplotypes associated with a susceptibility to myocardial infarction, ACS, stroke or PAOD include the haplotypes
20 shown in Tables 4, 5, 6, 7, 11, 12, and 19, as well as haplotypes comprising markers shown in Table 3.

Increased risk for MI, ACS, stroke or PAOD in individuals with a FLAP at-risk haplotype is logically conferred by increased production of leukotrienes in the arterial vessel wall or in bone-marrow derived inflammatory cells within the blood
25 and/or arterial vessel wall. It is shown herein that FLAP at-risk haplotypes are associated with high serum leukotriene E4 levels. It is also shown herein that FLAP at-risk haplotypes are associated with higher production of LTB4 *ex vivo*. It is further shown herein that serum leukotriene levels (specifically, leukotrieneE4) correlate with serum CRP levels in myocardial infarction patients. Therefore, FLAP
30 genetic variation drives high leukotriene levels (within the blood vessel and/or systemically) which in turn drive higher CRP levels which has been shown as a risk

factor for MI. Accordingly, individuals with a FLAP at-risk haplotype are likely to have elevated serum CRP as well as other serum inflammatory markers. The level of serum CRP or other serum inflammatory markers can be used as a surrogate for the level of arterial wall inflammation initiated by lipid deposition and atherogenesis
5 conferred by the presence of the at-risk FLAP haplotype.

In another embodiment of the invention, an individual who is at risk for MI, ACS, stroke or PAOD is an individual who has a polymorphism in a FLAP gene, in which the presence of the polymorphism is indicative of a susceptibility to MI, ACS, stroke or PAOD. The term “gene,” as used herein, refers to not only the sequence of
10 nucleic acids encoding a polypeptide, but also the promoter regions, transcription enhancement elements, splice donor/acceptor sites, and other non-transcribed nucleic acid elements. Representative polymorphisms include those presented in Table 3, below.

In a further embodiment of the invention, an individual who is at risk for MI,
15 ACS, stroke or PAOD is an individual who has an at-risk polymorphism in the 5-LO gene in the promoter region, as described herein.

In a fourth embodiment, an individual who is at risk for MI, ACS, stroke or PAOD is an individual who has an elevated inflammatory marker. An “elevated inflammatory marker,” as used herein, is the presence of an amount of an
20 inflammatory marker that is greater, by an amount that is statistically significant, than the amount that is typically found in control individual(s) or by comparison of disease risk in a population associated with the lowest band of measurement (*e.g.*, below the mean or median, the lowest quartile or the lowest quintile) compared to higher bands of measurement (*e.g.*, above the mean or median, the second, third or fourth quartile;
25 the second, third, fourth or fifth quintile). An “inflammatory marker” refers to a molecule that is indicative of the presence of inflammation in an individual, for example, C-reactive protein (CRP), serum amyloid A, fibrinogen, leukotriene levels (*e.g.*, leukotriene E4), leukotriene metabolites (*e.g.*, cysteinyl leukotriene 1), interleukin-6, tissue necrosis factor-alpha, soluble vascular cell adhesion molecules
30 (sVCAM), soluble intervascular adhesion molecules (sICAM), E-selectin, matrix metalloprotease type-1, matrix metalloprotease type-2, matrix metalloprotease type-3,

matrix metalloprotease type-9, myeloperoxidase (MPO), N-tyrosine) or other markers (see, e.g., Doggen, C.J.M. *et al.*, *J. Internal Med.*, 248:406-414 (2000); Ridker, P.M. *et al.*, *New Englnd. J. Med.* 1997: 336: 973-979, Rettersol, L. *et al.*, 2002: 160:433-440; Ridker, P.M. *et. al.*, *New England. J. Med.*, 2002: 347: 1557-1565; Bermudez, E.A. *et .al.*, *Arterioscler. Thromb. Vasc. Biol.* , 2002: 22:1668-1673). In certain
5 embodiments, the presence of such inflammatory markers can be measured in serum or urine.

 In a fifth embodiment, an individual who is at risk for MI, ACS, stroke or PAOD is an individual who has increased LDL cholesterol and/or decreased HDL
10 cholesterol levels. For example, the American Heart Association indicates that an LDL cholesterol level of less than 100 mg/dL is optimal; from 100-129 mg/dL is near/above optimal; from 130-159 mg/dL is borderline high; from 160-189 is high; and from 190 and up is very high. Therefore, an individual who is at risk for MI, ACS, stroke or PAOD because of an increased LDL cholesterol level is, for example,
15 an individual who has more than 100 mg/dL cholesterol, such as an individual who has a near/above optimal level, a borderline high level, a high level or a very high level. Similarly, the American Heart Association indicates that an HDL cholesterol level of less than 40 mg/dL is a major risk factor for heart disease; and an HDL cholesterol level of 60 mg/dL or more is protective against heart disease. Thus, an
20 individual who is at risk for MI, ACS, stroke or PAOD because of a decreased HDL cholesterol level is, for example, an individual who has less than 60 mg/dL HDL cholesterol, such as an individual who has less than 40 mg/dL HDL cholesterol.

 In a sixth embodiment, an individual who is at risk for MI, ACS, stroke or PAOD is an individual who has increased leukotriene synthesis. "Increased
25 leukotriene synthesis," as used herein, indicates an amount of production of leukotrienes that is greater, by an amount that is statistically significant, than the amount of production of leukotrienes that is typically found in control individual(s) or by comparison of leukotriene production in a population associated with the lowest band of measurement (e.g., below the mean or median, the lowest quartile or the
30 lowest quintile) compared to higher bands of measurement (e.g., above the mean or median, the second, third or fourth quartile; the second, third, fourth or fifth quintile).

For example, the FLAP at-risk haplotypes correlate with increased serum leukotriene synthesis levels, and with increased production of leukotrienes *ex vivo*. An individual can be assessed for the presence of increased leukotriene synthesis by a variety of methods. For example, an individual can be assessed for an increased risk of MI,
5 ACS, stroke, PAOD or atherosclerosis, by assessing the level of a leukotriene metabolite (e.g., LTE₄) in a sample (e.g., serum, plasma or urine) from the individual. Samples containing blood, cells, or tissue can also be obtained from an individual and used to assess leukotriene or leukotriene metabolite production *ex vivo* under appropriate assay conditions. An increased level of leukotriene metabolites, and/or an
10 increased level of leukotriene production *ex vivo*, is indicative of increased production of leukotrienes in the individual, and of an increased risk of MI, ACS, stroke, PAOD or atherosclerosis.

In a further embodiment, an individual who is at risk for MI, ACS, or stroke is an individual who has already experienced at least one MI, ACS event or stroke, or
15 who has stable angina, and is therefore at risk for a second MI, ACS event or stroke. In another embodiment, an individual who is at risk for MI, ACS, stroke or PAOD is an individual who has atherosclerosis or who requires treatment (e.g., angioplasty, stents, revascularization procedure) to restore blood flow in arteries.

In further embodiments, an individual who is at risk for MI, stroke or PAOD is
20 an individual having asymptomatic ankle/brachial index of less than 0.9; an individual who is at risk for stroke, is an individual who has had one or more transient ischemic attacks; who has had transient monocular blindness; has had a carotid endarterectomy; or has asymptomatic carotid stenosis; an individual who is at risk for PAOD, is an individual who has (or had) claudication, limb ischemia leading to
25 gangrene, ulceration or amputation, or has had a revascularization procedure.

In additional embodiments, an individual who is at risk for MI, ACS, stroke or PAOD is an individual who has diabetes; hypertension; hypercholesterolemia; elevated triglycerides (e.g., > 200 mg/dl); elevated lp(a); obesity; ankle/brachial index (ABI) less than 0.9; and/or is a past or current smoker.

30 Individuals at risk for MI, ACS, stroke or PAOD may fall into more than one of these representative target populations. For example, an individual may have

experienced at least one MI, ACS event, transient ischemic attack, transient monocular blindness, or stroke, and may also have an increased level of an inflammatory marker. As used therein, the term “individual in a target population” refers to an individual who is at risk for MI, ACS, stroke or PAOD who falls into at
5 least one of the representative target populations described above.

ASSESSMENT FOR AT-RISK HAPLOTYPES

A “haplotype,” as described herein, refers to a combination of genetic markers (“alleles”), such as those set forth in Table 3. In a certain embodiment, the haplotype
10 can comprise one or more alleles, two or more alleles, three or more alleles, four or more alleles, or five or more alleles. The genetic markers are particular “alleles” at “polymorphic sites” associated with FLAP. A nucleotide position at which more than one sequence is possible in a population (either a natural population or a synthetic population, *e.g.*, a library of synthetic molecules), is referred to herein as a
15 “polymorphic site”. Where a polymorphic site is a single nucleotide in length, the site is referred to as a single nucleotide polymorphism (“SNP”). For example, if at a particular chromosomal location, one member of a population has an adenine and another member of the population has a thymine at the same position, then this position is a polymorphic site, and, more specifically, the polymorphic site is a SNP.
20 Polymorphic sites can allow for differences in sequences based on substitutions, insertions or deletions. Each version of the sequence with respect to the polymorphic site is referred to herein as an “allele” of the polymorphic site. Thus, in the previous example, the SNP allows for both an adenine allele and a thymine allele.

Typically, a reference sequence is referred to for a particular sequence. Alleles
25 that differ from the reference are referred to as “variant” alleles. For example, the reference FLAP sequence is described herein by SEQ ID NO: 1. The term, “variant FLAP”, as used herein, refers to a sequence that differs from SEQ ID NO: 1, but is otherwise substantially similar. The genetic markers that make up the haplotypes described herein are FLAP variants.

30 Additional variants can include changes that affect a polypeptide, *e.g.*, the FLAP polypeptide. These sequence differences, when compared to a reference nucleotide

sequence, can include the insertion or deletion of a single nucleotide, or of more than one nucleotide, resulting in a frame shift; the change of at least one nucleotide, resulting in a change in the encoded amino acid; the change of at least one nucleotide, resulting in the generation of a premature stop codon; the deletion of several
5 nucleotides, resulting in a deletion of one or more amino acids encoded by the nucleotides; the insertion of one or several nucleotides, such as by unequal recombination or gene conversion, resulting in an interruption of the coding sequence of a reading frame; duplication of all or a part of a sequence; transposition; or a rearrangement of a nucleotide sequence, as described in detail above. Such sequence
10 changes alter the polypeptide encoded by a FLAP nucleic acid. For example, if the change in the nucleic acid sequence causes a frame shift, the frame shift can result in a change in the encoded amino acids, and/or can result in the generation of a premature stop codon, causing generation of a truncated polypeptide. Alternatively, a polymorphism associated with a susceptibility to MI, ACS, stroke or PAOD can be a
15 synonymous change in one or more nucleotides (*i.e.*, a change that does not result in a change in the amino acid sequence). Such a polymorphism can, for example, alter splice sites, affect the stability or transport of mRNA, or otherwise affect the transcription or translation of the polypeptide. The polypeptide encoded by the reference nucleotide sequence is the “reference” polypeptide with a particular
20 reference amino acid sequence, and polypeptides encoded by variant alleles are referred to as “variant” polypeptides with variant amino acid sequences.

Haplotypes are a combination of genetic markers, *e.g.*, particular alleles at polymorphic sites. The haplotypes described herein, *e.g.*, having markers such as those shown in Table 3, are found more frequently in individuals with MI, ACS,
25 stroke or PAOD than in individuals without MI, ACS, stroke or PAOD. Therefore, these haplotypes have predictive value for detecting a susceptibility to MI, ACS, stroke or PAOD in an individual. The haplotypes described herein are in some cases a combination of various genetic markers, *e.g.*, SNPs and microsatellites. Therefore, detecting haplotypes can be accomplished by methods known in the art for detecting
30 sequences at polymorphic sites, such as the methods described above.

In certain methods described herein, an individual who is at risk for MI, ACS, stroke or PAOD is an individual in whom an at-risk haplotype is identified. In one embodiment, the at-risk haplotype is one that confers a significant risk of MI, ACS, stroke or PAOD. In one embodiment, significance associated with a haplotype is measured by an odds ratio. In a further embodiment, the significance is measured by a percentage. In one embodiment, a significant risk is measured as an odds ratio of at least about 1.2, including by not limited to: 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, and 1.9. In a further embodiment, an odds ratio of at least 1.2 is significant. In a further embodiment, an odds ratio of at least about 1.5 is significant. In a further embodiment, a significant increase in risk is at least about 1.7 is significant. In a further embodiment, a significant increase in risk is at least about 20%, including but not limited to about 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, and 98%. In a further embodiment, a significant increase in risk is at least about 50%. It is understood however, that identifying whether a risk is medically significant may also depend on a variety of factors, including the specific disease, the haplotype, and often, environmental factors.

An at-risk haplotype in, or comprising portions of, the FLAP gene, in one where the haplotype is more frequently present in an individual at risk for MI, ACS, stroke or PAOD (affected), compared to the frequency of its presence in a healthy individual (control), and wherein the presence of the haplotype is indicative of susceptibility to MI, ACS, stroke or PAOD. As an example of a simple test for correlation would be a Fisher-exact test on a two by two table. Given a cohort of chromosomes the two by two table is constructed out of the number of chromosomes that include both of the haplotypes, one of the haplotype but not the other and neither of the haplotypes.

In certain embodiments at-risk haplotype is an at-risk haplotype within or near FLAP that significantly correlates with a haplotype such as a haplotype shown in Table 4; a haplotype shown in Table 5; a haplotype shown in Table 13; haplotype B4; haplotype B5; haplotype B6; haplotype A4; haplotype A5; or haplotype HapB. In other embodiments, an at-risk haplotype comprises an at-risk haplotype within or near FLAP that significantly correlates with susceptibility to myocardial infarction

or stroke. In a particular embodiment, a haplotype associated with a susceptibility to myocardial infarction, ACS, stroke or PAOD comprises markers DG00AAFIU, SG13S25, DG00AAJFF, DG00AAHII, SG13S32 and SG13S35 at the 13q12 locus. In another embodiment, a haplotype associated with a susceptibility to myocardial
5 infarction, ACS, stroke or PAOD comprises markers DG00AAFIU, SG13S25, DG00AAHII, SG13S30 and SG13S42 at the 13q12 locus. In a third embodiment, a haplotype associated with a susceptibility to myocardial infarction, ACS, stroke or PAOD comprises markers SG13S25, DG00AAHII, SG13S30 and SG13S42 at the 13q12 locus. In a fourth embodiment, a haplotype associated with a susceptibility to
10 myocardial infarction, ACS, stroke or PAOD comprises markers DG00AAFIU, SG13S25, DG00AAHID, B_SNP_310657 and SG13S32 at the 13q12 locus. In other embodiments, the at-risk haplotype is selected from the group consisting of: haplotype B4, B5, B6, A4 and A5. The at-risk haplotype can also comprise a combination of the markers in the haplotypes B4, B5, B6, A4 and/or A5. In further
15 embodiments, the at-risk haplotype can be haplotype HapB. In other embodiments, the at-risk haplotype comprises a polymorphism shown in Table 3.

Standard techniques for genotyping for the presence of SNPs and/or microsatellite markers can be used, such as fluorescent based techniques (Chen, *et al.*, *Genome Res.* 9, 492 (1999)), PCR, LCR, Nested PCR and other techniques for nucleic
20 acid amplification. In a preferred embodiment, the method comprises assessing in an individual the presence or frequency of SNPs and/or microsatellites in, comprising portions of, the FLAP gene, wherein an excess or higher frequency of the SNPs and/or microsatellites compared to a healthy control individual is indicative that the individual is susceptible to MI, ACS, stroke or PAOD. See, for example, Table 3
25 (below) for SNPs and markers that can form haplotypes that can be used as screening tools. These markers and SNPs can be identified in at-risk haplotypes. For example, an at-risk haplotype can include microsatellite markers and/or SNPs such as those set forth in Table 3. The presence of the haplotype is indicative of a susceptibility to MI, ACS, stroke or PAOD, and therefore is indicative of an
30 individual who falls within a target population for the treatment methods described herein.

Haplotype analysis involves defining a candidate susceptibility locus using LOD scores. The defined regions are then ultra-fine mapped with microsatellite markers with an average spacing between markers of less than 100Kb. All usable microsatellite markers that found in public databases and mapped within that region
5 can be used. In addition, microsatellite markers identified within the deCODE genetics sequence assembly of the human genome can be used. The frequencies of haplotypes in the patient and the control groups using an expectation-maximization algorithm can be estimated (Dempster A. *et al.*, 1977. *J. R. Stat. Soc. B*, 39:1-389). An implementation of this algorithm that can handle missing genotypes and
10 uncertainty with the phase can be used. Under the null hypothesis, the patients and the controls are assumed to have identical frequencies. Using a likelihood approach, an alternative hypothesis where a candidate at-risk-haplotype, which can include the markers described herein, is allowed to have a higher frequency in patients than controls, while the ratios of the frequencies of other haplotypes are assumed to be the
15 same in both groups is tested. Likelihoods are maximized separately under both hypotheses and a corresponding 1-df likelihood ratio statistic is used to evaluate the statistic significance.

To look for at-risk-haplotypes in the 1-lod drop, for example, association of all possible combinations of genotyped markers is studied, provided
20 those markers span a practical region. The combined patient and control groups can be randomly divided into two sets, equal in size to the original group of patients and controls. The haplotype analysis is then repeated and the most significant p-value registered is determined. This randomization scheme can be repeated, for example, over 100 times to construct an empirical distribution of p-values. In a preferred
25 embodiment, a p-value of <0.05 is indicative of an at-risk haplotype.

A detailed discussion of haplotype analysis follows.

Haplotype analysis

Our general approach to haplotype analysis involves using likelihood-based
30 inference applied to NEsted MOdels. The method is implemented in our program NEMO, which allows for many polymorphic markers, SNPs and microsatellites.

The method and software are specifically designed for case-control studies where the purpose is to identify haplotype groups that confer different risks. It is also a tool for studying LD structures.

When investigating haplotypes constructed from many markers, apart from
 5 looking at each haplotype individually, meaningful summaries often require putting haplotypes into groups. A particular partition of the haplotype space is a model that assumes haplotypes within a group have the same risk, while haplotypes in different groups can have different risks. Two models/partitions are nested when one, the alternative model, is a finer partition compared to the other, the null model, *i.e.*, the
 10 alternative model allows some haplotypes assumed to have the same risk in the null model to have different risks. The models are nested in the classical sense that the null model is a special case of the alternative model. Hence traditional generalized likelihood ratio tests can be used to test the null model against the alternative model. Note that, with a multiplicative model, if haplotypes h_i and h_j are assumed to have
 15 the same risk, it corresponds to assuming that $f_i/p_i = f_j/p_j$ where f and p denote haplotype frequencies in the affected population and the control population respectively.

One common way to handle uncertainty in phase and missing genotypes is a two-step method of first estimating haplotype counts and then treating the estimated
 20 counts as the exact counts, a method that can sometimes be problematic (*e.g.*, see the information measure section below) and may require randomization to properly evaluate statistical significance. In NEMO, maximum likelihood estimates, likelihood ratios and p-values are calculated directly, with the aid of the EM algorithm, for the observed data treating it as a missing-data problem.

25 NEMO allows complete flexibility for partitions. For example, the first haplotype problem described in the Methods section on Statistical analysis considers testing whether h_1 has the same risk as the other haplotypes h_2, \dots, h_k . Here the alternative grouping is $[h_1], [h_2, \dots, h_k]$ and the null grouping is $[h_1, \dots, h_k]$. The second haplotype problem in the same section involves three haplotypes $h_1 = G0$, h_2
 30 $= GX$ and $h_3 = AX$, and the focus is on comparing h_1 and h_2 . The alternative grouping is $[h_1], [h_2], [h_3]$ and the null grouping is $[h_1, h_2], [h_3]$. If composite alleles

exist, one could collapse these alleles into one at the data processing stage, and performed the test as described. This is a perfectly valid approach, and indeed, whether we collapse or not makes no difference if there were no missing information regarding phase. But, with the actual data, if each of the alleles making up a
 5 composite correlates differently with the SNP alleles, this will provide some partial information on phase. Collapsing at the data processing stage will unnecessarily increase the amount of missing information. A nested-models/partition framework can be used in this scenario. Let h_2 be split into $h_{2a}, h_{2b}, \dots, h_{2e}$, and h_3 be split into $h_{3a}, h_{3b}, \dots, h_{3e}$. Then the alternative grouping is $[h_1], [h_{2a}, h_{2b}, \dots, h_{2e}], [h_{3a}, h_{3b},$
 10 $\dots, h_{3e}]$ and the null grouping is $[h_1, h_{2a}, h_{2b}, \dots, h_{2e}], [h_{3a}, h_{3b}, \dots, h_{3e}]$. The same method can be used to handle composite where collapsing at the data processing stage is not even an option since L_C represents multiple haplotypes constructed from multiple SNPs. Alternatively, a 3-way test with the alternative grouping of $[h_1], [h_{2a}, h_{2b}, \dots, h_{2e}], [h_{3a}, h_{3b}, \dots, h_{3e}]$ versus the null grouping of $[h_1, h_{2a}, h_{2b}, \dots, h_{2e},$
 15 $h_{3a}, h_{3b}, \dots, h_{3e}]$ could also be performed. Note that the generalized likelihood ratio test-statistic would have two degrees of freedom instead of one.

Measuring information

Even though likelihood ratio tests based on likelihoods computed directly for
 20 the observed data, which have captured the information loss due to uncertainty in phase and missing genotypes, can be relied on to give valid p-values, it would still be of interest to know how much information had been lost due to the information being incomplete. Interestingly, one can measure information loss by considering a two-step procedure to evaluating statistical significance that appears natural but
 25 happens to be systematically anti-conservative. Suppose we calculate the maximum likelihood estimates for the population haplotype frequencies calculated under the alternative hypothesis that there are differences between the affected population and control population, and use these frequency estimates as estimates of the observed frequencies of haplotype counts in the affected sample and in the control sample.
 30 Suppose we then perform a likelihood ratio test treating these estimated haplotype counts as though they are the actual counts. We could also perform a Fisher's exact

test, but we would then need to round off these estimated counts since they are in general non-integers. This test will in general be anti-conservative because treating the estimated counts as if they were exact counts ignores the uncertainty with the counts, overestimates the effective sample size and underestimates the sampling variation. It means that the chi-square likelihood-ratio test statistic calculated this way, denoted by Λ^* , will in general be bigger than Λ , the likelihood-ratio test-statistic calculated directly from the observed data as described in methods. But Λ^* is useful because the ratio Λ/Λ^* happens to be a good measure of information, or $1 - (\Lambda/\Lambda^*)$ is a measure of the fraction of information lost due to missing information. This information measure for haplotype analysis is described in Nicolae and Kong, Technical Report 537, Department of Statistics, University of Statistics, University of Chicago, Revised for *Biometrics* (2003) as a natural extension of information measures defined for linkage analysis, and is implemented in NEMO.

15 *Statistical analysis.*

For single marker association to the disease, the Fisher exact test can be used to calculate two-sided p-values for each individual allele. All p-values are presented unadjusted for multiple comparisons unless specifically indicated. The presented frequencies (for microsatellites, SNPs and haplotypes) are allelic frequencies as opposed to carrier frequencies. To minimize any bias due the relatedness of the patients who were recruited as families for the linkage analysis, first and second-degree relatives can be eliminated from the patient list. Furthermore, the test can be repeated for association correcting for any remaining relatedness among the patients, by extending a variance adjustment procedure described in Risch, N. & Teng, J. (25 *Genome Res.*, 8:1278-1288 (1998)). The relative power of family-based and case-control designs for linkage disequilibrium studies of complex human diseases I. DNA pooling. (*ibid*) for sibships so that it can be applied to general familial relationships, and present both adjusted and unadjusted p-values for comparison. The differences are in general very small as expected. To assess the significance of single-marker association corrected for multiple testing we carried out a randomisation test using the same genotype data. Cohorts of patients and controls

can be randomized and the association analysis redone multiple times (e.g., up to 500,000 times) and the p-value is the fraction of replications that produced a p-value for some marker allele that is lower than or equal to the p-value we observed using the original patient and control cohorts.

- 5 For both single-marker and haplotype analyses, relative risk (RR) and the population attributable risk (PAR) can be calculated assuming a multiplicative model (haplotype relative risk model), (Terwilliger, J.D. & Ott, J., *Hum Hered*, 42, 337-46 (1992) and Falk, C.T. & Rubinstein, P, *Ann Hum Genet* 51 (Pt 3), 227-33 (1987)), i.e., that the risks of the two alleles/haplotypes a person carries multiply.
- 10 For example, if RR is the risk of A relative to a, then the risk of a person homozygote AA will be RR times that of a heterozygote Aa and RR^2 times that of a homozygote aa. The multiplicative model has a nice property that simplifies analysis and computations — haplotypes are independent, i.e., in Hardy-Weinberg equilibrium, within the affected population as well as within the control population.
- 15 As a consequence, haplotype counts of the affecteds and controls each have multinomial distributions, but with different haplotype frequencies under the alternative hypothesis. Specifically, for two haplotypes h_i and h_j , $\text{risk}(h_i)/\text{risk}(h_j) = (f_i/p_i)/(f_j/p_j)$, where f and p denote respectively frequencies in the affected population and in the control population. While there is some power loss if the true model is
- 20 not multiplicative, the loss tends to be mild except for extreme cases. Most importantly, p-values are always valid since they are computed with respect to null hypothesis.

In general, haplotype frequencies are estimated by maximum likelihood and tests of differences between cases and controls are performed using a generalized

25 likelihood ratio test (Rice, J.A. *Mathematical Statistics and Data Analysis*, 602 (International Thomson Publishing, (1995)). deCODE's haplotype analysis program called NEMO, which stands for NEsted MOdels, can be used to calculate all the haplotype results. To handle uncertainties with phase and missing genotypes, it is emphasized that we do not use a common two-step approach to association tests,

30 where haplotype counts are first estimated, possibly with the use of the EM algorithm, Dempster, (A.P., Laird, N.M. & Rubin, D.B., *Journal of the Royal*

Statistical Society B, 39, 1-38 (1971)) and then tests are performed treating the estimated counts as though they are true counts, a method that can sometimes be problematic and may require randomisation to properly evaluate statistical significance. Instead, with NEMO, maximum likelihood estimates, likelihood ratios
 5 and p-values are computed with the aid of the EM-algorithm directly for the observed data, and hence the loss of information due to uncertainty with phase and missing genotypes is automatically captured by the likelihood ratios. Even so, it is of interest to know how much information is retained, or lost, due to incomplete information. Described herein is such a measure that is natural under the likelihood
 10 framework. For a fixed set of markers, the simplest tests performed compare one selected haplotype against all the others. Call the selected haplotype h_1 and the others h_2, \dots, h_k . Let p_1, \dots, p_k denote the population frequencies of the haplotypes in the controls, and f_1, \dots, f_k denote the population frequencies of the haplotypes in the affecteds. Under the null hypothesis, $f_i = p_i$ for all i . The alternative model we use
 15 for the test assumes h_2, \dots, h_k to have the same risk while h_1 is allowed to have a different risk. This implies that while p_1 can be different from f_1 , $f_1/(f_2 + \dots + f_k) = p_1/(p_2 + \dots + p_k) = \beta_i$ for $i = 2, \dots, k$. Denoting f_i/p_1 by r_i , and noting that $\beta_2 + \dots + \beta_k = 1$, the test statistic based on generalized likelihood ratios is

$$\Lambda = 2 \left[\ell(\hat{r}, \hat{p}_1, \hat{\beta}_2, \dots, \hat{\beta}_{k-1}) - \ell(1, \tilde{p}_1, \tilde{\beta}_2, \dots, \tilde{\beta}_{k-1}) \right]$$

20 where ℓ denotes log_elikelihood and \sim and \wedge denote maximum likelihood estimates under the null hypothesis and alternative hypothesis respectively. Λ has asymptotically a chi-square distribution with 1-df, under the null hypothesis. Slightly more complicated null and alternative hypotheses can also be used. For example, let h_1 be G0, h_2 be GX and h_3 be AX. When comparing G0 against GX,
 25 *i.e.*, this is the test which gives estimated RR of 1.46 and p-value = 0.0002, the null assumes G0 and GX have the same risk but AX is allowed to have a different risk. The alternative hypothesis allows, for example, three haplotype groups to have different risks. This implies that, under the null hypothesis, there is a constraint that $f_1/p_1 = f_2/p_2$, or $w = [f_1/p_1]/[f_2/p_2] = 1$. The test statistic based on generalized
 30 likelihood ratios is

$$\Lambda = 2 \left[\ell(\hat{p}_1, \hat{f}_1, \hat{p}_2, \hat{w}) - \ell(\tilde{p}_1, \tilde{f}_1, \tilde{p}_2, 1) \right]$$

that again has asymptotically a chi-square distribution with 1-df under the null hypothesis. If there are composite haplotypes (for example, h_2 and h_3), that is handled in a natural manner under the nested models framework.

5 LD between pairs of SNPs can be calculated using the standard definition of D' and R^2 (Lewontin, R., *Genetics* 49, 49-67 (1964) and Hill, W.G. & Robertson, A. *Theor. Appl. Genet.* 22, 226-231 (1968)). Using NEMO, frequencies of the two marker allele combinations are estimated by maximum likelihood and deviation from linkage equilibrium is evaluated by a likelihood ratio test. The definitions of D' and R^2 are extended to include microsatellites by averaging over the values for all possible allele combination of the two markers weighted by the marginal allele probabilities. When plotting all marker combination to elucidate the LD structure in a particular region, we plot D' in the upper left corner and the p-value in the lower right corner. In the LD plots the markers can be plotted equidistant rather than
10 according to their physical location, if desired.
15

Statistical Methods for Linkage Analysis

Multipoint, affected-only allele-sharing methods can be used in the analyses to assess evidence for linkage. Results, both the LOD-score and the non-parametric linkage (NPL) score, can be obtained using the program Allegro (Gudbjartsson *et al.*,
20 *Nat. Genet.* 25:12-3, 2000). Our baseline linkage analysis uses the Spairs scoring function (Whittemore, A.S., Halpern, J. (1994), *Biometrics* 50:118-27; Kruglyak L, *et al.* (1996), *Am J Hum Genet* 58:1347-63), the exponential allele-sharing model (Kong, A. and Cox, N.J. (1997), *Am J Hum Genet* 61:1179-88) and a family weighting scheme that is halfway, on the log-scale, between weighting each affected
25 pair equally and weighting each family equally. The information measure we use is part of the Allegro program output and the information value equals zero if the marker genotypes are completely uninformative and equals one if the genotypes determine the exact amount of allele sharing by descent among the affected relatives (Gretarsdottir *et al.*, *Am. J. Hom. Genet.* 70:593-603, (2002)). We computed the P-

values two different ways and here report the less significant result. The first P-value can be computed on the basis of large sample theory; the distribution of $Z_{lr} = \sqrt{2[\log_e(10)\text{LOD}]}$ approximates a standard normal variable under the null hypothesis of no linkage (Kong, A. and Cox, N.J. (1997), *Am J Hum Genet* 61:1179-88). The second P-value can be calculated by comparing the observed LOD-score with its complete data sampling distribution under the null hypothesis (e.g., Gudbjartsson *et al.*, *Nat. Genet.* 25:12-3, 2000). When the data consist of more than a few families, these two P-values tend to be very similar.

METHODS OF TREATMENT

The present invention encompasses methods of treatment (prophylactic and/or therapeutic, as described above) for MI, ACS, stroke or PAOD in
5 individuals, such as individuals in the target populations described above, as well as for other diseases and conditions associated with FLAP or with other members of the leukotriene pathway (*e.g.*, for atherosclerosis). Members of the “leukotriene pathway,” as used herein, include polypeptides (*e.g.*, enzymes, receptors) and other molecules that are associated with production of leukotrienes: for example,
10 enzymes such as FLAP, 5-LO, other leukotriene biosynthetic enzymes (*e.g.*, leukotriene C4 synthetase, leukotriene A4 hydrolase); receptors or binding agents of the enzymes; leukotrienes such as LTA₄, LTB₄, LTC₄, LTD₄, LTE₄, Cys LT₁, and Cys LT₂; and receptors of leukotrienes (*e.g.*, leukotriene B₄ receptor 1 (BLT₁), leukotriene B₄ receptor 2 (BLT₂), cysteinyl leukotriene receptor 1
15 (CysLTR₁), cysteinyl leukotriene receptor 2 (CysLTR₂)).

In particular, the invention relates to methods of treatment for myocardial infarction or susceptibility to myocardial infarction (for example, for individuals in an at-risk population such as those described above); as well as methods of treatment for acute coronary syndrome (*e.g.*, unstable angina, non-ST-elevation
20 myocardial infarction (NSTEMI) or ST-elevation myocardial infarction (STEMI)); methods for reducing risk of MI, stroke or PAOD in persons with asymptomatic ankle/brachial index less than 0.9; for decreasing risk of a second myocardial infarction; for stroke or susceptibility to stroke; for transient ischemic attack; for transient monocular blindness; for decreasing risk of a second stroke; for PAOD or
25 susceptibility to PAOD; for ABI less than 0.9; for claudication or limb ischemia; for atherosclerosis, such as for patients requiring treatment (*e.g.*, angioplasty, stents, revascularization procedure) to restore blood flow in arteries (*e.g.*, coronary, carotid, and/or femoral arteries); for treatment of asymptomatic ankle/brachial index of less than 0.9; and/or for decreasing leukotriene synthesis
30 (*e.g.*, for treatment of MI, ACS, stroke or PAOD). The invention additionally pertains to use of one or more leukotriene synthesis inhibitors, as described herein,

for the manufacture of a medicament for the treatment of MI, ACS, stroke, PAOD and/or atherosclerosis, e.g., using the methods described herein.

In the methods of the invention, a “leukotriene synthesis inhibitor” is used. In one embodiment, a “leukotriene synthesis inhibitor” is an agent that inhibits
5 FLAP polypeptide activity and/or FLAP nucleic acid expression, as described herein (*e.g.*, a nucleic acid antagonist). In another embodiment, a leukotriene synthesis inhibitor is an agent that inhibits polypeptide activity and/or nucleic acid expression of another member of the leukotriene biosynthetic pathway (*e.g.*, 5-LO; LTC4S; LTA4H; LTB4DH). In still another embodiment, a leukotriene synthesis
10 inhibitor is an agent that alters activity or metabolism of a leukotriene (*e.g.*, an antagonist of a leukotriene; an antagonist of a leukotriene receptor). In preferred embodiments, the leukotriene synthesis inhibitor alters activity and/or nucleic acid expression of FLAP or of 5-LO, or alters interaction between FLAP and 5-LO.

Leukotriene synthesis inhibitors can alter polypeptide activity or nucleic acid
15 expression of a member of the leukotriene pathway by a variety of means, such as, for example, by catalytically degrading, downregulating or interfering with the expression, transcription or translation of a nucleic acid encoding the member of the leukotriene pathway; by altering posttranslational processing of the polypeptide; by altering transcription of splicing variants; or by interfering with
20 polypeptide activity (*e.g.*, by binding to the polypeptide, or by binding to another polypeptide that interacts with that member of the leukotriene pathway, such as a FLAP binding agent as described herein or some other binding agent of a member of the leukotriene pathway; by altering interaction among two or more members of the leukotriene pathway (*e.g.*, interaction between FLAP and 5-LO); or by
25 antagonizing activity of a member of the leukotriene pathway.

Representative leukotriene synthesis inhibitors include the following:

agents that inhibit activity of a member of the leukotriene biosynthetic pathway (*e.g.*, FLAP, 5-LO), LTC4S, LTA4H, LTB4DH, such as the agents
30 presented in the Agent Table below; agents that inhibit activity of receptors of members of the leukotriene pathway, such as FLAP receptors, LTA4

- receptors, LTB₄ receptors, LTC₄ receptors, LTD₄ receptors, TLE₄ receptors, Cys LT₁ receptors, Cys LT₂ receptors, 5-LO receptors; BLT₁; BLT₂; CysLTR₁; CysLTR₂; agents that bind to the members of the leukotriene pathway, such as FLAP binding agents (*e.g.*, 5-LO), agents that bind to
5 receptors of members of the leukotriene pathway (*e.g.*, leukotriene receptor antagonists); or agents that bind to a leukotriene (*e.g.*, to LTA₄, LTB₄, LTC₄, LTD₄, LTE₄, Cys LT₁, Cys LT₂) or otherwise affect (*e.g.*, increase or decrease) activity of the leukotriene;
- 10 antibodies to leukotrienes;
- antisense nucleic acids or small double-stranded interfering RNA, to nucleic acids encoding FLAP, 5-LO, or a leukotriene synthetase or other member of the leukotriene pathway, or fragments or derivatives thereof, including
15 antisense nucleic acids to nucleic acids encoding the FLAP, 5-LO or leukotriene synthetase polypeptides, and vectors comprising such antisense nucleic acids (*e.g.*, nucleic acid, cDNA, and/or mRNA, double-stranded interfering RNA, or a nucleic acid encoding an active fragment or derivative thereof, or an oligonucleotide; for example, the complement of one of SEQ ID
20 Nos. 1 or 3, or a nucleic acid complementary to the nucleic acid encoding SEQ ID NO: 2, or fragments or derivatives thereof);
- peptidomimetics; fusion proteins or prodrugs thereof; ribozymes; other small molecules; and
- 25 other agents that alter (*e.g.*, inhibit or antagonize) expression of a member of the leukotriene pathway, such as FLAP or 5-LO nucleic acid expression or polypeptide activity, or that regulate transcription of FLAP splicing variants or 5-LO splicing variants (*e.g.*, agents that affect which splicing variants are
30 expressed, or that affect the amount of each splicing variant that is expressed).

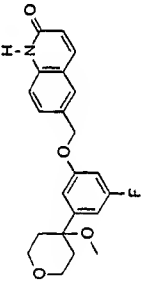
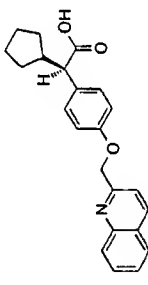
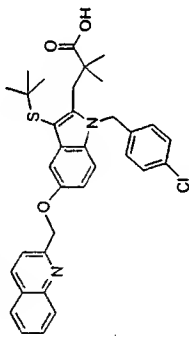
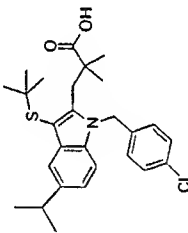
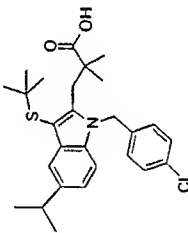
More than one leukotriene synthesis inhibitor can be used concurrently, if desired.

The therapy is designed to alter activity of a FLAP polypeptide, a 5-LO polypeptide, or another member of the leukotriene pathway in an individual, such as by inhibiting or antagonizing activity. For example, a leukotriene synthesis inhibitor can be administered in order to decrease synthesis of leukotrienes within the individual, or to downregulate or decrease the expression or availability of the FLAP nucleic acid or specific splicing variants of the FLAP nucleic acid.

Downregulation or decreasing expression or availability of a native FLAP nucleic acid or of a particular splicing variant could minimize the expression or activity of a defective nucleic acid or the particular splicing variant and thereby minimize the impact of the defective nucleic acid or the particular splicing variant. Similarly, for example, a leukotriene synthesis inhibitor can be administered in order to downregulate or decrease the expression or availability of the nucleic acid encoding 5-LO or specific splicing variants of the nucleic acid encoding 5-LO.

The leukotriene synthesis inhibitor(s) are administered in a therapeutically effective amount (*i.e.*, an amount that is sufficient to treat the disease or condition, such as by ameliorating symptoms associated with the disease or condition, preventing or delaying the onset of the disease or condition, and/or also lessening the severity or frequency of symptoms of the disease or condition). The amount which will be therapeutically effective in the treatment of a particular individual's disease or condition will depend on the symptoms and severity of the disease, and can be determined by standard clinical techniques. In addition, *in vitro* or *in vivo* assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the disease or disorder, and should be decided according to the judgment of a practitioner and each patient's circumstances. Effective doses may be extrapolated from dose-response curves derived from *in vitro* or animal model test systems.

In preferred embodiments of the invention, the leukotriene synthesis inhibitor agent is an agent that inhibits activity of FLAP and/or of 5-LO. Preferred agents include the following, as set forth in the Agent Table:

AstraZeneca	ZD-2138		6-((3-fluoro-5-(tetrahydro-4-methoxy-2H-pyran-4-yl)phenoxy)methyl)-1-methyl-2 (1H)-quinolinone (alternatively NH can be N-methyl)	EP 466452	5-LPO inhibitor
Bayer	BAY-X-1005		(R)-(+)-alpha-cyclopentyl-4-(2-quinolinylmethoxy)-Benzenesacetic acid	US 5970215 EP 344519, DE 19880531	FLAP inhibitor
Merck	MK-0591		1-((4-chlorophenyl)methyl)-3-((1,1-dimethylethyl)thio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)-1H-Indole-2-propanoic acid	EP 419049, US 19890822	FLAP inhibitor
Merck	MK-866		(3-(4-chlorobenzyl)-3-t-butylthio-5-isopropylindol-2-yl)2,2-dimethyl-propanoic acid		5-LPO inhibitor
Merck	MK-886		1-((4-chlorophenyl)methyl)-3-((1,1-dimethylethyl)thio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)-1H-Indole-2-propanoic acid	EP 419049, US 19890822	5-LPO inhibitor
Pfizer	CJ-13610		4-(3-(4-(2-Methylimidazol-1-yl)-phenylsulfanyl)-phenyl)-tetrahydro-pyran-4-carboxylic acid amide		5-LPO inhibitor

In preferred methods of the invention, the agents set forth in the Agent Table can be used for prophylactic and/or therapeutic treatment for diseases and conditions associated with FLAP or with other members of the leukotriene pathway, or with increased leukotriene synthesis. In particular, they can be used

5 for treatment for myocardial infarction or susceptibility to myocardial infarction, such as for individuals in an at-risk population as described above, (e.g., based on identified risk factors such as elevated cholesterol, elevated C-reactive protein, and/or genotype); for individuals suffering from acute coronary syndrome, such as unstable angina, non-ST-elevation myocardial infarction (NSTEMI) or ST-

10 elevation myocardial infarction (STEMI); methods for reducing risk of MI, stroke or PAOD in persons with asymptomatic ankle/brachial index less than 0.9; for decreasing risk of a subsequent myocardial infarction, such as in individuals who have already had one or more myocardial infarctions; for stroke or susceptibility to stroke; for decreasing risk of a second stroke; for PAOD or susceptibility to

15 PAOD; for treatment of atherosclerosis, such as in patients requiring treatment (e.g., angioplasty, stents, revascularization procedure) to restore blood flow in arteries (e.g., coronary, carotid, and/or femoral arteries); for treatment of asymptomatic ankle/brachial index of less than 0.9; and/or for decreasing leukotriene synthesis (e.g., for treatment of myocardial infarction, ACS, stroke or

20 PAOD

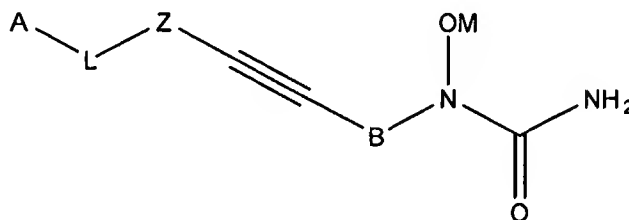
In one preferred embodiment of the invention, the leukotriene synthesis inhibitor is an inhibitor of FLAP such as 1-((4-chlorophenyl)methyl)-3-((1,1-dimethylethyl)thio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)-1H-Indole-2-propanoic acid otherwise known as MK-0591, (R)-(+)-alpha-cyclopentyl-4-(2-

25 quinolinylmethoxy)-Benzeneacetic acid otherwise known as BAY-x-1005, 3-(3-(1,1-dimethylethylthio-5-(quinoline-2-ylmethoxy)-1-(4-chloromethylphenyl)indole-2-yl)-2,2-dimethylpropionaldehyde oxime-0-2-acetic acid otherwise known as A-81834, their optically pure enantiomers, salts, chemical derivatives, analogues, or other compounds inhibiting FLAP that

30 effectively decrease leukotriene biosynthesis when administered to humans.

In another preferred embodiment of the invention, the leukotriene synthesis inhibitor is an inhibitor of 5LO such as zileuton, atreleuton, 6-((3-fluoro-5-(tetrahydro-4-methoxy-2H-pyran-4yl)phenoxy)methyl)-1-methyl-2(1H)-quinolinone otherwise known as ZD-2138, 1-((4-chlorophenyl)methyl)-3-
 5 ((1,1dimethylethyl)thio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)-1H-Indole-2-propanoic acid otherwise known as MK-886, 4-(3-(4-(2-Methylimidazol-1-yl)-phenylsulfanyl)-phenyl)-tetrahydro-pyran-4-carboxylic acid amide otherwise known as CJ-13610, their optically pure enantiomers, salts, chemical
 10 derivatives, analogues or other compounds inhibiting 5-LO that effectively decrease leukotriene biosynthesis when administered to humans.

The compound can be represented by the following formula:

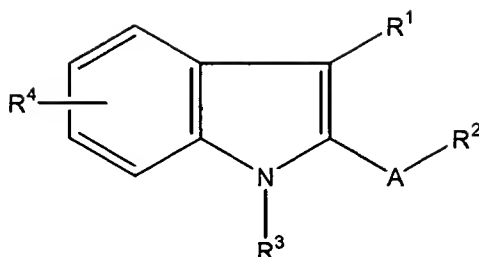


15

or a pharmaceutically acceptable salt thereof, wherein M is selected from the group consisting of hydrogen, a pharmaceutically acceptable cation, and a pharmaceutically acceptable metabolically cleavable group; B is a straight or branched divalent alkylene group of from one to twelve carbon atoms; Z is
 20 thiazolyl, optionally substituted with alkyl of from one to six carbon atoms or haloalkyl of from one to six carbon atoms; L is selected from the group consisting of (a) alkylene of from 1-6 carbon atoms, (b) alkenylene of from 2-6 carbon atoms, (c) alkynylene of from 2-6 carbon atoms, (d) hydroxyalkyl of 1-6 carbon atoms, (e) >C=O, (f) >C=N-OR₁, where R₁ is hydrogen or C₁-C₆ alkyl,
 25 (g) -(CHR₁)_n (CO)(CHR₂)_m, where n and m are independently selected from an integer from one to six and R₁ and R₂ are independently selected from hydrogen

and C₁-C₆-alkyl, (h) -(CHR₁)_n C=NOR₂, where R₁, R₂ and n are as defined above; (i) -(CHR₁)_n ON=CR₂, where R₁, R₂ and n are as defined above; (j) -(CHR₁)_n -O-(CHR₂)_m -, where R₁, R₂, n and m are as defined above, (k) -(CHR₁)_n -NR₂ (CHR₃)_m -, where R₁, R₂, n and m are as defined above and R₃ is selected from hydrogen and C₁-C₆-alkyl; (l) -(CHR₁)_n -S- (CHR₂)_m -, where R₁, R₂, n and m are as defined above; and (m) -(CHR₁)_n -(SO₂)-(CHR₂)_m -, where R₁, R₂, n and m are as defined above; A is carbocyclic aryl optionally substituted with alkyl of from one to six carbon atoms, haloalkyl of from one to six carbon atoms, hydroxyalkyl of from one to six carbon atoms, alkoxy of from one to twelve carbon atoms, alkoxyalkoxyl in which the two alkoxy portions may each independently contain from one to six carbon atoms, alkylthio of from one to six carbon atoms, hydroxy, halogen, cyano, amino, alkylamino of from one to six carbon atoms, dialkylamino in which the two alkyl groups may independently contain from one to six carbon atoms, alkanoylamino of from two to eight carbon atoms, N-alkanoyl-N-alkylamino in which the alkanoyl is of from two to eight carbon atoms and the alkyl group is of from one to six carbon atoms, alkylaminocarbonyl of from two to eight carbon atoms, dialkylaminocarbonyl in which the two alkyl groups are independently of from one to six carbon atoms, carboxyl, alkoxy carbonyl or from two to eight carbon atoms, phenyl, optionally substituted with alkyl of from one to six carbon atoms, haloalkyl of from one to six carbon atoms, alkoxy of from one to six carbon atoms, hydroxy or halogen, phenoxy, optionally substituted with alkyl of from one to six carbon atoms, haloalkyl of from one to six carbon atoms, alkoxy of from one to six carbon atoms, hydroxy or halogen, and phenylthio, optionally substituted with alkyl of from one to six carbon atoms, haloalkyl of from one to six carbon atoms, alkoxy of from one to six carbon atoms, hydroxy or halogen. Preferably, the compound is a compound or pharmaceutically acceptable salt thereof having the name (R)-N-{3-[-5-(4-fluorophenylmethyl)thiazo-2-yl]-1-methyl-2-propynyl}-N-hydroxyurea. See U.S. Patent No. 4,615,596, incorporated herein by reference.

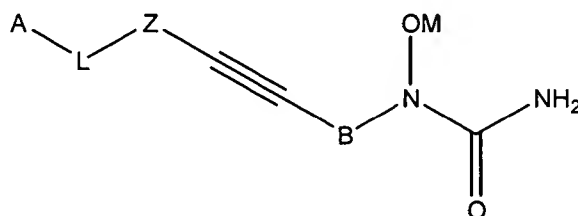
The compound is represented by the following formula:



or a pharmaceutically acceptable salt thereof, wherein A is selected from the group consisting of straight or branched divalent alkylene of from one to twelve carbon atoms and divalent cycloalkylene of from three to eight carbon atoms; R₁ is selected from the group consisting of hydrogen, alkylthio of from one to six carbon atoms, phenylthio, optionally substituted with alkyl of from one to six carbon atoms, alkoxy of from one to six carbon atoms, or halogen, phenylalkylthio in which the alkyl portion contains from one to six carbon atoms, and the phenyl group is optionally substituted with alkyl of from one to six carbon atoms, alkoxy of from one to six carbon atoms, or halogen, R₂ is selected from the group consisting of -COOB wherein B is selected from hydrogen, a pharmaceutically acceptable cation, or a metabolically cleavable group, -COOalkyl where the alkyl portion contains from one to six carbon atoms, -COOalkylcarbocyclicaryl where the alkyl portion contains from one to six carbon atoms and the aryl portion is optionally substituted with alkyl of from one to six carbon atoms, alkoxy of from one to six carbon atoms, or halogen, -CONR₅ R₆ wherein R₅ is selected from the group consisting of hydrogen, hydroxyl, alkyl of from one to six carbon atoms, and alkoxy of from one to six carbon atoms, and R₆ is selected from the group consisting of hydrogen and alkyl of from one to six carbon atoms, -COR₆, and -OH; R₃ is selected from the group consisting of phenylalkyl in which the alkyl portion contains from one to six carbon atoms, and the phenyl group is optionally substituted with alkyl of from one to six carbon atoms, alkoxy of from one to six carbon atoms, or halogen, R₄ is selected from the group consisting of thiazolylalkyloxy in which the alkyl portion contains from one to six carbon atoms, and the heteroaryl portion is optionally substituted with alkyl of from one to six carbon atoms,

alkoxy of from one to six carbon atoms, or halogen, and thiazolyloxy optionally substituted with alkyl of from one to six carbon atoms, alkoxy of from one to six carbon atoms, or halogen. See U.S. Patent No. 5,288,743, incorporated herein by reference.

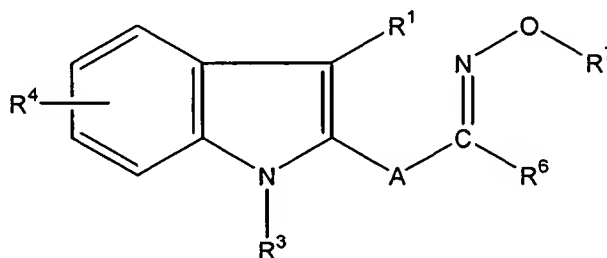
5 The compound can be represented by the formula:



10 or a pharmaceutically acceptable salt thereof, wherein M is selected from the group consisting of hydrogen, and a pharmaceutically acceptable cation; B is a straight or branched divalent alkylene group of from one to twelve carbon atoms; Z is selected from the group consisting of: (a) furyl, optionally substituted with alkyl of from one to six carbon atoms, or haloalkyl of from one to six carbon atoms, and (b) thienyl, optionally substituted with alkyl of from one to six carbon atoms, or haloalkyl of from one to six carbon atoms; and L is alkylene of from 1-6 carbon atoms; A is phenyl optionally substituted with alkyl of from one to six carbon atoms, haloalkyl of from one to six carbon atoms, hydroxyalkyl of from one to six carbon atoms, alkoxy of from one to twelve carbon atoms, alkoxyalkoxyl in which the two alkoxy portions may each independently contain from one to six carbon atoms, alkylthio of from one to six carbon atoms, hydroxy, halogen, cyano, amino, alkylamino of from one to six carbon atoms, dialkylamino in which the two alkyl groups may independently contain from one to six carbon atoms, alkanoylamino of from two to eight carbon atoms, N-alkanoyl-N-alkylamino in which the alkanoyl is of from two to eight carbon atoms and the alkyl group is of from one to six carbon atoms, alkylaminocarbonyl of from two to eight carbon atoms, dialkylaminocarbonyl in

which the two alkyl groups are independently of from one to six carbon atoms, carboxyl, alkoxycarbonyl of from two to eight carbon atoms, phenyl, optionally substituted with alkyl of from one to six carbon atoms, haloalkyl of from one to six carbon atoms, alkoxy of from one to six carbon atoms, hydroxy or halogen, phenoxy, optionally substituted with alkyl of from one to six carbon atoms, haloalkyl of from one to six carbon atoms, alkoxy of from one to six carbon atoms, hydroxy or halogen, or phenylthio, optionally substituted with alkyl of from one to six carbon atoms, haloalkyl of from one to six carbon atoms, alkoxy of from one to six carbon atoms, hydroxy or halogen. Preferably, the compound is a compound or a pharmaceutically acceptable salt thereof selected from the group consisting of: N-{3-(5-(4-fluorophenylmethyl)fur-2-yl)-3-butyne-2-yl}-N-hydroxyurea; N-{3-(5-(4-fluorophenylmethyl)-2-thienyl)-1-methyl-2-propynyl}-N-hydroxyurea; (R)-N-{3-(5-(4-fluorophenylmethyl)-2-thienyl)-1-methyl-2-propynyl}-N-hydroxyurea; and (R)-N-{3-(5-(4-chlorophenylmethyl)-2-thienyl)-1-methyl-2-propynyl}-N-hydroxyurea; (S)-N-{3-[5-(4-fluorophenylmethyl)-2-thienyl]-1-methyl-2-propynyl}-N-hydroxyurea. See U.S. Patent No. 5,288,751, incorporated by reference herein.

The compound can be represented by the formula:



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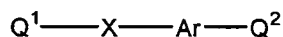
or a pharmaceutically acceptable salt thereof, wherein A is selected from the group consisting of straight or branched divalent alkylene of one to twelve carbon atoms, straight or branched divalent alkenylene of two to twelve carbon atoms, and divalent cycloalkylene of three to eight carbon atoms; R¹ is alkylthio

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of one to six carbon atoms; R⁶ is selected from the group consisting of hydrogen and alkyl of one to six carbon atoms; R⁷ is selected from the group consisting of (carboxyl)alkyl in which the alkyl portion is of one to six carbon atoms, (alkoxycarbonyl)alkyl in which the alkoxycarbonyl portion is of two to six
 5 carbon atoms and the alkyl portion is of one to six carbon atoms, (aminocarbonyl)alkyl in which the alkyl portion is of one to six carbon atoms, ((alkylamino)carbonyl)alkyl in which each alkyl portion independently is of one to six carbon atoms, and ((dialkylamino)carbonyl)alkyl in which each alkyl portion independently is of one to six carbon atoms; R³ is phenylalkyl in which
 10 the alkyl portion is of one to six carbon atoms; R⁴ is 2-, 3- or 6-quinolylmethoxy, optionally substituted with alkyl of one to six carbon atoms, haloalkyl of one to six carbon atoms, alkoxy of one to twelve carbon atoms, halogen, or hydroxy. Preferably the compound is selected from the group consisting of: 3-(3-1,1-
 15 dimethylethylthio)-5-(quinolin-2-ylmethoxy)-1-(4-chlorophenylmethyl)-indol-2-yl)-2,2-dimethylpropionaldehyde oxime-O-2 acetic acid; 3-(3-(1,1-dimethylethylthio)-5-(quinolin-2-ylmethoxy)-1-(4-chloro-phenylmethyl) indol-2-yl)-2,2-dimethylpropionaldehyde oxime-O-2-(3-methyl)butyric acid; 3-(3-(1,1-dimethylethylthio)-5-(6,7-dichloroquinolin-2-ylmethoxy)-1-(4-
 20 chlorophenylmethyl) indol-2-yl)-2,2-dimethylpropionaldehyde oxime-O-2-acetic acid; and 3-(3-(1,1-dimethylethylthio)-5-(6-fluoroquinolin-2-ylmethoxy)-1-(4chlorophenylmethyl) indol-2-yl)-2,2-dimethylpropionaldehyde oxime-O-2-propionic acid; or a pharmaceutically acceptable salt or ester thereof. See U.S. Patent No. 5,459,150, incorporated by reference herein.

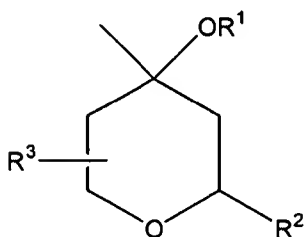
The compound can be represented by the formula:

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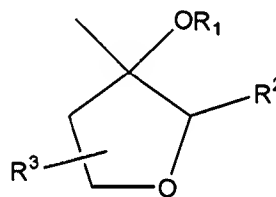


or pharmaceutically acceptable salts thereof, wherein Q is a 9-, 10- or 11-membered bicyclic heterocyclic moiety containing one or two nitrogen
 30 heteroatoms and optionally containing a further heteroatom selected from nitrogen, oxygen and sulphur, and Q may optionally bear up to four substituents

selected from halogeno, hydroxy, cyano, formyl, oxo, thioxo, (1-4C)alkyl, (3-4C)alkenyl, (3-4C)alkynyl, (1-4C)alkoxy, fluoro-(1-4C)alkyl, hydroxy-(1-4C)alkyl, (2-5C)alkanoyl, phenyl, benzoyl and benzyl, and wherein said phenyl, benzoyl and benzyl substituents may optionally bear one or two substituents
 5 selected from halogeno, (1-4C)alkyl and (1-4C)alkoxy;
 X is oxy, thio, sulphinyl or sulphonyl; Ar is phenylene, pyridinediyl, pyrimidinediyl, thiophenediyl, furandiyl, thiazolediyl, oxazolediyl, thiadiazolediyl or oxadiazolediyl which may optionally bear one or two substituents selected from halogeno, cyano, trifluoromethyl, hydroxy, amino, (1-4C)alkyl, (1-4C)alkoxy, (1-4C)alkylamino and di-(1-4C)alkylamino; and Q is
 10 selected from the groups of the formulae II and III:



II

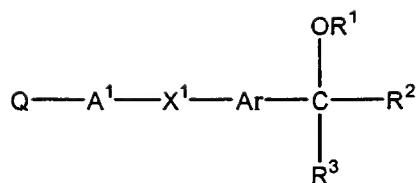


III

15 wherein R is hydrogen, (2-5C)alkanoyl or benzoyl, and wherein said benzoyl group may optionally bear one or two substituents selected from halogeno, (1-4C)alkyl and (1-4C)alkoxy; R is (1-4C)alkyl; and R is hydrogen or (1-4C)alkyl; or R and R are linked to form a methylene, vinylene, ethylene or trimethylene group. Preferably, the compound is selected from the group consisting of:
 20 (2S,4R)-4-[5-fluoro-3-(1-methyl-2-oxo-1,2,3,4-tetrahydroquinolin-6-ylthio)phenyl]-4-hydroxy-2-ethyltetrahydropyran, (2S,4R)-4-[5-fluoro-3-(1-methyl-2-oxo-1,2,3,4-tetrahydroquinolin-6-ylsulphonyl)phenyl]-4-hydroxy-2-methyltetrahydropyran, (2S,4R)-4-hydroxy-2-methyl-4-[2-(1-methyl-2-oxo-1,2,3,4-tetrahydroquinolin-6-ylthio)thiazol-5-yl]tetrahydropyran, (2S,4R)-4-
 25 hydroxy-2-methyl-4-[2-(1-methyl-2-oxo-1,2,3,4-tetrahydroquinolin-6-

ylsulphonyl)thiazol-5-yl]tetrahydropyran, (2S,4R)-4-[2-(7-fluoro-1-methyl-2-
 oxo-1,2,3,4-tetrahydroquinolin-6-ylthio)thiazol-5-yl]-4-hydroxy-2-
 methyltetrahydropyran, (2S,4R)-4-hydroxy-2-methyl-4-[2-(1-methyl-2-
 oxoindolin-5-ylthio)thiazol-5-yl]tetrahydropyran, (2S,4R)-4-hydroxy-2-methyl-
 4-[2-(1-methyl-2-oxo-1,2,3,4-tetrahydroquinolin-6-ylthio)thien-4-
 5 yl]tetrahydropyran, (2S,4R)-4-hydroxy-2-methyl-4-[2-(1-methyl-2-oxo-1,2,3,4-
 tetrahydroquinolin-6-ylsulphonyl)thien-4-yl]tetrahydropyran, (2S,4R)-4-
 hydroxy-2-methyl-4-[2-(1-methyl-2-oxo-1,2,3,4-tetrahydroquinolin-6-
 ylthio)thien-5-yl]tetrahydropyran, (2S,4R)-4-hydroxy-2-methyl-4-[2-(1-methyl-
 10 2-oxo-1,2-dihydroquinolin-6-ylthio)thien-4-yl]tetrahydropyran, (2S,4R)-4-
 hydroxy-2-methyl-4-[2-(1,8-dimethyl-2-oxo-1,2,3,4-tetrahydroquinolin-6-
 ylthio)thien-4-yl]tetrahydropyran, 4-[2-(8-fluoro-1-methyl-2-oxo-1,2,3,4-
 tetrahydroquinolin-6-ylthio)thien-4-yl]-4-hydroxy-2-methyltetrahydropyran, 4-
 [2-(7-fluoro-1-methyl-2-oxo-1,2,3,4-tetrahydroquinolin-6-ylthio)thien-4-yl]-4-
 15 hydroxy-2-methyltetrahydropyran, (2S,4R)-4-hydroxy-2-methyl-4-[2-(1-methyl-
 2-oxoindolin-5-ylthio)thien-4-yl]tetrahydropyran, (2S,4R)-4-hydroxy-2-methyl-
 4-[3-(1-methyl-2-oxo-1,2,3,4-tetrahydroquinolin-6-
 ylthio)phenyl]tetrahydropyran, (2S,4R)-4-hydroxy-2-methyl-4-[3-(1-methyl-2-
 oxo-1,2,3,4-tetrahydroquinolin-6-ylsulphonyl)phenyl]tetrahydropyran, (2S,4R)-
 20 4-[3-(1-ethyl-2-oxo-1,2,3,4-tetrahydroquinolin-6-ylthio)phenyl]-4-hydroxy-2-
 methyltetrahydropyran, (2S,4R)-4-[3-(7-fluoro-1-methyl-2-oxo-1,2,3,4-
 tetrahydroquinolin-6-ylthio)phenyl]-4-hydroxy-2-methyltetrahydropyran,
 (2S,4R)-4-hydroxy-2-methyl-4-[3-(1-methyl-2-oxo-1,2-dihydroquinolin-6-
 ylthio)phenyl]tetrahydropyran, (2S,4R)-4-[3-(8-chloro-1-methyl-2-oxo-1,2,3,4-
 25 tetrahydroquinolin-6-ylthio)phenyl]-4-hydroxy-2-methyltetrahydropyran and
 (2S,4R)-4-hydroxy-2-methyl-4-[3-(1-methyl-2-oxoindolin-5-
 ylthio)phenyl]tetrahydropyran. See EP 623614 B1, incorporated herein by
 reference.

The compound can be represented by the formula:

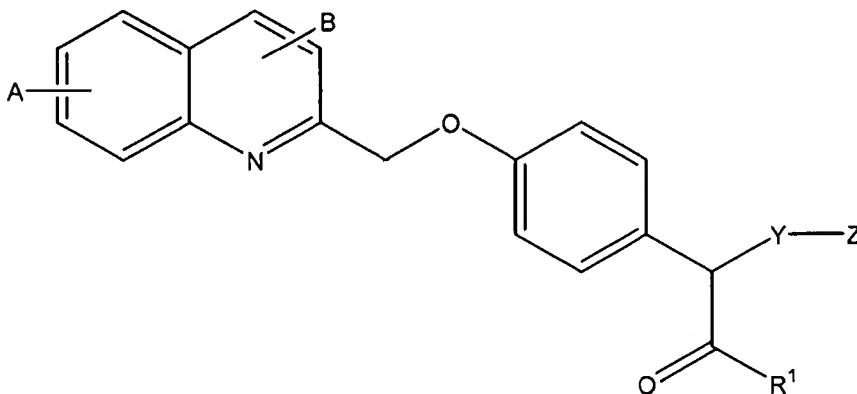


wherein Q is a 10-membered bicyclic heterocyclic moiety containing one or two nitrogen heteroatoms which bears one or two thioxo substituents, and which heterocyclic moiety may optionally bear one, two or three further substituents selected from halogeno, hydroxy, cyano, amino, (1-4C)alkyl, (1-4C)alkoxy, fluoro-(1-4C)alkyl, (1-4C)alkylamino, di-[(1-4C)alkyl]amino, amino-(1-4C)alkyl, (1-4C)alkylamino-(1-4C)alkyl, di-[(1-4C)alkyl]amino-(1-4C)alkyl, phenyl and phenyl-(1-4C)alkyl, and wherein said phenyl or phenyl-(1-4C)alkyl substituent may optionally bear a substituent selected from halogeno, (1-4C)alkyl and (1-4C)alkoxy;

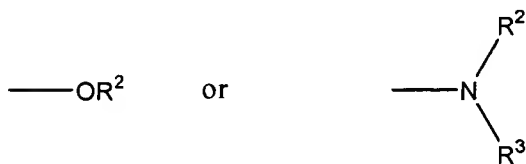
wherein A is a direct link to X or is (1-3C)alkylene; wherein X is oxy, thio, sulphinyl, sulphonyl or imino; wherein Ar is phenylene which may optionally bear one or two substituents selected from halogeno, hydroxy, amino, nitro, cyano, carbamoyl, ureido, (1-4C)alkyl, (1-4C)alkoxy, (1-4C)alkylamino, di-[(1-4C)alkyl]amino, fluoro-(1-4C)alkyl and (2-4C)alkanoylamino; or Ar is pyridylene; wherein R is (1-4C)alkyl, (3-4C)alkenyl or (3-4C)alkynyl; and wherein R and R together form a group of the formula -A-X-A- which, together with the carbon atom to which A and A are attached, defines a ring having 5 to 7 ring atoms, wherein A and A, which may be the same or different, each is (1-3C)alkylene and X is oxy, thio, sulphinyl or sulphonyl, and which ring may bear one, two or three substituents, which may be the same or different, selected from hydroxy, (1-4C)alkyl and (1-4C)alkoxy; or wherein R and R together form a group of the formula -A-X-A- which, together with the oxygen atom to which A is attached and with the carbon atom to which A is attached, defines a ring having 5 to 7 ring atoms, wherein A and A, which may be the same or different, each is (1-3C)alkylene and X is oxy, thio, sulphinyl or sulphonyl, and which ring

may bear one, two or three (1-4C)alkyl substituents, and wherein R is (1-4C)alkyl, (2-4C)alkenyl or (2-4C)alkynyl; or a pharmaceutically-acceptable salt thereof. Preferably, the compound is selected from the group consisting of: 4-(5-fluoro-3-(1-methyl-2-thioxo-1,2-dihydroquinolin-6-ylmethoxy)phenyl]-4-ethoxytetrahydropyran and 4-(5-fluoro-3-(1-methyl-2-thioxo-1,2,3,4-tetrahydroquinolin-6-ylmethoxy)phenyl]-4-methoxytetrahydropyran, 4-(5-fluoro-3-(1-methyl-2-thioxo-1,2,3,4-tetrahydroquinolin-6-ylthio)phenyl]-4-methoxytetrahydropyran and pharmaceutically-acceptable salt thereof. See EP 466452 B1, incorporated herein by reference.

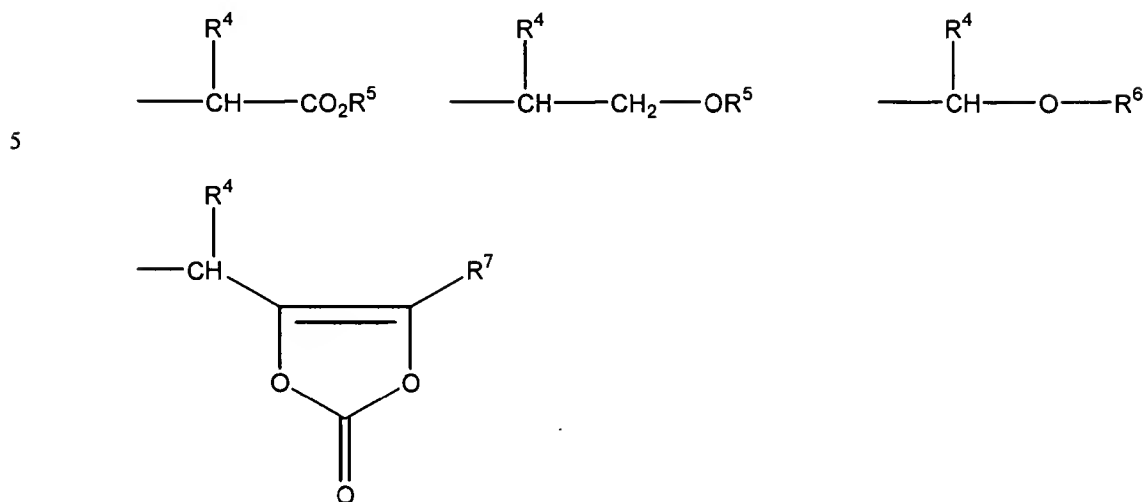
The compound can be a substituted 4-(quinolin-2-ylmethoxy)phenylacetic acid derivative represented by the following formula:



or pharmaceutically acceptable salt thereof, wherein R¹ represents a group of the formula:

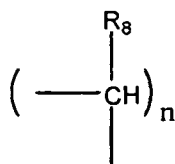


R^2 and R^3 are identical or different and represent hydrogen, lower alkyl, phenyl, benzyl or a group of the formula:



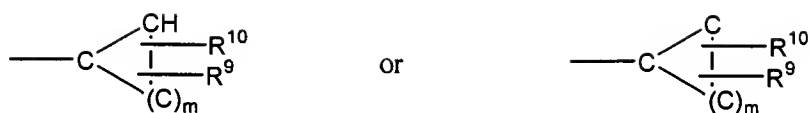
10 R^4 represents hydrogen, lower alkyl, phenyl or benzyl, which can optionally be substituted by hydroxyl, carboxyl, lower alkoxy carbonyl, lower alkylthio, heteroaryl or carbamoyl, R^5 represents hydrogen, lower alkyl, phenyl or benzyl, R^6 represents a group of the formula $-\text{COR}^5$ or $-\text{CO}^2 R^5$, R^7 represents hydrogen, lower alkyl or phenyl, Y represents a group of the formula:

15



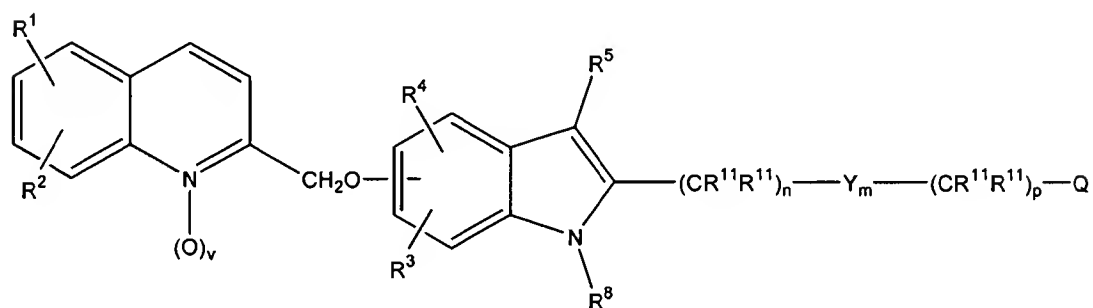
20 wherein R^8 represents hydrogen, lower alkyl or phenyl and n denotes a number of 0 to 5, Z represents norbornyl, or represents a group of the formula:

-52-



wherein R^9 and R^{10} are identical or different and denote hydrogen, lower alkyl or phenyl, or R^9 and R^{10} can together form a saturated carbocyclic ring having up to 6 carbon atoms and m denotes a number from 1 to 6, and A and B are identical or different and denote hydrogen, lower alkyl or halogen, or a pharmaceutically acceptable salt thereof. Preferably the compounds are selected from the group consisting of: 2-[4-(quinolin-2-yl-methoxy)phenyl]-2-cyclopentylacetic acid, 2-[4-(quinolin-2-yl-methoxy)phenyl]-2-cyclohexylacetic acid, and 2-[4-(quinolin-2-yl-methoxy)phenyl]-2-cycloheptylacetic acid, (+)-enantiomer of 2-[4-(quinolin-2-yl-methoxy)phenyl]-2-cyclopentylacetic acid, (-)-enantiomer of 2-[4-(quinolin-2-yl-methoxy)phenyl]-2-cyclopentylacetic acid and pharmaceutically acceptable salts thereof. See U.S. Patent No. 4,970,215, incorporated herein by reference.

The compound can be represented by the formula:



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wherein R , R , R and R are independently hydrogen, halogen, lower alkyl, lower alkenyl, lower alkynyl, $-\text{CF}_3$, $-\text{CN}$, $-\text{NO}_2$, $-\text{N}_3$, $-\text{C}(\text{OH})\text{RR}$, $-\text{CO}_2\text{R}$, $-\text{SR}$,

-S(O)R, -S(O)₂R, -S(O)₂NRR, -OR, -NRR, -C(O)R or -(CH₂)_tR; R is hydrogen, -CH₃, -CF₃, -C(O)H, X-R or X-R; R and R are independently: alkyl, -(CH₂)_uPh(R)₂ or -(CH₂)_uTh(R)₂; R is -CF₃ or R; R is hydrogen or X-R; each R is independently hydrogen or lower alkyl, or two R's on same carbon atom are

5 joined to form a cycloalkyl ring of 3 to 6 carbon atoms; R is hydrogen, lower alkyl or -CH₂R;

R is lower alkyl or -(CH₂)_rR; R is -CF₃ or R; R is hydrogen, -C(O)R, R, or two R 's on the same nitrogen may be joined to form a monocyclic heterocyclic ring of 4 to 6 atoms containing up to 2 heteroatoms chosen from O, S or N; R is

10 hydrogen, -CF₃, lower alkyl, lower alkenyl, lower alkynyl or -(CH₂)_rR; R is -(CH₂)_s-C(RR)-(CH₂)_s-R or -CH₂C(O)NRR; R is hydrogen or lower alkyl; R is a) a monocyclic or bicyclic heterocyclic ring containing from 3 to 9 nuclear carbon atoms and 1 or 2 nuclear hetero-atoms selected from N, S or O and with each ring in the heterocyclic radical being formed of 5 or 6 atoms, or b) the

15 radical W-R; R is alkyl or C(O)R;

R is phenyl substituted with 1 or 2 R groups; R is hydrogen, halogen, lower alkyl, lower alkoxy, lower alkylthio, lower alkylsulfonyl, lower alkylcarbonyl, -CF₃, -CN, -NO₂ or -N₃; R is alkyl, cycloalkyl, monocyclic monoheterocyclic ring;

20 R is the residual structure of a standard amino acid, or R and R attached to the same N can cyclize to form a proline residue; m is 0 to 1; n is 0 to 3; p is 1 to 3 when m is 1; p is 0 to 3 when m is 0; r is 0 to 2; s is 0 to 3; t is 0 to 2; u is 0 to 3; v is 0 or 1;

W is 0, S or NR; X is 0, or NR; X is C(O), CRR, S, S(O) or S(O)₂; X is C(O), CRR, S(O)₂ or a bond; Y is X or X; Q is -CO₂R, -C(O)NHS(O)₂R, -NHS(O)₂R,

25 -S(O)₂NHR -C(O)NRR, -CO₂R, -C(O)NRR, -CH₂OH, or 1H- or 2H-tetrazol-5-yl;

and the pharmaceutically acceptable salts thereof. Preferred embodiments of the

30 compounds are selected from the following and pharmaceutically acceptable salts thereof:

- 3-[N-(p-chlorobenzyl)-3-(t-butylthio)-5-(quinolin-2-ylmethoxy)indol-2-yl]-
2,2-dimethylpropanoic acid;
- 3-[N-(p-chlorobenzyl)-3-methyl-5-(quinolin-2-ylmethoxy)indol-2-
5 yl]-2,2-dimethylpropanoic acid;
- 3-[N-(p-t-butylthiobenzyl)-3-(t-butylthio)-5-(quinolin-2-
ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid;
- 3-[N-(p-chlorobenzyl)-3-(phenylthio)-5-(quinolin-2-
ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid;
- 10 3-[N-(p-chlorobenzyl)-3-(phenylsulfonyl)-5-(quinolin-2-
ylmethoxy)indol-2-yl]-2,2-dimethyl propanoic acid, N-oxide;
- 3-[N-(p-chlorobenzyl)-3-(phenylsulfonyl)-5-(quinolin-2-
ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid;
- 3-[N-(p-chlorobenzyl)-3-(phenylsulfinyl)-5-(quinolin-2-
15 ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid;
- 3-[N-(p-chlorobenzyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-
dimethylpropanoic acid;;
- 3-[N-(p-chlorobenzyl)-3-benzoyl-5-(quinolin-2-ylmethoxy)indol-2-
yl]-2,2-dimethylpropanoic acid;
- 20 3-[N-(p-chlorobenzyl)-3-benzyl-5-(quinolin-2-ylmethoxy)indol-2-
yl]-2,2-dimethylpropanoic acid;
- 3-[N-(p-chlorobenzyl)-3-(3,3-dimethyl-1-oxo-1-butyl)-5-(quinolin-2-
ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid;
- 2-[N-(p-chlorobenzyl)-3-(t-butylthio)-5-(quinolin-2-ylmethoxy)indol-
25 2-yl]ethoxyethanoic acid;
- 3-[N-(p-chlorobenzyl)-3-(3,3-dimethyl-1-butyl)-5-(quinolin-2-
ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid;
- 3-[N-(p-chlorobenzyl)-3-(t-butylthio)-5-(quinolin-2-ylmethoxy)indol-
2-yl]-2-methylpropanoic acid;
- 30 3-[N-(p-chlorobenzyl)-3-methyl-5-(6,7-dichloroquinolin-2-
ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid;

- 3-[N-(p-chlorobenzyl)-3-methyl-5-(7-chloroquinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid;
- 3-[N-(p-chlorobenzyl)-4-allyl-5-(quinolin-2-ylmethoxy)-3-(t-butylthio)indol-2-yl]-2,2-dimethylpropanoic acid;
- 5 3-[N-(p-chlorobenzyl)-4-allyl-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid;
- 3-[N-(p-chlorobenzyl)-6-(quinolin-2-ylmethoxy)-3-(t-butylthio)indol-2-yl]-2,2-dimethylpropanoic acid;
- 3-[N-(p-chlorobenzyl)-4-(quinolin-2-ylmethoxy)-3-(t-butylthio)indol-2-yl]-2,2-dimethylpropanoic acid;
- 10 3-[N-(p-chlorobenzyl)-7-(quinolin-2-ylmethoxy)-3-(t-butylthio)indol-2-yl]-2,2-dimethylpropanoic acid;
- 2-[2-[N-(p-chlorobenzyl)-3-(t-butylthio)-5-(quinolin-2-ylmethoxy)indol-2-yl]ethoxy]propanoic acid;
- 15 3-[N-(p-chlorobenzyl)-4-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid;;
- 3-[N-methyl-3-(p-chlorobenzoyl)-6-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
- 3-[N-methyl-3-(p-chlorobenzyl)-6-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
- 20 3-[N-(4-chlorobenzyl)-3-i-propoxy-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
- 3-[N-(4-chlorobenzyl)-3-(t-butylthio)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2-ethylpropanoic acid,
- 25 3-[N-(4-chlorobenzyl)-3-trifluoroacetyl-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
- 3-[N-(4-chlorobenzyl)-3-(3,3-dimethyl-1-oxo-1-butyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2-methylpropanoic acid,
- 3-[3-(3,3-dimethyl-1-oxo-1-butyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
- 30 3-[N-(4-trifluoromethylbenzyl)-3-(3,3-dimethyl-1-oxo-1-butyl)-5-

- (quinolin-2-yl-methoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
3-[N-benzyl-3-(3,3-dimethyl-1-oxo-1-butyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
3-[N-(3-methoxybenzyl)-3-(3,3-dimethyl-1-oxo-1-butyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
5 3-[N-allyl-3-(3,3-dimethyl-1-oxo-1-butyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
3-[N-(4-methoxybenzyl)-3-(3,3-dimethyl-1-oxo-1-butyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
10 3-[N-methyl-3-(3,3-dimethyl-1-oxo-3-butyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
3-[3-(4-chlorobenzyl)-6-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid.
3-[N-(phenylsulfonyl)-3-(4-chlorobenzyl)-6-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
15 3-[N-benzyl-3-(4-chlorobenzyl)-6-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
3-[N-(4-chlorobenzyl)-3-(t-butylsulfonyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
20 3-[N-(4-chlorobenzyl)-3-(t-butylsulfinyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
3-[N-allyl-3-(4-chlorobenzyl)-6-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
3-[N-(n-propyl)-3-(4-chlorobenzyl)-6-(quinoline-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
25 3-[N-ethyl-3-(4-chlorobenzyl)-6-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
3-[N-(4-chlorobenzyl)-3-(4-t-butylbenzoyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
30 3-[N-(4-chlorobenzyl)-3-(4-chlorobenzoyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,

- 3-[N-(4-chlorobenzyl)-3-(1,1-dimethylethyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
3-[N-(4-chlorobenzyl)-3-acetyl-5-(quinolin-2-ylmethoxy)indol-2-yl]-
2,2-dimethylpropanoic acid
- 5 3-[N-(4-chlorobenzyl)-3-cyclopropanecarbonyl-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
3-[N-(4-chlorobenzyl)-3-(3-cyclopentylpropanoyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
3-[N-(4-chlorobenzyl)-3-(3-methylbutanoyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
- 10 3-[N-(4-chlorobenzyl)-3-propanoyl-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
3-[N-(4-chlorobenzyl)-3-(2-methylpropanoyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
- 15 3-[N-(4-chlorobenzyl)-3-trimethylacetyl-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
3-[N-(4-chlorobenzyl)-3-phenylacetyl-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
3-[N-(4-fluorobenzyl)-3-(3,3-dimethyl-1-oxo-1-butyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
- 20 3-[N-(4-bromobenzyl)-3-(3,3-dimethyl-1-oxo-1-butyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
3-[N-(4-iodobenzyl)-3-(3,3-dimethyl-1-oxo-1-butyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
- 25 3-[N-(4-chlorobenzyl)-3-(1,1-dimethylbutyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
3-[N-(4-chlorobenzyl)-3-(1,1-dimethylpropyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
3-[N-(3-fluorobenzyl)-3-(1,1-dimethylethyl)-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
- 30 3-[N-(4-chlorobenzyl)-3-(3-methylethyl)-5-(quinolin-2-

- ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
 3-[N-(4-chlorobenzyl)-3-cyclopropyl-5-(quinolin-2-ylmethoxy)indol-
 2-yl]-2,2-dimethylpropanoic acid,
 3-[N-(4-chlorobenzyl)-3-(1-methyl-1-cyclopropyl)-5-(quinolin-2-
 5 ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
 3-[N-(4-chlorobenzyl)-3-cyclopentyl-5-(quinolin-2-ylmethoxy)indol-
 2-yl]-2,2-dimethylpropanoic acid,
 3-[N-(4-chlorobenzyl)-3-cyclohexyl-5-(quinolin-2-ylmethoxy)indol-
 2-yl]-2,2-dimethylpropanoic acid,
 10 3-[N-(4-chlorobenzyl)-3-(α , α -dimethylbenzyl)-5-(
 (quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
 3-[N-(4-chlorobenzyl)-3-(2-{4-chloro- α , α -
 dimethylbenzyl})-5-(quinolin-2-ylmethoxy)indol-2-yl]-2,2-
 dimethylpropanoic acid,
 15 3-[N-(4-chlorobenzyl)-3-(1-adamantyl)-5-(quinolin-2-
 ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
 3-[N-(4-chlorobenzyl)-3-((1-adamantyl)methyl)-5-(quinolin-2-
 ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
 3-[N-(1,1-dimethylethyl)-3-(4-chlorobenzyl)-6-(quinolin-2-
 20 ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
 3-[N-(1,1-dimethylpropyl)-3-(4-chlorobenzyl)-6-(quinoline-2-
 ylmethoxy)indol-2-yl]-2,2-dimethylpropanoic acid,
 3-[N-(4-chlorobenzyl)-3-(3,3-dimethyl-1-oxo-1-butyl)-5-(quinolin-2-
 ylmethoxy)indol-2-yl]-2,2-diethylpropanoic acid,
 25 methyl 3-[N-(4-chlorobenzyl)-3,6-bis(acetyl)-5-(quinolin-2-
 ylmethoxy)indol-2-yl]-2,2 dimethyl propanoate or
 methyl 3-[N-(4-chlorobenzyl)-3,6-bis(cyclopropanecarbonyl)-5-
 (quinolin-2-ylmethoxy)indol-2-yl]-2,2-dimethyl propanoate. See EP
 419049 B1, incorporated herein by reference.

30 The term "alkyl" refers to a monovalent group derived from a straight
 or branched chain saturated hydrocarbon by the removal of a single hydrogen

atom. Alkyl groups are exemplified by methyl, ethyl, *n*- and iso-propyl, *n*-,
sec-, iso- and tert-butyl, and the like. The term "hydroxyalkyl" represents an
alkyl group, as defined above, substituted by one to three hydroxyl groups
with the proviso that no more than one hydroxy group may be attached to a
5 single carbon atom of the alkyl group. The term "alkylamino" refers to a
group having the structure -NHR' wherein R' is alkyl, as previously defined,
examples of alkylamino include methylamino, ethylamino, iso-propylamino
and the like. The term "alkylaminocarbonyl" refers to an alkylamino group,
as previously defined, attached to the parent molecular moiety through a
10 carbonyl group. Examples of alkylaminocarbonyl include methylamino-
carbonyl, ethylaminocarbonyl, iso-propylaminocarbonyl and the like. The
term "alkylthio" refers to an alkyl group, as defined above, attached to the
parent molecular moiety through a sulfur atom and includes such examples
as methylthio, ethylthio, propylthio, *n*-, sec- and tert-butylthio and the like.
15 The term "alkanoyl" represents an alkyl group, as defined above, attached to
the parent molecular moiety through a carbonyl group. Alkanoyl groups are
exemplified by formyl, acetyl, propionyl, butanoyl and the like. The term
"alkanoylamino" refers to an alkanoyl group, as previously defined, attached
to the parent molecular moiety through a nitrogen atom. Examples of
20 alkanoylamino include formamido, acetamido, and the like. The term "N-
alkanoyl-N-alkylamino" refers to an alkanoyl group, as previously defined,
attached to the parent molecular moiety through an aminoalkyl group.
Examples of N-alkanoyl-N-alkylamino include N-methylformamido, N-
methyl-acetamido, and the like. The terms "alkoxy" or "alkoxyl" denote an
25 alkyl group, as defined above, attached to the parent molecular moiety
through an oxygen atom. Representative alkoxy groups include methoxyl,
ethoxyl, propoxyl, butoxyl, and the like. The term "alkoxyalkoxyl" refers to
an alkyl group, as defined above, attached through an oxygen to an alkyl
group, as defined above, attached in turn through an oxygen to the parent
30 molecular moiety. Examples of alkoxyalkoxyl include methoxymethoxyl,
methoxyethoxyl, ethoxyethoxyl and the like. The term "alkoxyalkyl" refers

to an alkoxy group, as defined above, attached through an alkylene group to the parent molecular moiety. The term "alkoxycarbonyl" represents an ester group; *i.e.*, an alkoxy group, attached to the parent molecular moiety through a carbonyl group such as methoxycarbonyl, ethoxycarbonyl, and the like.

- 5 The term "alkenyl" denotes a monovalent group derived from a hydrocarbon containing at least one carbon-carbon double bond by the removal of a single hydrogen atom. Alkenyl groups include, for example, ethenyl, propenyl, butenyl, 1-methyl-2-buten-1-yl and the like. The term "alkylene" denotes a divalent group derived from a straight or branched chain saturated
- 10 hydrocarbon by the removal of two hydrogen atoms, for example methylene, 1,2-ethylene, 1,1-ethylene, 1,3-propylene, 2,2-dimethylpropylene, and the like. The term "alkenylene" denotes a divalent group derived from a straight or branched chain hydrocarbon containing at least one carbon-carbon double bond. Examples of alkenylene include $-\text{CH}=\text{CH}-$, $-\text{CH}_2\text{CH}=\text{CH}-$, -
- 15 $\text{C}(\text{CH}_3)=\text{CH}-$, $-\text{CH}_2\text{CH}=\text{CHCH}_2-$, and the like. The term "cycloalkylene" refers to a divalent group derived from a saturated carbocyclic hydrocarbon by the removal of two hydrogen atoms, for example cyclopentylene, cyclohexylene, and the like. The term "cycloalkyl" denotes a monovalent group derived from a monocyclic or bicyclic saturated carbocyclic ring
- 20 compound by the removal of a single hydrogen atom. Examples include cyclopropyl, cyclobutyl, cyclopentyl, cyclohexyl, bicyclo[2.2.1]heptanyl, and bicyclo[2.2.2]octanyl. The term "alkynylene" refers to a divalent group derived by the removal of two hydrogen atoms from a straight or branched chain acyclic hydrocarbon group containing a carbon-carbon triple bond.
- 25 Examples of alkynylene include $-\text{CH}\equiv\text{CH}-$, $-\text{CH}\equiv\text{CH}-\text{CH}_2-$, $-\text{CH}\equiv\text{CH}-\text{CH}(\text{CH}_3)-$, and the like. The term "carbocyclic aryl" denotes a monovalent carbocyclic ring group derived by the removal of a single hydrogen atom from a monocyclic or bicyclic fused or non-fused ring system obeying the "4n+2 p electron" or Huckel aromaticity rule. Examples of carbocyclic aryl
- 30 groups include phenyl, 1- and 2-naphthyl, biphenyl, fluorenyl, and the like. The term "(carbocyclic aryl)alkyl" refers to a carbocyclic aryl ring group as

defined above, attached to the parent molecular moiety through an alkylene group. Representative (carbocyclic aryl)alkyl groups include phenylmethyl, phenylethyl, phenylpropyl, 1-naphthylmethyl, and the like. The term "carbocyclicarylalkoxy" refers to a carbocyclicaryl alkyl group, as defined

5 above, attached to the parent molecular moiety through an oxygen atom. The term "carbocyclic aryloxyalkyl" refers to a carbocyclic aryl group, as defined above, attached to the parent molecular moiety through an oxygen atom and thence through an alkylene group. Such groups are exemplified by phenoxymethyl, 1- and 2-naphthylloxymethyl, phenoxyethyl and the like.

10 The term "(carbocyclic aryl)alkoxyalkyl" denotes a carbocyclic aryl group as defined above, attached to the parent molecular moiety through an alkoxyalkyl group. Representative (carbocyclic aryl)alkoxyalkyl groups include phenylmethoxymethyl, phenylethoxymethyl, 1- and 2-naphthylmethoxyethyl, and the like. "Carbocyclic arylthioalkyl" represents a

15 carbocyclic aryl group as defined above, attached to the parent molecular moiety through a sulfur atom and thence through an alkylene group and are typified by phenylthiomethyl, 1- and 2-naphthylthioethyl and the like. The term "dialkylamino" refers to a group having the structure -NR'R" wherein R' and R" are independently selected from alkyl, as previously defined.

20 Additionally, R' and R" taken together may optionally be -(CH₂)_{kk} -- where kk is an integer of from 2 to 6. Examples of dialkylamino include, dimethylamino, diethylaminocarbonyl, methylethylamino, piperidino, and the like. The term "halo or halogen" denotes fluorine, chlorine, bromine or iodine. The term "haloalkyl" denotes an alkyl group, as defined above,

25 having one, two, or three halogen atoms attached thereto and is exemplified by such groups as chloromethyl, bromoethyl, trifluoromethyl, and the like. The term "hydroxyalkyl" represents an alkyl group, as defined above, substituted by one to three hydroxyl groups with the proviso that no more than one hydroxy group may be attached to a single carbon atom of the alkyl

30 group. The term "phenoxy" refers to a phenyl group attached to the parent molecular moiety through an oxygen atom. The term "phenylthio" refers to a

phenyl group attached to the parent molecular moiety through a sulfur atom. The term "pyridyloxy" refers to a pyridyl group attached to the parent molecular moiety through an oxygen atom. The terms "heteroaryl" or "heterocyclic aryl" as used herein refers to substituted or unsubstituted 5- or 6-membered ring aromatic groups containing one oxygen atom, one, two, three, or four nitrogen atoms, one nitrogen and one sulfur atom, or one nitrogen and one oxygen atom. The term heteroaryl also includes bi- or tricyclic groups in which the aromatic heterocyclic ring is fused to one or two benzene rings. Representative heteroaryl groups are pyridyl, thienyl, indolyl, pyrazinyl, isoquinolyl, pyrrolyl, pyrimidyl, benzothienyl, furyl, benzo[b]furyl, imidazolyl, thiazolyl, carbazolyl, and the like. The term "heteroarylalkyl" denotes a heteroaryl group, as defined above, attached to the parent molecular moiety through an alkylene group. The term "heteroaryloxy" denotes a heteroaryl group, as defined above, attached to the parent molecular moiety through an oxygen atom. The term "heteroarylalkoxy" denotes a heteroarylalkyl group, as defined above, attached to the parent molecular moiety through an oxygen atom.

NUCLEIC ACID THERAPEUTIC AGENTS

In another embodiment, a nucleic acid of the invention; a nucleic acid complementary to a nucleic acid of the invention; or a portion of such a nucleic acid (*e.g.*, an oligonucleotide as described below); or a nucleic acid encoding a member of the leukotriene pathway (*e.g.*, 5-LO), can be used in "antisense" therapy, in which a nucleic acid (*e.g.*, an oligonucleotide) which specifically hybridizes to the mRNA and/or genomic DNA of a nucleic acid is administered or generated *in situ*. The antisense nucleic acid that specifically hybridizes to the mRNA and/or DNA inhibits expression of the polypeptide encoded by that mRNA and/or DNA, *e.g.*, by inhibiting translation and/or transcription. Binding of the antisense nucleic acid can be by conventional base pair complementarity, or, for example, in the case of

binding to DNA duplexes, through specific interaction in the major groove of the double helix.

An antisense construct can be delivered, for example, as an expression plasmid as described above. When the plasmid is transcribed in the cell, it produces RNA that is complementary to a portion of the mRNA and/or DNA that encodes the polypeptide for the member of the leukotriene pathway (*e.g.*, FLAP or 5-LO). Alternatively, the antisense construct can be an oligonucleotide probe that is generated *ex vivo* and introduced into cells; it then inhibits expression by hybridizing with the mRNA and/or genomic DNA of the polypeptide. In one embodiment, the oligonucleotide probes are modified oligonucleotides that are resistant to endogenous nucleases, *e.g.*, exonucleases and/or endonucleases, thereby rendering them stable *in vivo*. Exemplary nucleic acid molecules for use as antisense oligonucleotides are phosphoramidate, phosphothioate and methylphosphonate analogs of DNA (see also U.S. Pat. Nos. 5,176,996, 5,264,564 and 5,256,775). Additionally, general approaches to constructing oligomers useful in antisense therapy are also described, for example, by Van der Krol *et al.* (*Biotechniques* 6:958-976 (1988)); and Stein *et al.* (*Cancer Res.* 48:2659-2668 (1988)). With respect to antisense DNA, oligodeoxyribonucleotides derived from the translation initiation site are preferred.

To perform antisense therapy, oligonucleotides (mRNA, cDNA or DNA) are designed that are complementary to mRNA encoding the polypeptide. The antisense oligonucleotides bind to mRNA transcripts and prevent translation. Absolute complementarity, although preferred, is not required. A sequence "complementary" to a portion of an RNA, as referred to herein, indicates that a sequence has sufficient complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double-stranded antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid, as described in detail above. Generally, the longer the

hybridizing nucleic acid, the more base mismatches with an RNA it may contain and still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures.

5 The oligonucleotides used in antisense therapy can be DNA, RNA, or chimeric mixtures or derivatives or modified versions thereof, single-stranded or double-stranded. The oligonucleotides can be modified at the base moiety, sugar moiety, or phosphate backbone, for example, to improve stability of the molecule, hybridization, etc. The oligonucleotides can
10 include other appended groups such as peptides (*e.g.* for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, *Proc. Natl. Acad. Sci. USA* 86:6553-6556 (1989); Lemaitre *et al.*, *Proc. Natl. Acad. Sci. USA* 84:648-652 (1987); PCT International Publication No. WO 88/09810) or the blood-brain barrier (see,
15 *e.g.*, PCT International Publication No. WO 89/10134), or hybridization-triggered cleavage agents (see, *e.g.*, Krol *et al.*, *BioTechniques* 6:958-976 (1988)) or intercalating agents. (See, *e.g.*, Zon, *Pharm.Res.* 5: 539-549 (1988)). To this end, the oligonucleotide may be conjugated to another molecule (*e.g.*, a peptide, hybridization triggered cross-linking agent,
20 transport agent, hybridization-triggered cleavage agent).

 The antisense molecules are delivered to cells that express the member of the leukotriene pathway *in vivo*. A number of methods can be used for delivering antisense DNA or RNA to cells; *e.g.*, antisense molecules can be injected directly into the tissue site, or modified antisense molecules,
25 designed to target the desired cells (*e.g.*, antisense linked to peptides or antibodies that specifically bind receptors or antigens expressed on the target cell surface) can be administered systematically. Alternatively, in a preferred embodiment, a recombinant DNA construct is utilized in which the antisense oligonucleotide is placed under the control of a strong promoter
30 (*e.g.*, pol III or pol II). The use of such a construct to transfect target cells in the patient results in the transcription of sufficient amounts of single stranded

5 RNAs that will form complementary base pairs with the endogenous transcripts and thereby prevent translation of the mRNA. For example, a vector can be introduced *in vivo* such that it is taken up by a cell and directs the transcription of an antisense RNA. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art and described above. For example, a plasmid, cosmid, YAC or viral vector can be used to prepare the recombinant DNA construct that can be introduced directly into the tissue site. Alternatively, viral vectors can be used which selectively infect the desired tissue, in which case administration may be accomplished by another route (*e.g.*, systemically).

15 In another embodiment of the invention, small double-stranded interfering RNA (RNA interference (RNAi)) can be used. RNAi is a post-transcription process, in which double-stranded RNA is introduced, and sequence-specific gene silencing results, through catalytic degradation of the targeted mRNA. See, *e.g.*, Elbashir, S.M. *et al.*, *Nature* 411:494-498 (2001); Lee, N.S., *Nature Biotech.* 19:500-505 (2002); Lee, S-K. *et al.*, *Nature Medicine* 8(7):681-686 (2002); the entire teachings of these references are incorporated herein by reference.

20 Endogenous expression of a member of the leukotriene pathway (*e.g.*, FLAP, 5-LO) can also be reduced by inactivating or “knocking out” the gene or its promoter using targeted homologous recombination (*e.g.*, see Smithies *et al.*, *Nature* 317:230-234 (1985); Thomas & Capecchi, *Cell* 51:503-512 (1987); Thompson *et al.*, *Cell* 5:313-321 (1989)). For example, an altered, non-functional gene of a member of the leukotriene pathway (or a completely unrelated DNA sequence) flanked by DNA homologous to the endogenous gene (either the coding regions or regulatory regions of the gene) can be used, with or without a selectable marker and/or a negative selectable marker, to transfect cells that express the gene *in vivo*. Insertion of the DNA construct, via targeted homologous recombination, results in

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inactivation of the gene. The recombinant DNA constructs can be directly administered or targeted to the required site *in vivo* using appropriate vectors, as described above. Alternatively, expression of non-altered genes can be increased using a similar method: targeted homologous recombination can be used to insert a DNA construct comprising a non-altered functional gene, or the complement thereof, or a portion thereof, in place of an gene in the cell, as described above. In another embodiment, targeted homologous recombination can be used to insert a DNA construct comprising a nucleic acid that encodes a polypeptide variant that differs from that present in the cell.

Alternatively, endogenous expression of a member of the leukotriene pathway can be reduced by targeting deoxyribonucleotide sequences complementary to the regulatory region of the member of the leukotriene pathway (*i.e.*, the promoter and/or enhancers) to form triple helical structures that prevent transcription of the gene in target cells in the body. (See generally, Helene, C., *Anticancer Drug Des.*, 6(6):569-84 (1991); Helene, C. *et al.*, *Ann. N.Y. Acad. Sci.* 660:27-36 (1992); and Maher, L. J., *Bioassays* 14(12):807-15 (1992)). Likewise, the antisense constructs described herein, by antagonizing the normal biological activity of one of the members of the leukotriene pathway, can be used in the manipulation of tissue, *e.g.*, tissue differentiation, both *in vivo* and *for ex vivo* tissue cultures. Furthermore, the anti-sense techniques (*e.g.*, microinjection of antisense molecules, or transfection with plasmids whose transcripts are anti-sense with regard to a nucleic acid RNA or nucleic acid sequence) can be used to investigate the role of one or more members of the leukotriene pathway in the development of disease-related conditions. Such techniques can be utilized in cell culture, but can also be used in the creation of transgenic animals.

The therapeutic agents as described herein can be delivered in a composition, as described above, or by themselves. They can be administered systemically, or can be targeted to a particular tissue. The therapeutic agents can be produced by a variety of means, including

chemical synthesis; recombinant production; *in vivo* production (*e.g.*, a transgenic animal, such as U.S. Pat. No. 4,873,316 to Meade *et al.*), for example, and can be isolated using standard means such as those described herein. In addition, a combination of any of the above methods of treatment
5 (*e.g.*, administration of non-altered polypeptide in conjunction with antisense therapy targeting altered mRNA for a member of the leukotriene pathway; administration of a first splicing variant in conjunction with antisense therapy targeting a second splicing variant) can also be used.

The invention additionally pertains to use of such therapeutic agents,
10 as described herein, for the manufacture of a medicament for the treatment of MI, ACS, stroke, PAOD and/or atherosclerosis, *e.g.*, using the methods described herein.

MONITORING PROGRESS OF TREATMENT

15 The current invention also pertains to methods of monitoring the response of an individual, such as an individual in one of the target populations described above, to treatment with a leukotriene synthesis inhibitor.

Because the level of inflammatory markers can be elevated in
20 individuals who are in the target populations described above, an assessment of the level of inflammatory markers of the individual both before, and during, treatment with the leukotriene synthesis inhibitor will indicate whether the treatment has successfully decreased production of leukotrienes in the arterial vessel wall or in bone-marrow derived inflammatory cells. For
25 example, in one embodiment of the invention, an individual who is a member of a target population as described above (*e.g.*, an individual at risk for MI, ACS, stroke or PAOD, such as an individual who is at-risk due to a FLAP haplotype) can be assessed for response to treatment with a leukotriene synthesis inhibitor, by examining leukotriene levels or
30 leukotriene metabolite levels in the individual. Blood, serum, plasma or urinary leukotrienes (*e.g.*, leukotriene E4, cysteinyl leukotriene 1), or *ex vivo*

production of leukotrienes (*e.g.*, in blood samples stimulated with a calcium ionophore to produce leukotrienes), or leukotriene metabolites, can be measured before, and during or after treatment with the leukotriene synthesis inhibitor. The leukotriene or leukotriene metabolite level before treatment is compared with the leukotriene or leukotriene metabolite level during or after treatment. The efficacy of treatment is indicated by a decrease in leukotriene production: a level of leukotriene or leukotriene metabolite during or after treatment that is significantly lower than the level of leukotriene or leukotriene metabolite before treatment, is indicative of efficacy. A level that is lower during or after treatment can be shown, for example, by decreased serum or urinary leukotrienes, or decreased *ex vivo* production of leukotrienes, or decreased leukotriene metabolites. A level that is “significantly lower”, as used herein, is a level that is less than the amount that is typically found in control individual(s), or is less in a comparison of disease risk in a population associated with the other bands of measurement (*e.g.*, the mean or median, the highest quartile or the highest quintile) compared to lower bands of measurement (*e.g.*, the mean or median, the other quartiles; the other quintiles).

For example, in one embodiment of the invention, the level of a leukotriene or leukotriene metabolite is assessed in an individual before treatment with a leukotriene synthesis inhibitor; and during or after treatment with the leukotriene synthesis inhibitor, and the levels are compared. A level of the leukotriene or leukotriene metabolite during or after treatment that is significantly lower than the level of the leukotriene or leukotriene metabolite before treatment, is indicative of efficacy of treatment with the leukotriene synthesis inhibitor. In another embodiment, production of a leukotriene or a leukotriene metabolite is stimulated in a first test sample from the individual, using a calcium ionophore, before treatment with a leukotriene synthesis inhibitor, and is also stimulated in a second test sample from the individual, using a calcium ionophore, during or after treatment with the leukotriene synthesis inhibitor, and the level of production in the first test sample is

compared with with the level of production of the leukotriene or leukotriene metabolite in the second test sample. A level of the leukotriene or leukotriene metabolite in the second test sample that is significantly lower than the level of the leukotriene or leukotriene metabolite in the first test sample, is indicative of efficacy of treatment with the leukotriene synthesis inhibitor.

In another embodiment of the invention, an individual who is a member of a target population of individuals at risk for MI, ACS, stroke or PAOD (*e.g.*, an individual in a target population described above, such as an individual at-risk due to elevated C-reactive protein) can be assessed for response to treatment with a leukotriene synthesis inhibitor, by examining levels of inflammatory markers in the individual. For example, levels of an inflammatory marker in an appropriate test sample (*e.g.*, serum, plasma or urine) can be measured before, and during or after treatment with the leukotriene synthesis inhibitor. The level of the inflammatory marker before treatment is compared with the level of the inflammatory marker during or after treatment. The efficacy of treatment is indicated by a decrease in the level of the inflammatory marker, that is, a level of the inflammatory marker during or after treatment that is significantly lower (*e.g.*, significantly lower), than the level of inflammatory marker before treatment, is indicative of efficacy. Representative inflammatory markers include: C-reactive protein (CRP), serum amyloid A, fibrinogen, a leukotriene, a leukotriene metabolite (*e.g.*, cysteinyl leukotriene 1), interleukin-6, tissue necrosis factor-alpha, soluble vascular cell adhesion molecules (sVCAM), soluble intervascular adhesion molecules (sICAM), E-selectin, matrix metalloprotease type-1, matrix metalloprotease type-2, matrix metalloprotease type-3, matrix metalloprotease type-9, myeloperoxidase (MPO), and N-tyrosine. In a preferred embodiment, the marker is CRP or MPO.

ASSESSMENT OF INCREASED RISK

The present invention additionally pertains to methods for assessing an individual (e.g., an individual who is in a target population as described herein, such as an individual who is at risk for MI, ACS, stroke or PAOD),
5 for for an increased risk of MI, ACS, atherosclerosis, stroke, transient ischemic attack, transient monocular blindness, asymptomatic carotid stenosis, PAOD, claudication, or limb ischemia. The methods comprise assessing the level of a leukotriene metabolite (e.g., LTE4, LTD4, LTB4) in the individual, wherein an increased level of leukotriene metabolite is
10 indicative of an increased risk. The level can be measured in any appropriate tissue or fluid sample, such as blood, serum, plasma, or urine. In one particular embodiment, the sample comprises neutrophils. The level of the leukotriene metabolite can be measured by standard methods, such as the methods described herein. For example, in one embodiment, production of a
15 leukotriene metabolite is stimulated in a first test sample from the individual, using a calcium ionophore. The level of production is compared with a control level. The control level is a level that is typically found in control individual(s), such as individual who are not at risk for MI, ACS, stroke or PAOD; alternatively, a control level is the level that is found by comparison
20 of disease risk in a population associated with the lowest band of measurement (e.g., below the mean or median, the lowest quartile or the lowest quintile) compared to higher bands of measurement (e.g., above the mean or median, the second, third or fourth quartile; the second, third, fourth or fifth quintile). A level of production of the leukotriene metabolite that is
25 significantly greater than the control level, is indicative of an increased risk. Individuals at increased risk are candidates for treatments described herein.

PHARMACEUTICAL COMPOSITIONS

The present invention also pertains to pharmaceutical compositions
30 comprising agents described herein, for example, an agent that is a

leukotriene synthesis inhibitor as described herein. For instance, a leukotriene synthesis inhibitor can be formulated with a physiologically acceptable carrier or excipient to prepare a pharmaceutical composition. The carrier and composition can be sterile. The formulation should suit the mode of administration.

Suitable pharmaceutically acceptable carriers include but are not limited to water, salt solutions (*e.g.*, NaCl), saline, buffered saline, alcohols, glycerol, ethanol, gum arabic, vegetable oils, benzyl alcohols, polyethylene glycols, gelatin, carbohydrates such as lactose, amylose or starch, dextrose, magnesium stearate, talc, silicic acid, viscous paraffin, perfume oil, fatty acid esters, hydroxymethylcellulose, polyvinyl pyrrolidone, etc., as well as combinations thereof. The pharmaceutical preparations can, if desired, be mixed with auxiliary agents, *e.g.*, lubricants, preservatives, stabilizers, wetting agents, emulsifiers, salts for influencing osmotic pressure, buffers, coloring, flavoring and/or aromatic substances and the like which do not deleteriously react with the active agents.

The composition, if desired, can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents. The composition can be a liquid solution, suspension, emulsion, tablet, pill, capsule, sustained release formulation, or powder. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides. Oral formulation can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, polyvinyl pyrrolidone, sodium saccharine, cellulose, magnesium carbonate, etc.

Methods of introduction of these compositions include, but are not limited to, intradermal, intramuscular, intraperitoneal, intraocular, intravenous, subcutaneous, topical, oral and intranasal. Other suitable methods of introduction can also include gene therapy (as described below), rechargeable or biodegradable devices, particle acceleration devices ("gene guns") and slow release polymeric devices. The pharmaceutical

compositions of this invention can also be administered as part of a combinatorial therapy with other agents.

The composition can be formulated in accordance with the routine procedures as a pharmaceutical composition adapted for administration to human beings. For example, compositions for intravenous administration typically are solutions in sterile isotonic aqueous buffer. Where necessary, the composition may also include a solubilizing agent and a local anesthetic to ease pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water free concentrate in a hermetically sealed container such as an ampule or sachette indicating the quantity of active agent. Where the composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water, saline or dextrose/water. Where the composition is administered by injection, an ampule of sterile water for injection or saline can be provided so that the ingredients may be mixed prior to administration.

For topical application, nonsprayable forms, viscous to semi-solid or solid forms comprising a carrier compatible with topical application and having a dynamic viscosity preferably greater than water, can be employed. Suitable formulations include but are not limited to solutions, suspensions, emulsions, creams, ointments, powders, enemas, lotions, sols, liniments, salves, aerosols, etc., which are, if desired, sterilized or mixed with auxiliary agents, *e.g.*, preservatives, stabilizers, wetting agents, buffers or salts for influencing osmotic pressure, etc. The agent may be incorporated into a cosmetic formulation. For topical application, also suitable are sprayable aerosol preparations wherein the active ingredient, preferably in combination with a solid or liquid inert carrier material, is packaged in a squeeze bottle or in admixture with a pressurized volatile, normally gaseous propellant, *e.g.*, pressurized air.

Agents described herein can be formulated as neutral or salt forms.

Pharmaceutically acceptable salts include those formed with free amino groups such as those derived from hydrochloric, phosphoric, acetic, oxalic, tartaric acids, etc., and those formed with free carboxyl groups such as those derived from sodium, potassium, ammonium, calcium, ferric hydroxides, isopropylamine, triethylamine, 2-ethylamino ethanol, histidine, procaine, etc.

The agents are administered in a therapeutically effective amount. The amount of agents which will be therapeutically effective in the treatment of a particular disorder or condition will depend on the nature of the disorder or condition, and can be determined by standard clinical techniques. In addition, *in vitro* or *in vivo* assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the symptoms, and should be decided according to the judgment of a practitioner and each patient's circumstances. Effective doses may be extrapolated from dose-response curves derived from *in vitro* or animal model test systems.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Optionally associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration. The pack or kit can be labeled with information regarding mode of administration, sequence of drug administration (*e.g.*, separately, sequentially or concurrently), or the like. The pack or kit may also include means for reminding the patient to take the therapy. The pack or kit can be a single unit dosage of the combination therapy or it can be a plurality of unit dosages. In particular, the agents can be separated, mixed together in any combination, present in a single vial or tablet. Agents assembled in a blister pack or other dispensing means is preferred. For the purpose of this invention, unit dosage is intended to mean

a dosage that is dependent on the individual pharmacodynamics of each agent and administered in FDA approved dosages in standard time courses.

NUCLEIC ACIDS OF THE INVENTION

5 *FLAP Nucleic Acids, Portions and Variants*

In addition, the invention pertains to isolated nucleic acid molecules comprising a human FLAP nucleic acid. The term, "FLAP nucleic acid," as used herein, refers to an isolated nucleic acid molecule encoding FLAP
10 polypeptide. The FLAP nucleic acid molecules of the present invention can be RNA, for example, mRNA, or DNA, such as cDNA and genomic DNA. DNA molecules can be double-stranded or single-stranded; single stranded RNA or DNA can be either the coding, or sense strand or the non-coding, or antisense strand. The nucleic acid molecule can include all or a portion of
15 the coding sequence of the gene or nucleic acid and can further comprise additional non-coding sequences such as introns and non-coding 3' and 5' sequences (including regulatory sequences, for example, as well as promoters, transcription enhancement elements, splice donor/acceptor sites, etc.).

20 For example, a FLAP nucleic acid can consist of SEQ ID NOs: 1 or 3 or the complement thereof, or to a portion or fragment of such an isolated nucleic acid molecule (*e.g.*, cDNA or the nucleic acid) that encodes FLAP polypeptide (*e.g.*, a polypeptide such as SEQ ID NO: 2). In a preferred embodiment, the isolated nucleic acid molecule comprises a nucleic acid
25 molecule selected from the group consisting of SEQ ID NOs: 1 or 3, or their complement thereof.

Additionally, the nucleic acid molecules of the invention can be fused to a marker sequence, for example, a sequence that encodes a polypeptide to assist in isolation or purification of the polypeptide. Such sequences include,
30 but are not limited to, those that encode a glutathione-S-transferase (GST)

fusion protein and those that encode a hemagglutinin A (HA) polypeptide marker from influenza.

5 An "isolated" nucleic acid molecule, as used herein, is one that is separated from nucleic acids that normally flank the gene or nucleic acid sequence (as in genomic sequences) and/or has been completely or partially purified from other transcribed sequences (*e.g.*, as in an RNA library). For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs, or culture medium when produced by recombinant techniques, or
10 chemical precursors or other chemicals when chemically synthesized. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstances, the material may be purified to essential homogeneity, for example as determined by PAGE or column
15 chromatography such as HPLC. In certain embodiments, an isolated nucleic acid molecule comprises at least about 50, 80 or 90% (on a molar basis) of all macromolecular species present. With regard to genomic DNA, the term "isolated" also can refer to nucleic acid molecules that are separated from the chromosome with which the genomic DNA is naturally associated. For
20 example, the isolated nucleic acid molecule can contain less than about 5 kb, including but not limited to 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotides which flank the nucleic acid molecule in the genomic DNA of the cell from which the nucleic acid molecule is derived.

The nucleic acid molecule can be fused to other coding or regulatory
25 sequences and still be considered isolated. Thus, recombinant DNA contained in a vector is included in the definition of "isolated" as used herein. Also, isolated nucleic acid molecules include recombinant DNA molecules in heterologous host cells, as well as partially or substantially purified DNA molecules in solution. "Isolated" nucleic acid molecules also
30 encompass *in vivo* and *in vitro* RNA transcripts of the DNA molecules of the present invention. An isolated nucleic acid molecule or nucleic acid

sequence can include a nucleic acid molecule or nucleic acid sequence that is synthesized chemically or by recombinant means. Therefore, recombinant DNA contained in a vector is included in the definition of "isolated" as used herein. Also, isolated nucleotide sequences include recombinant DNA
5 molecules in heterologous organisms, as well as partially or substantially purified DNA molecules in solution. *In vivo* and *in vitro* RNA transcripts of the DNA molecules of the present invention are also encompassed by "isolated" nucleotide sequences. Such isolated nucleotide sequences are useful in the manufacture of the encoded polypeptide, as probes for isolating
10 homologous sequences (*e.g.*, from other mammalian species), for gene mapping (*e.g.*, by *in situ* hybridization with chromosomes), or for detecting expression of the nucleic acid in tissue (*e.g.*, human tissue), such as by Northern blot analysis.

The present invention also pertains to nucleic acid molecules which
15 are not necessarily found in nature but which encode a FLAP polypeptide (*e.g.*, a polypeptide having an amino acid sequence comprising an amino acid sequence of SEQ ID NOs: 2), or another splicing variant of a FLAP polypeptide or polymorphic variant thereof. Thus, for example, DNA
20 molecules that comprise a sequence that is different from the naturally occurring nucleic acid sequence but which, due to the degeneracy of the genetic code, encode a FLAP polypeptide of the present invention are also the subjects of this invention. The invention also encompasses nucleotide sequences encoding portions (fragments), or encoding variant polypeptides such as analogues or derivatives of a FLAP polypeptide. Such variants can
25 be naturally occurring, such as in the case of allelic variation or single nucleotide polymorphisms, or non-naturally-occurring, such as those induced by various mutagens and mutagenic processes. Intended variations include, but are not limited to, addition, deletion and substitution of one or more nucleotides that can result in conservative or non-conservative amino
30 acid changes, including additions and deletions. Preferably the nucleotide (and/or resultant amino acid) changes are silent or conserved; that is, they

do not alter the characteristics or activity of a FLAP polypeptide. In one preferred embodiment, the nucleotide sequences are fragments that comprise one or more polymorphic microsatellite markers. In another preferred embodiment, the nucleotide sequences are fragments that
5 comprise one or more single nucleotide polymorphisms in a FLAP nucleic acid (*e.g.*, the single nucleotide polymorphisms set forth in Table 3, below).

Other alterations of the nucleic acid molecules of the invention can include, for example, labeling, methylation, internucleotide modifications such as uncharged linkages (*e.g.*, methyl phosphonates, phosphotriesters, phosphoamidates, carbamates), charged linkages (*e.g.*, phosphorothioates, phosphorodithioates), pendent moieties (*e.g.*, polypeptides), intercalators
10 (*e.g.*, acridine, psoralen), chelators, alkylators, and modified linkages (*e.g.*, alpha anomeric nucleic acids). Also included are synthetic molecules that mimic nucleic acid molecules in the ability to bind to a designated sequence via hydrogen bonding and other chemical interactions. Such molecules
15 include, for example, those in which peptide linkages substitute for phosphate linkages in the backbone of the molecule.

The invention also pertains to nucleic acid molecules that hybridize under high stringency hybridization conditions, such as for selective
20 hybridization, to a nucleic acid sequence described herein (*e.g.*, nucleic acid molecules which specifically hybridize to a nucleic acid sequence encoding polypeptides described herein, and, optionally, have an activity of the polypeptide). In one embodiment, the invention includes variants described herein which hybridize under high stringency hybridization conditions (*e.g.*,
25 for selective hybridization) to a nucleic acid sequence comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1 or 3 or the complement thereof. In another embodiment, the invention includes variants described herein which hybridize under high stringency hybridization conditions (*e.g.*, for selective hybridization) to a nucleic acid
30 sequence encoding an amino acid sequence of SEQ ID NO: 2 or a

polymorphic variant thereof. In a preferred embodiment, the variant that hybridizes under high stringency hybridizations has an activity of a FLAP.

Such nucleic acid molecules can be detected and/or isolated by specific hybridization (*e.g.*, under high stringency conditions). “Specific hybridization,” as used herein, refers to the ability of a first nucleic acid to hybridize to a second nucleic acid in a manner such that the first nucleic acid does not hybridize to any nucleic acid other than to the second nucleic acid (*e.g.*, when the first nucleic acid has a higher similarity to the second nucleic acid than to any other nucleic acid in a sample wherein the hybridization is to be performed). “Stringency conditions” for hybridization is a term of art which refers to the incubation and wash conditions, *e.g.*, conditions of temperature and buffer concentration, which permit hybridization of a particular nucleic acid to a second nucleic acid; the first nucleic acid may be perfectly (*i.e.*, 100%) complementary to the second, or the first and second may share some degree of complementarity that is less than perfect (*e.g.*, 70%, 75%, 85%, 95%). For example, certain high stringency conditions can be used which distinguish perfectly complementary nucleic acids from those of less complementarity. “High stringency conditions”, “moderate stringency conditions” and “low stringency conditions” for nucleic acid hybridizations are explained on pages 2.10.1-2.10.16 and pages 6.3.1-6.3.6 in *Current Protocols in Molecular Biology* (Ausubel, F.M. *et al.*, “*Current Protocols in Molecular Biology*”, John Wiley & Sons, (1998), the entire teachings of which are incorporated by reference herein). The exact conditions which determine the stringency of hybridization depend not only on ionic strength (*e.g.*, 0.2X SSC, 0.1X SSC), temperature (*e.g.*, room temperature, 42°C, 68°C) and the concentration of destabilizing agents such as formamide or denaturing agents such as SDS, but also on factors such as the length of the nucleic acid sequence, base composition, percent mismatch between hybridizing sequences and the frequency of occurrence of subsets of that sequence within other non-identical sequences. Thus, equivalent conditions can be determined by varying one or more of these parameters

while maintaining a similar degree of identity or similarity between the two nucleic acid molecules. Typically, conditions are used such that sequences at least about 60%, at least about 70%, at least about 80%, at least about 90% or at least about 95% or more identical to each other remain hybridized to one another. By varying hybridization conditions from a level of stringency at which no hybridization occurs to a level at which hybridization is first observed, conditions which will allow a given sequence to hybridize (*e.g.*, selectively) with the most similar sequences in the sample can be determined.

Exemplary conditions are described in Krause, M.H. and S.A. Aaronson, *Methods in Enzymology* 200: 546-556 (1991), and in, Ausubel, *et al.*, "*Current Protocols in Molecular Biology*", John Wiley & Sons, (1998), which describes the determination of washing conditions for moderate or low stringency conditions. Washing is the step in which conditions are usually set so as to determine a minimum level of complementarity of the hybrids. Generally, starting from the lowest temperature at which only homologous hybridization occurs, each °C by which the final wash temperature is reduced (holding SSC concentration constant) allows an increase by 1% in the maximum extent of mismatching among the sequences that hybridize. Generally, doubling the concentration of SSC results in an increase in T_m of -17°C. Using these guidelines, the washing temperature can be determined empirically for high, moderate or low stringency, depending on the level of mismatch sought.

For example, a low stringency wash can comprise washing in a solution containing 0.2X SSC/0.1% SDS for 10 minutes at room temperature; a moderate stringency wash can comprise washing in a prewarmed solution (42°C) solution containing 0.2X SSC/0.1% SDS for 15 minutes at 42°C; and a high stringency wash can comprise washing in prewarmed (68°C) solution containing 0.1X SSC/0.1%SDS for 15 minutes at 68°C. Furthermore, washes can be performed repeatedly or sequentially to obtain a desired result as known in the art. Equivalent conditions can be

determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleic acid molecule and the primer or probe used.

5 The percent homology or identity of two nucleotide or amino acid sequences can be determined by aligning the sequences for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of a first sequence for optimal alignment). The nucleotides or amino acids at corresponding positions are then compared, and the percent identity between
10 the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % identity = # of identical positions/total # of positions x 100). When a position in one sequence is occupied by the same nucleotide or amino acid residue as the corresponding position in the other sequence, then the molecules are homologous at that position. As used
15 herein, nucleic acid or amino acid “homology” is equivalent to nucleic acid or amino acid “identity”. In certain embodiments, the length of a sequence aligned for comparison purposes is at least 30%, for example, at least 40%, in certain embodiments at least 60%, and in other embodiments at least 70%, 80%, 90% or 95% of the length of the reference sequence. The actual
20 comparison of the two sequences can be accomplished by well-known methods, for example, using a mathematical algorithm. A preferred, non-limiting example of such a mathematical algorithm is described in Karlin *et al.*, *Proc. Natl. Acad. Sci. USA* 90:5873-5877 (1993). Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) as
25 described in Altschul *et al.*, *Nucleic Acids Res.* 25:389-3402 (1997). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (*e.g.*, NBLAST) can be used. In one embodiment, parameters for sequence comparison can be set at score=100, wordlength=12, or can be varied (*e.g.*, W=5 or W=20).

30 Another preferred, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and

Miller, *CABIOS* 4(1): 11-17 (1988). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package (Accelrys, Cambridge, UK). When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight
5 residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art and include ADVANCE and ADAM as described in Torellis and Robotti, *Comput. Appl. Biosci.* 10:3-5 (1994); and FASTA described in Pearson and Lipman, *Proc. Natl. Acad. Sci. USA* 85:2444-8 (1988).

10 In another embodiment, the percent identity between two amino acid sequences can be accomplished using the GAP program in the GCG software package using either a BLOSUM63 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. In yet another embodiment, the percent identity between two nucleic acid sequences can be
15 accomplished using the GAP program in the GCG software package using a gap weight of 50 and a length weight of 3.

The present invention also provides isolated nucleic acid molecules that contain a fragment or portion that hybridizes under highly stringent conditions to a nucleic acid sequence comprising SEQ ID NO: 1 or 3 or the
20 complement of SEQ ID NO: 1 or 3, and also provides isolated nucleic acid molecules that contain a fragment or portion that hybridizes under highly stringent conditions to a nucleic acid sequence encoding an amino acid sequence of the invention or polymorphic variant thereof. The nucleic acid fragments of the invention are at least about 15, for example, at least about
25 18, 20, 23 or 25 nucleotides, and can be 30, 40, 50, 100, 200 or more nucleotides in length. Longer fragments, for example, 30 or more nucleotides in length, encoding antigenic polypeptides described herein are particularly useful, such as for the generation of antibodies as described below.

Probes and Primers

In a related aspect, the nucleic acid fragments of the invention are used as probes or primers in assays such as those described herein. “Probes” or “primers” are oligonucleotides that hybridize in a base-specific manner to a complementary strand of nucleic acid molecules. Such probes and primers include polypeptide nucleic acids, as described in Nielsen *et al.* (*Science* 254:1497-1500 (1991)).

A probe or primer comprises a region of nucleic acid that hybridizes to at least about 15, for example about 20-25, and in certain embodiments about 40, 50 or 75, consecutive nucleotides of a nucleic acid of the invention, such as a nucleic acid comprising a contiguous nucleic acid sequence of SEQ ID NOs: 1 or 3 or the complement of SEQ ID Nos: 1 or 3, or a nucleic acid sequence encoding an amino acid sequence of SEQ ID NO: 2 or polymorphic variant thereof. In preferred embodiments, a probe or primer comprises 100 or fewer nucleotides, in certain embodiments, from 6 to 50 nucleotides, for example, from 12 to 30 nucleotides. In other embodiments, the probe or primer is at least 70% identical to the contiguous nucleic acid sequence or to the complement of the contiguous nucleotide sequence, for example, at least 80% identical, in certain embodiments at least 90% identical, and in other embodiments at least 95% identical, or even capable of selectively hybridizing to the contiguous nucleic acid sequence or to the complement of the contiguous nucleotide sequence. Often, the probe or primer further comprises a label, *e.g.*, radioisotope, fluorescent compound, enzyme, or enzyme co-factor.

The nucleic acid molecules of the invention such as those described above can be identified and isolated using standard molecular biology techniques and the sequence information provided herein. For example, nucleic acid molecules can be amplified and isolated using the polymerase chain reaction and synthetic oligonucleotide primers based on one or more of SEQ ID NOs: 1 or 3, or the complement thereof, or designed based on nucleotides based on sequences encoding one or more of the amino acid

sequences provided herein. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (Eds. Innis *et al.*, Academic Press, San Diego, CA, 1990); Mattila *et al.*, *Nucl. Acids Res.* 19:4967 (1991); Eckert *et al.*, *PCR Methods and Applications* 1:17 (1991); PCR (eds. McPherson *et al.*, IRL Press, Oxford); and U.S. Patent 4,683,202. The nucleic acid molecules can be amplified using cDNA, mRNA or genomic DNA as a template, cloned into an appropriate vector and characterized by DNA sequence analysis.

Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4:560 (1989), Landegren *et al.*, *Science* 241:1077 (1988), transcription amplification (Kwoh *et al.*, *Proc. Natl. Acad. Sci. USA* 86:1173 (1989)), and self-sustained sequence replication (Guatelli *et al.*, *Proc. Nat. Acad. Sci. USA* 87:1874 (1990)) and nucleic acid based sequence amplification (NASBA). The latter two amplification methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

The amplified DNA can be labeled, for example, radiolabeled, and used as a probe for screening a cDNA library derived from human cells, mRNA in zap express, ZIPLOX or other suitable vector. Corresponding clones can be isolated, DNA can obtained following *in vivo* excision, and the cloned insert can be sequenced in either or both orientations by art recognized methods to identify the correct reading frame encoding a polypeptide of the appropriate molecular weight. For example, the direct analysis of the nucleic acid molecules of the present invention can be accomplished using well-known methods that are commercially available. See, for example, Sambrook *et al.*, *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind *et al.*, *Recombinant DNA Laboratory Manual*, (Acad. Press, 1988)). Using these or similar

methods, the polypeptide and the DNA encoding the polypeptide can be isolated, sequenced and further characterized.

Antisense nucleic acid molecules of the invention can be designed using the nucleotide sequences of SEQ ID NOs: 1 or 3 and/or the
5 complement of one or more of SEQ ID NOs: 1 or 3 and/or a portion of one or more of SEQ ID NOs: 1 or 3 or the complement of one or more of SEQ ID NOs: 1 or 3 and/or a sequence encoding the amino acid sequences of SEQ ID NOs: 2 or encoding a portion of one or more of SEQ ID NOs: 1 or 3 or their complement. They can be constructed using chemical synthesis and
10 enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid molecule (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of
15 the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Alternatively, the antisense nucleic acid molecule can be produced biologically using an expression vector into which a nucleic acid molecule has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from
20 the inserted nucleic acid molecule will be of an antisense orientation to a target nucleic acid of interest).

The nucleic acid sequences can also be used to compare with endogenous DNA sequences in patients to identify one or more of the disorders related to FLAP, and as probes, such as to hybridize and discover
25 related DNA sequences or to subtract out known sequences from a sample. The nucleic acid sequences can further be used to derive primers for genetic fingerprinting, to raise anti-polypeptide antibodies using DNA immunization techniques, and as an antigen to raise anti-DNA antibodies or elicit immune responses. Portions or fragments of the nucleotide sequences identified
30 herein (and the corresponding complete gene sequences) can be used in numerous ways as polynucleotide reagents. For example, these sequences

can be used to: (i) map their respective genes on a chromosome; and, thus, locate gene regions or nucleic acid regions associated with genetic disease; (ii) identify an individual from a minute biological sample (tissue typing); and (iii) aid in forensic identification of a biological sample. Additionally, the nucleotide sequences of the invention can be used to identify and express recombinant polypeptides for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding polypeptide is expressed, either constitutively, during tissue differentiation, or in diseased states. The nucleic acid sequences can additionally be used as reagents in the screening and/or diagnostic assays described herein, and can also be included as components of kits (*e.g.*, reagent kits) for use in the screening and/or diagnostic assays described herein.

Vectors

Another aspect of the invention pertains to nucleic acid constructs containing a nucleic acid molecule of SEQ ID NOs: 1 or 3 or the complement thereof (or a portion thereof). Yet another aspect of the invention pertains to nucleic acid constructs containing a nucleic acid molecule encoding an amino acid of SEQ ID NO: 2 or polymorphic variant thereof. The constructs comprise a vector (*e.g.*, an expression vector) into which a sequence of the invention has been inserted in a sense or antisense orientation. As used herein, the term “vector” refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a “plasmid”, which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host

cell, and thereby are replicated along with the host genome. Moreover, certain vectors, such as expression vectors, are capable of directing the expression of genes or nucleic acids to which they are operably linked. In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses) that serve equivalent functions.

Preferred recombinant expression vectors of the invention comprise a nucleic acid molecule of the invention in a form suitable for expression of the nucleic acid molecule in a host cell. This means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operably linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, “operably linked” or “operatively linked” is intended to mean that the nucleic acid sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleic acid sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term “regulatory sequence” is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel, “Gene Expression Technology”, *Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleic acid sequence in many types of host cell and those which direct expression of the nucleic acid sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed and the level of expression of polypeptide desired. The expression vectors of the invention can be introduced into host

cells to thereby produce polypeptides, including fusion polypeptides, encoded by nucleic acid molecules as described herein.

The recombinant expression vectors of the invention can be designed for expression of a polypeptide of the invention in prokaryotic or eukaryotic cells, *e.g.*, bacterial cells such as *E. coli*, insect cells (using baculovirus expression vectors), yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel, *supra*. Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms “host cell” and “recombinant host cell” are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but also to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, a nucleic acid molecule of the invention can be expressed in bacterial cells (*e.g.*, *E. coli*), insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms “transformation” and “transfection” are intended to refer to a variety of art-recognized techniques for introducing a foreign nucleic acid molecule (*e.g.*, DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or

transfecting host cells can be found in Sambrook, *et al.* (*supra*), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene or nucleic acid that encodes a selectable marker (*e.g.*, for resistance to antibiotics) is generally introduced into the host cells along with the gene or nucleic acid of interest. Preferred selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid molecules encoding a selectable marker can be introduced into a host cell on the same vector as the nucleic acid molecule of the invention or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid molecule can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene or nucleic acid will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic host cell or eukaryotic host cell in culture can be used to produce (*i.e.*, express) a polypeptide of the invention. Accordingly, the invention further provides methods for producing a polypeptide using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding a polypeptide of the invention has been introduced) in a suitable medium such that the polypeptide is produced. In another embodiment, the method further comprises isolating the polypeptide from the medium or the host cell.

The host cells of the invention can also be used to produce nonhuman transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which a nucleic acid molecule of the invention has been introduced (*e.g.*, an exogenous FLAP nucleic acid, or an exogenous nucleic acid encoding a FLAP polypeptide). Such host cells can then be used to create non-human

transgenic animals in which exogenous nucleotide sequences have been introduced into the genome or homologous recombinant animals in which endogenous nucleotide sequences have been altered. Such animals are useful for studying the function and/or activity of the nucleic acid sequence and polypeptide encoded by the sequence and for identifying and/or evaluating modulators of their activity. As used herein, a “transgenic animal” is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal include a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens and amphibians. A transgene is exogenous DNA which is integrated into the genome of a cell from which a transgenic animal develops and which remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, an “homologous recombinant animal” is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, *e.g.*, an embryonic cell of the animal, prior to development of the animal.

Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009, U.S. Pat. No. 4,873,191 and in Hogan, *Manipulating the Mouse Embryo* (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986). Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley, *Current Opinion in BioTechnology* 2:823-829 (1991) and in PCT Publication Nos. WO 90/11354, WO 91/01140, WO 92/0968, and WO 93/04169. Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut *et*

al., *Nature* 385:810-813 (1997) and PCT Publication Nos. WO 97/07668 and WO 97/07669.

POLYPEPTIDES OF THE INVENTION

5 The present invention also pertains to isolated polypeptides encoded by FLAP nucleic acids ("FLAP polypeptides"), and fragments and variants thereof, as well as polypeptides encoded by nucleotide sequences described herein (*e.g.*, other splicing variants). The term "polypeptide" refers to a polymer of amino acids, and not to a specific length; thus, peptides,
10 oligopeptides and proteins are included within the definition of a polypeptide. As used herein, a polypeptide is said to be "isolated" or "purified" when it is substantially free of cellular material when it is isolated from recombinant and non-recombinant cells, or free of chemical precursors or other chemicals when it is chemically synthesized. A polypeptide,
15 however, can be joined to another polypeptide with which it is not normally associated in a cell (*e.g.*, in a "fusion protein") and still be "isolated" or "purified."

 The polypeptides of the invention can be purified to homogeneity. It is understood, however, that preparations in which the polypeptide is not
20 purified to homogeneity are useful. The critical feature is that the preparation allows for the desired function of the polypeptide, even in the presence of considerable amounts of other components. Thus, the invention encompasses various degrees of purity. In one embodiment, the language "substantially free of cellular material" includes preparations of the
25 polypeptide having less than about 30% (by dry weight) other proteins (*i.e.*, contaminating protein), less than about 20% other proteins, less than about 10% other proteins, or less than about 5% other proteins.

 When a polypeptide is recombinantly produced, it can also be substantially free of culture medium, *i.e.*, culture medium represents less
30 than about 20%, less than about 10%, or less than about 5% of the volume of the polypeptide preparation. The language "substantially free of chemical

precursors or other chemicals” includes preparations of the polypeptide in which it is separated from chemical precursors or other chemicals that are involved in its synthesis. In one embodiment, the language “substantially free of chemical precursors or other chemicals” includes preparations of the polypeptide having less than about 30% (by dry weight) chemical precursors or other chemicals, less than about 20% chemical precursors or other chemicals, less than about 10% chemical precursors or other chemicals, or less than about 5% chemical precursors or other chemicals.

In one embodiment, a polypeptide of the invention comprises an amino acid sequence encoded by a nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 or 3, or the complement of SEQ ID NO: 1 or 3, or portions thereof, or a portion or polymorphic variant thereof. However, the polypeptides of the invention also encompass fragment and sequence variants. Variants include a substantially homologous polypeptide encoded by the same genetic locus in an organism, *i.e.*, an allelic variant, as well as other splicing variants. Variants also encompass polypeptides derived from other genetic loci in an organism, but having substantial homology to a polypeptide encoded by a nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1 or 3 or their complement, or portions thereof, or having substantial homology to a polypeptide encoded by a nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of nucleotide sequences encoding SEQ ID NO: 2 or polymorphic variants thereof. Variants also include polypeptides substantially homologous or identical to these polypeptides but derived from another organism, *i.e.*, an ortholog. Variants also include polypeptides that are substantially homologous or identical to these polypeptides that are produced by chemical synthesis. Variants also include polypeptides that are substantially homologous or identical to these polypeptides that are produced by recombinant methods.

As used herein, two polypeptides (or a region of the polypeptides) are substantially homologous or identical when the amino acid sequences are at least about 45-55%, in certain embodiments at least about 70-75%, and in other embodiments at least about 80-85%, and in others greater than about 90% or more homologous or identical. A substantially homologous amino acid sequence, according to the present invention, will be encoded by a nucleic acid molecule hybridizing to SEQ ID NO: 1 or 3 or portion thereof, under stringent conditions as more particularly described above, or will be encoded by a nucleic acid molecule hybridizing to a nucleic acid sequence encoding SEQ ID NO: 2 or a portion thereof or polymorphic variant thereof, under stringent conditions as more particularly described thereof.

The invention also encompasses polypeptides having a lower degree of identity but having sufficient similarity so as to perform one or more of the same functions performed by a polypeptide encoded by a nucleic acid molecule of the invention. Similarity is determined by conserved amino acid substitution. Such substitutions are those that substitute a given amino acid in a polypeptide by another amino acid of like characteristics. Conservative substitutions are likely to be phenotypically silent. Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile; interchange of the hydroxyl residues Ser and Thr, exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln, exchange of the basic residues Lys and Arg and replacements among the aromatic residues Phe and Tyr. Guidance concerning which amino acid changes are likely to be phenotypically silent are found in Bowie *et al.*, *Science* 247:1306-1310 (1990).

A variant polypeptide can differ in amino acid sequence by one or more substitutions, deletions, insertions, inversions, fusions, and truncations or a combination of any of these. Further, variant polypeptides can be fully functional or can lack function in one or more activities. Fully functional variants typically contain only conservative variation or variation in non-

critical residues or in non-critical regions. Functional variants can also contain substitution of similar amino acids that result in no change or an insignificant change in function. Alternatively, such substitutions may positively or negatively affect function to some degree. Non-functional
5 variants typically contain one or more non-conservative amino acid substitutions, deletions, insertions, inversions, or truncation or a substitution, insertion, inversion, or deletion in a critical residue or critical region.

Amino acids that are essential for function can be identified by methods known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis (Cunningham *et al.*, *Science* 244:1081-1085 (1989)).
10 The latter procedure introduces single alanine mutations at every residue in the molecule. The resulting mutant molecules are then tested for biological activity *in vitro*, or *in vitro* proliferative activity. Sites that are critical for polypeptide activity can also be determined by structural analysis such as
15 crystallization, nuclear magnetic resonance or photoaffinity labeling (Smith *et al.*, *J. Mol. Biol.* 224:899-904 (1992); de Vos *et al.*, *Science* 255:306-312 (1992)).

The invention also includes fragments of the polypeptides of the invention. Fragments can be derived from a polypeptide encoded by a
20 nucleic acid molecule comprising SEQ ID NO: 1 or 3, or the complement of SEQ ID NO: 1 or 3 (or other variants). However, the invention also encompasses fragments of the variants of the polypeptides described herein. As used herein, a fragment comprises at least 6 contiguous amino acids. Useful fragments include those that retain one or more of the biological
25 activities of the polypeptide as well as fragments that can be used as an immunogen to generate polypeptide-specific antibodies.

Biologically active fragments (peptides which are, for example, 6, 9, 12, 15, 16, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) can comprise a domain, segment, or motif that has been identified by
30 analysis of the polypeptide sequence using well-known methods, *e.g.*, signal peptides, extracellular domains, one or more transmembrane segments or

loops, ligand binding regions, zinc finger domains, DNA binding domains, acylation sites, glycosylation sites, or phosphorylation sites.

5 Fragments can be discrete (not fused to other amino acids or polypeptides) or can be within a larger polypeptide. Further, several fragments can be comprised within a single larger polypeptide. In one embodiment a fragment designed for expression in a host can have heterologous pre- and pro-polypeptide regions fused to the amino terminus of the polypeptide fragment and an additional region fused to the carboxyl terminus of the fragment.

10 The invention thus provides chimeric or fusion polypeptides. These comprise a polypeptide of the invention operatively linked to a heterologous protein or polypeptide having an amino acid sequence not substantially homologous to the polypeptide. "Operatively linked" indicates that the polypeptide and the heterologous protein are fused in-frame. The
15 heterologous protein can be fused to the N-terminus or C-terminus of the polypeptide. In one embodiment the fusion polypeptide does not affect function of the polypeptide *per se*. For example, the fusion polypeptide can be a GST-fusion polypeptide in which the polypeptide sequences are fused to the C-terminus of the GST sequences. Other types of fusion polypeptides
20 include, but are not limited to, enzymatic fusion polypeptides, for example beta-galactosidase fusions, yeast two-hybrid GAL fusions, poly-His fusions and Ig fusions. Such fusion polypeptides, particularly poly-His fusions, can facilitate the purification of recombinant polypeptide. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of a polypeptide
25 can be increased using a heterologous signal sequence. Therefore, in another embodiment, the fusion polypeptide contains a heterologous signal sequence at its N-terminus.

30 EP-A-O 464 533 discloses fusion proteins comprising various portions of immunoglobulin constant regions. The Fc is useful in therapy and diagnosis and thus results, for example, in improved pharmacokinetic properties (EP-A 0232 262). In drug discovery, for example, human proteins

have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists. Bennett *et al.*, *Journal of Molecular Recognition*, 8:52-58 (1995) and Johanson *et al.*, *The Journal of Biological Chemistry*, 270,16:9459-9471 (1995). Thus, this invention also encompasses
5 soluble fusion polypeptides containing a polypeptide of the invention and various portions of the constant regions of heavy or light chains of immunoglobulins of various subclasses (IgG, IgM, IgA, IgE).

A chimeric or fusion polypeptide can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the
10 different polypeptide sequences are ligated together in-frame in accordance with conventional techniques. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of nucleic acid fragments can be carried out using anchor primers which give rise to complementary
15 overhangs between two consecutive nucleic acid fragments which can subsequently be annealed and re-amplified to generate a chimeric nucleic acid sequence (see Ausubel *et al.*, *Current Protocols in Molecular Biology*, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST protein). A nucleic acid
20 molecule encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the polypeptide.

The isolated polypeptide can be purified from cells that naturally express it, purified from cells that have been altered to express it
25 (recombinant), or synthesized using known protein synthesis methods. In one embodiment, the polypeptide is produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the polypeptide is cloned into an expression vector, the expression vector introduced into a host cell and the polypeptide expressed in the host cell. The polypeptide can
30 then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques.

The polypeptides of the present invention can be used to raise antibodies or to elicit an immune response. The polypeptides can also be used as a reagent, *e.g.*, a labeled reagent, in assays to quantitatively determine levels of the polypeptide or a molecule to which it binds (*e.g.*, a ligand) in biological fluids. The polypeptides can also be used as markers for cells or tissues in which the corresponding polypeptide is preferentially expressed, either constitutively, during tissue differentiation, or in diseased states. The polypeptides can be used to isolate a corresponding binding agent, *e.g.*, ligand, such as, for example, in an interaction trap assay, and to screen for peptide or small molecule antagonists or agonists of the binding interaction. For example, because members of the leukotriene pathway including FLAP bind to receptors, the leukotriene pathway polypeptides can be used to isolate such receptors.

ANTIBODIES OF THE INVENTION

Polyclonal and/or monoclonal antibodies that specifically bind one form of the polypeptide or nucleic acid product (*e.g.*, a polypeptide encoded by a nucleic acid having a SNP as set forth in Table 3), but not to another form of the polypeptide or nucleic acid product, are also provided. Antibodies are also provided which bind a portion of either polypeptide encoded by nucleic acids of the invention (*e.g.*, SEQ ID NO: 1 or SEQ ID NO: 3, or the complement of SEQ ID NO: 1 or SEQ ID NO: 3), or to a polypeptide encoded by nucleic acids of the invention that contain a polymorphic site or sites. The invention also provides antibodies to the polypeptides and polypeptide fragments of the invention, or a portion thereof, or having an amino acid sequence encoded by a nucleic acid molecule comprising all or a portion of SEQ ID NOS: 1 or 3, or the complement thereof, or another variant or portion thereof.

The term “antibody” as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, *i.e.*, molecules that contain an antigen binding site that

specifically binds an antigen. A molecule that specifically binds to a polypeptide of the invention is a molecule that binds to that polypeptide or a fragment thereof, but does not substantially bind other molecules in a sample, *e.g.*, a biological sample, which naturally contains the polypeptide.

5 Examples of immunologically active portions of immunoglobulin molecules include F(ab) and F(ab')₂ fragments which can be generated by treating the antibody with an enzyme such as pepsin. The invention provides polyclonal and monoclonal antibodies that bind to a polypeptide of the invention. The term "monoclonal antibody" or "monoclonal antibody composition", as used
10 herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope of a polypeptide of the invention. A monoclonal antibody composition thus typically displays a single binding affinity for a particular polypeptide of the invention with which it immunoreacts.

15 Polyclonal antibodies can be prepared as described above by immunizing a suitable subject with a desired immunogen, *e.g.*, polypeptide of the invention or fragment thereof. The antibody titer in the immunized subject can be monitored over time by standard techniques, such as with an enzyme linked immunosorbent assay (ELISA) using immobilized
20 polypeptide. If desired, the antibody molecules directed against the polypeptide can be isolated from the mammal (*e.g.*, from the blood) and further purified by well-known techniques, such as protein A chromatography to obtain the IgG fraction. At an appropriate time after immunization, *e.g.*, when the antibody titers are highest, antibody-producing
25 cells can be obtained from the subject and used to prepare monoclonal antibodies by standard techniques, such as the hybridoma technique originally described by Kohler and Milstein, *Nature* 256:495-497 (1975), the human B cell hybridoma technique (Kozbor *et al.*, *Immunol. Today* 4:72 (1983)); the EBV-hybridoma technique (Cole *et al.*, *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, 1985, Inc., pp. 77-96); or trioma
30 techniques. The technology for producing hybridomas is well known (see

generally *Current Protocols in Immunology* (1994) Coligan *et al.* (eds.) John Wiley & Sons, Inc., New York, NY). Briefly, an immortal cell line (typically a myeloma) is fused to lymphocytes (typically splenocytes) from a mammal immunized with an immunogen as described above, and the culture supernatants of the resulting hybridoma cells are screened to identify a hybridoma producing a monoclonal antibody that binds a polypeptide of the invention.

Any of the many well known protocols used for fusing lymphocytes and immortalized cell lines can be applied for the purpose of generating a monoclonal antibody to a polypeptide of the invention (see, *e.g.*, *Current Protocols in Immunology, supra*; Galfre *et al.*, *Nature* 266:55052 (1977); R.H. Kenneth, in *Monoclonal Antibodies: A New Dimension In Biological Analyses*, Plenum Publishing Corp., New York, New York (1980); and Lerner, *Yale J. Biol. Med.* 54:387-402 (1981). Moreover, the ordinarily skilled worker will appreciate that there are many variations of such methods that also would be useful.

Alternative to preparing monoclonal antibody-secreting hybridomas, a monoclonal antibody to a polypeptide of the invention can be identified and isolated by screening a recombinant combinatorial immunoglobulin library (*e.g.*, an antibody phage display library) with the polypeptide to thereby isolate immunoglobulin library members that bind the polypeptide. Kits for generating and screening phage display libraries are commercially available (*e.g.*, the Pharmacia *Recombinant Phage Antibody System*, Catalog No. 27-9400-01; and the Stratagene *SurfZAP™* Phage Display Kit, Catalog No. 240612). Additionally, examples of methods and reagents particularly amenable for use in generating and screening antibody display library can be found in, for example, U.S. Patent No. 5,223,409; PCT Publication No. WO 92/18619; PCT Publication No. WO 91/17271; PCT Publication No. WO 92/20791; PCT Publication No. WO 92/15679; PCT Publication No. WO 93/01288; PCT Publication No. WO 92/01047; PCT Publication No. WO 92/09690; PCT Publication No. WO 90/02809; Fuchs *et al.*, *Bio/Technology*

9: 1370-1372 (1991); Hay *et al.*, *Hum. Antibod. Hybridomas* 3:81-85 (1992); Huse *et al.*, *Science* 246:1275-1281 (1989); Griffiths *et al.*, *EMBO J.* 12:725-734 (1993).

5 Additionally, recombinant antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art.

10 In general, antibodies of the invention (*e.g.*, a monoclonal antibody) can be used to isolate a polypeptide of the invention by standard techniques, such as affinity chromatography or immunoprecipitation. A polypeptide-specific antibody can facilitate the purification of natural polypeptide from cells and of recombinantly produced polypeptide expressed in host cells.

15 Moreover, an antibody specific for a polypeptide of the invention can be used to detect the polypeptide (*e.g.*, in a cellular lysate, cell supernatant, or tissue sample) in order to evaluate the abundance and pattern of expression of the polypeptide. Antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example,

20 determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish

25 peroxidase, alkaline phosphatase, β -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an

30 example of a luminescent material includes luminol; examples of

bioluminescent materials include luciferase, luciferin and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

As described above, antibodies to leukotrienes can be used in the methods of the invention. The methods described herein can be used to generate such antibodies for use in the methods.

DIAGNOSTIC ASSAYS

The nucleic acids, probes, primers, polypeptides and antibodies described herein can be used in methods of diagnosis of a susceptibility to MI, ACS, stroke or PAOD, or to another disease or condition associated with an MI gene, such as FLAP, as well as in kits useful for diagnosis of a susceptibility to MI, ACS, stroke or PAOD, or to another disease or condition associated with FLAP. In one embodiment, the kit useful for diagnosis of susceptibility to MI, ACS, stroke or PAOD, or to another disease or condition associated with FLAP comprises primers as described herein, wherein the primers contain one or more of the SNPs identified in Table 3.

In one embodiment of the invention, diagnosis of susceptibility to MI, ACS, stroke or PAOD (or diagnosis of susceptibility to another disease or condition associated with FLAP), is made by detecting a polymorphism in a FLAP nucleic acid as described herein. The polymorphism can be an alteration in a FLAP nucleic acid, such as the insertion or deletion of a single nucleotide, or of more than one nucleotide, resulting in a frame shift alteration; the change of at least one nucleotide, resulting in a change in the encoded amino acid; the change of at least one nucleotide, resulting in the generation of a premature stop codon; the deletion of several nucleotides, resulting in a deletion of one or more amino acids encoded by the nucleotides; the insertion of one or several nucleotides, such as by unequal recombination or gene conversion, resulting in an interruption of the coding sequence of the gene or nucleic acid; duplication of all or a part of the gene or nucleic acid; transposition of all or a part of the gene or nucleic acid; or

rearrangement of all or a part of the gene or nucleic acid. More than one such alteration may be present in a single gene or nucleic acid. Such sequence changes cause an alteration in the polypeptide encoded by a FLAP nucleic acid. For example, if the alteration is a frame shift alteration, the frame shift can result in a change in the encoded amino acids, and/or can result in the generation of a premature stop codon, causing generation of a truncated polypeptide. Alternatively, a polymorphism associated with a disease or condition associated with a FLAP nucleic acid or a susceptibility to a disease or condition associated with a FLAP nucleic acid can be a synonymous alteration in one or more nucleotides (*i.e.*, an alteration that does not result in a change in the polypeptide encoded by a FLAP nucleic acid). Such a polymorphism may alter splicing sites, affect the stability or transport of mRNA, or otherwise affect the transcription or translation of the nucleic acid. A FLAP nucleic acid that has any of the alteration described above is referred to herein as an “altered nucleic acid.”

In a first method of diagnosing a susceptibility to MI, ACS, stroke or PAOD, hybridization methods, such as Southern analysis, Northern analysis, or *in situ* hybridizations, can be used (see *Current Protocols in Molecular Biology*, Ausubel, F. *et al.*, eds., John Wiley & Sons, including all supplements through 1999). For example, a biological sample from a test subject (a “test sample”) of genomic DNA, RNA, or cDNA, is obtained from an individual suspected of having, being susceptible to or predisposed for, or carrying a defect for, a susceptibility to a disease or condition associated with a FLAP nucleic acid (the “test individual”). The individual can be an adult, child, or fetus. The test sample can be from any source which contains genomic DNA, such as a blood sample, sample of amniotic fluid, sample of cerebrospinal fluid, or tissue sample from skin, muscle, buccal or conjunctival mucosa, placenta, gastrointestinal tract or other organs. A test sample of DNA from fetal cells or tissue can be obtained by appropriate methods, such as by amniocentesis or chorionic villus sampling. The DNA, RNA, or cDNA sample is then examined to determine whether a

polymorphism in an MI nucleic acid is present, and/or to determine which splicing variant(s) encoded by the FLAP is present. The presence of the polymorphism or splicing variant(s) can be indicated by hybridization of the nucleic acid in the genomic DNA, RNA, or cDNA to a nucleic acid probe. A
5 “nucleic acid probe,” as used herein, can be a DNA probe or an RNA probe; the nucleic acid probe can contain at least one polymorphism in a FLAP nucleic acid or contains a nucleic acid encoding a particular splicing variant of a FLAP nucleic acid. The probe can be any of the nucleic acid molecules described above (*e.g.*, the nucleic acid, a fragment, a vector comprising the
10 nucleic acid, a probe or primer, etc.).

To diagnose a susceptibility to MI, ACS, stroke or PAOD (or another disease or condition associated with FLAP), the test sample containing a FLAP nucleic acid is contacted with at least one nucleic acid probe to form a hybridization sample. A preferred probe for detecting mRNA or genomic
15 DNA is a labeled nucleic acid probe capable of hybridizing to mRNA or genomic DNA sequences described herein. The nucleic acid probe can be, for example, a full-length nucleic acid molecule, or a portion thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to
20 appropriate mRNA or genomic DNA. For example, the nucleic acid probe can be all or a portion of one of SEQ ID NOs: 1 and 3, or the complement thereof or a portion thereof; or can be a nucleic acid encoding all or a portion of one of SEQ ID NO: 2. Other suitable probes for use in the diagnostic assays of the invention are described above (see *e.g.*, probes and primers
25 discussed under the heading, “Nucleic Acids of the Invention”).

The hybridization sample is maintained under conditions that are sufficient to allow specific hybridization of the nucleic acid probe to a FLAP nucleic acid. “Specific hybridization,” as used herein, indicates exact hybridization (*e.g.*, with no mismatches). Specific hybridization can be
30 performed under high stringency conditions or moderate stringency conditions, for example, as described above. In a particularly preferred

embodiment, the hybridization conditions for specific hybridization are high stringency.

Specific hybridization, if present, is then detected using standard methods. If specific hybridization occurs between the nucleic acid probe and
5 FLAP nucleic acid in the test sample, then the FLAP has the polymorphism, or is the splicing variant, that is present in the nucleic acid probe. More than one nucleic acid probe can also be used concurrently in this method. Specific hybridization of any one of the nucleic acid probes is indicative of a polymorphism in the FLAP nucleic acid, or of the presence of a particular
10 splicing variant encoding the FLAP nucleic acid, and is therefore diagnostic for a susceptibility to a disease or condition associated with FLAP (*e.g.*, MI, ACS, stroke or PAOD).

In Northern analysis (see *Current Protocols in Molecular Biology*, Ausubel, F. *et al.*, eds., John Wiley & Sons, *supra*) the hybridization
15 methods described above are used to identify the presence of a polymorphism or a particular splicing variant, associated with a susceptibility to a disease or condition associated with FLAP (*e.g.*, MI, ACS, stroke or PAOD). For Northern analysis, a test sample of RNA is obtained from the individual by appropriate means. Specific hybridization of a
20 nucleic acid probe, as described above, to RNA from the individual is indicative of a polymorphism in a FLAP nucleic acid, or of the presence of a particular splicing variant encoded by a FLAP nucleic acid, and is therefore diagnostic for susceptibility to a disease or condition associated with FLAP (*e.g.*, MI, ACS, stroke or PAOD).

25 For representative examples of use of nucleic acid probes, see, for example, U.S. Patents No. 5,288,611 and 4,851,330.

Alternatively, a peptide nucleic acid (PNA) probe can be used instead of a nucleic acid probe in the hybridization methods described above. PNA is a DNA mimic having a peptide-like, inorganic backbone, such as N-(2-
30 aminoethyl)glycine units, with an organic base (A, G, C, T or U) attached to the glycine nitrogen via a methylene carbonyl linker (see, for example,

Nielsen, P.E. *et al.*, *Bioconjugate Chemistry* 5, American Chemical Society, p. 1 (1994). The PNA probe can be designed to specifically hybridize to a nucleic acid having a polymorphism associated with a susceptibility to a disease or condition associated with FLAP (*e.g.*, MI). Hybridization of the PNA probe to a FLAP nucleic acid as described herein is diagnostic for the susceptibility to the disease or condition.

In another method of the invention, mutation analysis by restriction digestion can be used to detect an altered nucleic acid, or nucleic acids containing a polymorphism(s), if the mutation or polymorphism in the nucleic acid results in the creation or elimination of a restriction site. A test sample containing genomic DNA is obtained from the individual. Polymerase chain reaction (PCR) can be used to amplify a FLAP nucleic acid (and, if necessary, the flanking sequences) in the test sample of genomic DNA from the test individual. RFLP analysis is conducted as described (see *Current Protocols in Molecular Biology, supra*). The digestion pattern of the relevant DNA fragment indicates the presence or absence of the alteration or polymorphism in the FLAP nucleic acid, and therefore indicates the presence or absence of the susceptibility to a disease or condition associated with FLAP (*e.g.*, MI, ACS, stroke or PAOD).

Sequence analysis can also be used to detect specific polymorphisms in the FLAP nucleic acid. A test sample of DNA or RNA is obtained from the test individual. PCR or other appropriate methods can be used to amplify the nucleic acid, and/or its flanking sequences, if desired. The sequence of a FLAP nucleic acid, or a fragment of the nucleic acid, or cDNA, or fragment of the cDNA, or mRNA, or fragment of the mRNA, is determined, using standard methods. The sequence of the nucleic acid, nucleic acid fragment, cDNA, cDNA fragment, mRNA, or mRNA fragment is compared with the known nucleic acid sequence of the nucleic acid, cDNA (*e.g.*, one or more of SEQ ID NOs: 1 or 3, and/or the complement of SEQ ID NO: 1 or 3), or a nucleic acid sequence encoding SEQ ID NO: 2 or a fragment thereof) or mRNA, as appropriate. The presence of a polymorphism in the FLAP

indicates that the individual has a susceptibility to a disease associated with FLAP (*e.g.*, MI, ACS, stroke or PAOD).

Allele-specific oligonucleotides can also be used to detect the presence of polymorphism(s) in the FLAP nucleic acid, through the use of dot-blot hybridization of amplified oligonucleotides with allele-specific oligonucleotide (ASO) probes (see, for example, Saiki, R. *et al.*, *Nature* 324:163-166 (1986)). An "allele-specific oligonucleotide" (also referred to herein as an "allele-specific oligonucleotide probe") is an oligonucleotide of approximately 10-50 base pairs, for example, approximately 15-30 base pairs, that specifically hybridizes to a FLAP nucleic acid, and that contains a polymorphism associated with a susceptibility to a disease or condition associated with FLAP (*e.g.*, MI, ACS, stroke or PAOD). An allele-specific oligonucleotide probe that is specific for particular polymorphisms in a FLAP nucleic acid can be prepared, using standard methods (see *Current Protocols in Molecular Biology, supra*). To identify polymorphisms in the nucleic acid associated with susceptibility to disease, a test sample of DNA is obtained from the individual. PCR can be used to amplify all or a fragment of a FLAP nucleic acid, and its flanking sequences. The DNA containing the amplified FLAP nucleic acid (or fragment of the nucleic acid) is dot-blotted, using standard methods (see *Current Protocols in Molecular Biology, supra*), and the blot is contacted with the oligonucleotide probe. The presence of specific hybridization of the probe to the amplified FLAP is then detected. Specific hybridization of an allele-specific oligonucleotide probe to DNA from the individual is indicative of a polymorphism in the FLAP, and is therefore indicative of a susceptibility to a disease or condition associated with FLAP (*e.g.*, MI, ACS, stroke or PAOD).

An allele-specific primer hybridizes to a site on target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, *Nucleic Acid Res.* 17, 2427-2448 (1989). This primer is used in conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from

the two primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, *e.g.*, WO 93/22456).

With the addition of such analogs as locked nucleic acids (LNAs), the size of primers and probes can be reduced to as few as 8 bases. LNAs are a novel class of bicyclic DNA analogs in which the 2' and 4' positions in the furanose ring are joined via an O-methylene (oxy-LNA), S-methylene (thio-LNA), or amino methylene (amino-LNA) moiety. Common to all of these LNA variants is an affinity toward complementary nucleic acids, which is by far the highest reported for a DNA analog. For example, particular all oxy-LNA nonamers have been shown to have melting temperatures of 64°C and 74°C when in complex with complementary DNA or RNA, respectively, as opposed to 28°C for both DNA and RNA for the corresponding DNA nonamer. Substantial increases in T_m are also obtained when LNA monomers are used in combination with standard DNA or RNA monomers. For primers and probes, depending on where the LNA monomers are included (*e.g.*, the 3' end, the 5' end, or in the middle), the T_m could be increased considerably.

In another embodiment, arrays of oligonucleotide probes that are complementary to target nucleic acid sequence segments from an individual, can be used to identify polymorphisms in a FLAP nucleic acid. For example, in one embodiment, an oligonucleotide array can be used. Oligonucleotide arrays typically comprise a plurality of different oligonucleotide probes that are coupled to a surface of a substrate in different known locations. These oligonucleotide arrays, also described as

“Genechips™,” have been generally described in the art, for example, U.S. Pat. No. 5,143,854 and PCT patent publication Nos. WO 90/15070 and WO 92/10092. These arrays can generally be produced using mechanical synthesis methods or light directed synthesis methods that incorporate a combination of photolithographic methods and solid phase oligonucleotide synthesis methods. See Fodor *et al.*, *Science* 251:767-777 (1991); Pirrung *et al.*, U.S. Pat. 5,143,854; (see also PCT Application WO 90/15070); Fodor *et al.*, PCT Publication WO 92/10092; and U.S. Pat. 5,424,186, the entire teachings of each of which are incorporated by reference herein. Techniques for the synthesis of these arrays using mechanical synthesis methods are described in, *e.g.*, U.S. Pat. 5,384,261, the entire teachings of which are incorporated by reference herein. In another example, linear arrays can be utilized.

Once an oligonucleotide array is prepared, a nucleic acid of interest is hybridized with the array and scanned for polymorphisms. Hybridization and scanning are generally carried out by methods described herein and also in, *e.g.*, published PCT Application Nos. WO 92/10092 and WO 95/11995, and U.S. Pat. No. 5,424,186, the entire teachings of which are incorporated by reference herein. In brief, a target nucleic acid sequence that includes one or more previously identified polymorphic markers is amplified using well-known amplification techniques, *e.g.*, PCR. Typically, this involves the use of primer sequences that are complementary to the two strands of the target sequence both upstream and downstream from the polymorphism.

Asymmetric PCR techniques may also be used. Amplified target, generally incorporating a label, is then hybridized with the array under appropriate conditions. Upon completion of hybridization and washing of the array, the array is scanned to determine the position on the array to which the target sequence hybridizes. The hybridization data obtained from the scan is typically in the form of fluorescence intensities as a function of location on the array. In a reverse method, a probe, containing a polymorphism, can be

coupled to a solid surface and PCR amplicons are then added to hybridize to these probes.

Although primarily described in terms of a single detection block, e.g., detection of a single polymorphism arrays can include multiple
5 detection blocks, and thus be capable of analyzing multiple, specific polymorphisms. It will generally be understood that detection blocks may be grouped within a single array or in multiple, separate arrays so that varying, optimal conditions may be used during the hybridization of the target to the array. For example, it may often be desirable to provide for the detection of
10 those polymorphisms that fall within G-C rich stretches of a genomic sequence, separately from those falling in A-T rich segments. This allows for the separate optimization of hybridization conditions for each situation.

Additional uses of oligonucleotide arrays for detection of polymorphisms can be found, for example, in U.S. Patents Nos. 5,858,659
15 and 5,837,832, the entire teachings of which are incorporated by reference herein. Other methods of nucleic acid analysis can be used to detect polymorphisms in a nucleic acid described herein, or variants encoded by a nucleic acid described herein. Representative methods include direct manual sequencing (Church and Gilbert, *Proc. Natl. Acad. Sci. USA* 81:1991-1995
20 (1988); Sanger, F. *et al.*, *Proc. Natl. Acad. Sci., USA* 74:5463-5467 (1977); Beavis *et al.* U.S. Pat. No. 5,288,644); automated fluorescent sequencing; single-stranded conformation polymorphism assays (SSCP); clamped denaturing gel electrophoresis (CDGE); denaturing gradient gel electrophoresis (DGGE) (Sheffield, V.C. *et al.*, *Proc. Natl. Acad. Sci. USA*
25 86:232-236 (1989)), mobility shift analysis (Orita, M. *et al.*, *Proc. Natl. Acad. Sci. USA* 86:2766-2770 (1989)), restriction enzyme analysis (Flavell *et al.*, *Cell* 15:25 (1978); Geever, *et al.*, *Proc. Natl. Acad. Sci. USA* 78:5081 (1981)); heteroduplex analysis; chemical mismatch cleavage (CMC) (Cotton *et al.*, *Proc. Natl. Acad. Sci. USA* 85:4397-4401 (1985)); RNase protection
30 assays (Myers, R.M. *et al.*, *Science* 230:1242 (1985)); use of polypeptides

which recognize nucleotide mismatches, such as *E. coli* mutS protein; allele-specific PCR, for example.

In one embodiment of the invention, diagnosis of a susceptibility to a disease or condition associated with FLAP (*e.g.*, MI, ACS, stroke or PAOD)
5 can also be made by expression analysis by quantitative PCR (kinetic thermal cycling). This technique utilizing TaqMan[®] can be used to allow the identification of polymorphisms and whether a patient is homozygous or heterozygous. The technique can assess the presence of an alteration in the expression or composition of the polypeptide encoded by a FLAP nucleic
10 acid or splicing variants encoded by a FLAP nucleic acid. Further, the expression of the variants can be quantified as physically or functionally different.

In another embodiment of the invention, diagnosis of a susceptibility to MI, ACS, stroke or PAOD (or of another disease or condition associated
15 with FLAP) can also be made by examining expression and/or composition of a FLAP polypeptide, by a variety of methods, including enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. A test sample from an individual is assessed for the presence of an alteration in the expression and/or an alteration in
20 composition of the polypeptide encoded by a FLAP nucleic acid, or for the presence of a particular variant encoded by a FLAP nucleic acid. An alteration in expression of a polypeptide encoded by a FLAP nucleic acid can be, for example, an alteration in the quantitative polypeptide expression (*i.e.*, the amount of polypeptide produced); an alteration in the composition of a
25 polypeptide encoded by a FLAP nucleic acid is an alteration in the qualitative polypeptide expression (*e.g.*, expression of an altered FLAP polypeptide or of a different splicing variant). In a preferred embodiment, diagnosis of a susceptibility to a disease or condition associated with FLAP is made by detecting a particular splicing variant encoded by that FLAP
30 variant, or a particular pattern of splicing variants.

Both such alterations (quantitative and qualitative) can also be present. An “alteration” in the polypeptide expression or composition, refers to an alteration in expression or composition in a test sample, as compared with the expression or composition of polypeptide by a FLAP nucleic acid in a control sample. A control sample is a sample that corresponds to the test sample (*e.g.*, is from the same type of cells), and is from an individual who is not affected by the disease or a susceptibility to a disease or condition associated with a FLAP nucleic acid. An alteration in the expression or composition of the polypeptide in the test sample, as compared with the control sample, is indicative of a susceptibility to a disease or condition associated with FLAP (*e.g.*, MI, ACS, stroke or PAOD). Similarly, the presence of one or more different splicing variants in the test sample, or the presence of significantly different amounts of different splicing variants in the test sample, as compared with the control sample, is indicative of a susceptibility to a disease or condition associated with a FLAP nucleic acid. Various means of examining expression or composition of the polypeptide encoded by a FLAP nucleic acid can be used, including: spectroscopy, colorimetry, electrophoresis, isoelectric focusing and immunoassays (*e.g.*, David *et al.*, U.S. Pat. 4,376,110) such as immunoblotting (see also *Current Protocols in Molecular Biology*, particularly Chapter 10). For example, in one embodiment, an antibody capable of binding to the polypeptide (*e.g.*, as described above), preferably an antibody with a detectable label, can be used. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (*e.g.*, Fab or F(ab')₂) can be used. The term “labeled”, with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (*i.e.*, physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling

of a DNA probe with biotin such that it can be detected with fluorescently labeled streptavidin.

Western blotting analysis, using an antibody as described above that specifically binds to a polypeptide encoded by an altered FLAP (*e.g.*, by a
5 FLAP having a SNP as shown in Table 3), or an antibody that specifically binds to a polypeptide encoded by a non-altered nucleic acid, or an antibody that specifically binds to a particular splicing variant encoded by a nucleic acid, can be used to identify the presence in a test sample of a particular splicing variant or of a polypeptide encoded by a polymorphic or altered
10 FLAP, or the absence in a test sample of a particular splicing variant or of a polypeptide encoded by a non-polymorphic or non-altered nucleic acid. The presence of a polypeptide encoded by a polymorphic or altered nucleic acid, or the absence of a polypeptide encoded by a non-polymorphic or non-altered nucleic acid, is diagnostic for a susceptibility to a disease or condition
15 associated with FLAP, as is the presence (or absence) of particular splicing variants encoded by the FLAP nucleic acid.

In one embodiment of this method, the level or amount of polypeptide encoded by a FLAP nucleic acid in a test sample is compared with the level or amount of the polypeptide encoded by the FLAP in a
20 control sample. A level or amount of the polypeptide in the test sample that is higher or lower than the level or amount of the polypeptide in the control sample, such that the difference is statistically significant, is indicative of an alteration in the expression of the polypeptide encoded by the FLAP, and is diagnostic for a susceptibility to a disease or condition associated with that
25 FLAP. Alternatively, the composition of the polypeptide encoded by a FLAP nucleic acid in a test sample is compared with the composition of the polypeptide encoded by the FLAP in a control sample (*e.g.*, the presence of different splicing variants). A difference in the composition of the polypeptide in the test sample, as compared with the composition of the
30 polypeptide in the control sample, is diagnostic for a susceptibility to a disease or condition associated with that FLAP. In another embodiment,

both the level or amount and the composition of the polypeptide can be assessed in the test sample and in the control sample. A difference in the amount or level of the polypeptide in the test sample, compared to the control sample; a difference in composition in the test sample, compared to the control sample; or both a difference in the amount or level, and a difference in the composition, is indicative of a susceptibility to a disease or condition associated with FLAP (*e.g.*, MI).

The invention further pertains to a method for the diagnosis and identification of susceptibility to myocardial infarction, ACS, stroke or PAOD in an individual, by identifying an at-risk haplotype in FLAP. In one embodiment, the at-risk haplotype is one which confers a significant risk of MI, ACS, stroke or PAOD. In one embodiment, significance associated with a haplotype is measured by an odds ratio. In a further embodiment, the significance is measured by a percentage. In one embodiment, a significant risk is measured as an odds ratio of at least about 1.2, including by not limited to: 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, and 1.9. In a further embodiment, an odds ratio of at least 1.2 is significant. In a further embodiment, an odds ratio of at least about 1.5 is significant. In a further embodiment, a significant increase in risk is at least about 1.7 is significant. In a further embodiment, a significant increase in risk is at least about 20%, including but not limited to about 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95, and 98%. In a further embodiment, a significant increase in risk is at least about 50%. It is understood however, that identifying whether a risk is medically significant may also depend on a variety of factors, including the specific disease, the haplotype, and often, environmental factors.

The invention also pertains to methods of diagnosing a susceptibility to myocardial infarction, ACS, stroke or PAOD in an individual, comprising screening for an at-risk haplotype in the FLAP nucleic acid that is more frequently present in an individual susceptible to myocardial infarction (affected), compared to the frequency of its presence in a healthy individual

(control), wherein the presence of the haplotype is indicative of susceptibility to myocardial infarction. Standard techniques for genotyping for the presence of SNPs and/or microsatellite markers that are associated with myocardial infarction, ACS, stroke or PAOD can be used, such as
5 fluorescent based techniques (Chen, *et al.*, *Genome Res.* 9, 492 (1999), PCR, LCR, Nested PCR and other techniques for nucleic acid amplification. In a preferred embodiment, the method comprises assessing in an individual the presence or frequency of SNPs and/or microsatellites in the FLAP nucleic acid that are associated with myocardial infarction, ACS, stroke or PAOD,
10 wherein an excess or higher frequency of the SNPs and/or microsatellites compared to a healthy control individual is indicative that the individual is susceptible to myocardial infarction, ACS, stroke or PAOD.

See table 9 for SNPs that comprise haplotypes that can be used as screening tools. See also Table 3 that sets forth SNPs and markers for use as screening
15 tools.

In one embodiment, the at-risk haplotype is characterized by the presence of polymorphism(s) represented in Table 3. For example, DG00AAFIU, where the SNP can be a "C" or a "T"; SG13S25, where the SNP can be a "G" or an "A"; DG00AAJFF, where the SNP can be a "G" or
20 an "A"; DG00AAHII, where the SNP can be a "G" or an "A"; DG00AAHID, where the SNP can be a "T" or an "A"; B_SNP_310657, where the SNP can be a "G" or an "A"; SG13S30, where the SNP can be a "G" or a "T"; SG13S32, where the SNP can be a "C" or an "A"; SG13S42, where the SNP can be a "G" or an "A"; and SG13S35, where the SNP can be
25 a "G" or an "A".

Kits (*e.g.*, reagent kits) useful in the methods of diagnosis comprise components useful in any of the methods described herein, including for example, hybridization probes or primers as described herein (*e.g.*, labeled probes or primers), reagents for detection of labeled molecules, restriction
30 enzymes (*e.g.*, for RFLP analysis), allele-specific oligonucleotides, antibodies which bind to altered or to non-altered (native) FLAP polypeptide,

means for amplification of nucleic acids comprising a FLAP, or means for analyzing the nucleic acid sequence of a nucleic acid described herein, or for analyzing the amino acid sequence of a polypeptide as described herein, etc. In one embodiment, a kit for diagnosing susceptibility to MI, ACS, stroke or PAOD can comprise primers for nucleic acid amplification of a region in the FLAP nucleic acid comprising an at-risk haplotype that is more frequently present in an individual having MI, ACS, stroke or PAOD or susceptible to MI, ACS, stroke or PAOD. The primers can be designed using portions of the nucleic acids flanking SNPs that are indicative of MI. In a particularly preferred embodiment, the primers are designed to amplify regions of the FLAP nucleic acid associated with an at-risk haplotype for MI, ACS, stroke or PAOD, as shown in Table 9, or more particularly the haplotype defined by the following SNP markers: In one embodiment, a haplotype associated with a susceptibility to myocardial infarction, ACS, stroke or PAOD comprises markers DG00AAFIU, SG13S25, DG00AAJFF, DG00AAHII, SG13S32 and SG13S35 at the 13q12 locus. In one particular embodiment, the presence of the alleles T, G, G, G, A and G at DG00AAFIU, SG13S25, DG00AAJFF, DG00AAHII, SG13S32 and SG13S35, respectively (the B6 haplotype), is diagnostic of susceptibility to myocardial infarction, ACS, stroke or PAOD. In another embodiment, a haplotype associated with a susceptibility to myocardial infarction, ACS, stroke or PAOD comprises markers DG00AAFIU, SG13S25, DG00AAHII, SG13S30 and SG13S42 at the 13q12 locus. In one particular embodiment, the presence of the alleles T, G, G, G and A at DG00AAFIU, SG13S25, DG00AAHII, SG13S30 and SG13S42, respectively (the B5 haplotype), is diagnostic of susceptibility to myocardial infarction, ACS, stroke or PAOD. In a third embodiment, a haplotype associated with a susceptibility to myocardial infarction, ACS, stroke or PAOD comprises markers SG13S25, DG00AAHII, SG13S30 and SG13S42 at the 13q12 locus. In one particular embodiment, the presence of the alleles G, G, G and A at SG13S25, DG00AAHII, SG13S30 and SG13S42, respectively (the B4 haplotype), is diagnostic of susceptibility to myocardial

infarction, ACS, stroke or PAOD. In a fourth embodiment, a haplotype associated with a susceptibility to myocardial infarction, ACS, stroke or PAOD comprises markers DG00AAFIU, SG13S25, DG00AAHID, B_SNP_310657 and SG13S32 at the 13q12 locus. In one particular embodiment, the presence of the alleles T, G, T, G and A at DG00AAFIU, SG13S25, DG00AAHID, B_SNP_310657 and SG13S32, respectively (the A5 haplotype), is diagnostic of susceptibility to myocardial infarction, ACS, stroke or PAOD. In a fifth embodiment, a haplotype associated with a susceptibility to myocardial infarction, ACS, stroke or PAOD comprises markers SG13S25, DG00AAHID, B_SNP_310657 and SG13S32 at the 13q12 locus. In one particular embodiment, the presence of the alleles G, T, G and A at SG13S25, DG00AAHID, B_SNP_310657 and SG13S32, respectively (the A4 haplotype), is diagnostic of susceptibility to myocardial infarction, ACS, stroke or PAOD.

SCREENING ASSAYS AND AGENTS IDENTIFIED THEREBY

The invention provides methods (also referred to herein as “screening assays”) for identifying the presence of a nucleotide that hybridizes to a nucleic acid of the invention, as well as for identifying the presence of a polypeptide encoded by a nucleic acid of the invention. In one embodiment, the presence (or absence) of a nucleic acid molecule of interest (*e.g.*, a nucleic acid that has significant homology with a nucleic acid of the invention) in a sample can be assessed by contacting the sample with a nucleic acid comprising a nucleic acid of the invention (*e.g.*, a nucleic acid having the sequence of one of SEQ ID NOs: 1 or 3 or the complement thereof, or a nucleic acid encoding an amino acid having the sequence of SEQ ID NO: 2, or a fragment or variant of such nucleic acids), under stringent conditions as described above, and then assessing the sample for the presence (or absence) of hybridization. In a preferred embodiment, high stringency conditions are conditions appropriate for selective hybridization. In another embodiment, a sample containing a nucleic acid molecule of

interest is contacted with a nucleic acid containing a contiguous nucleic acid sequence (*e.g.*, a primer or a probe as described above) that is at least partially complementary to a part of the nucleic acid molecule of interest (*e.g.*, a FLAP nucleic acid), and the contacted sample is assessed for the presence or absence of hybridization. In a preferred embodiment, the nucleic acid containing a contiguous nucleic acid sequence is completely complementary to a part of the nucleic acid molecule of interest.

In any of these embodiments, all or a portion of the nucleic acid of interest can be subjected to amplification prior to performing the hybridization.

In another embodiment, the presence (or absence) of a polypeptide of interest, such as a polypeptide of the invention or a fragment or variant thereof, in a sample can be assessed by contacting the sample with an antibody that specifically hybridizes to the polypeptide of interest (*e.g.*, an antibody such as those described above), and then assessing the sample for the presence (or absence) of binding of the antibody to the polypeptide of interest.

In another embodiment, the invention provides methods for identifying agents (*e.g.*, fusion proteins, polypeptides, peptidomimetics, prodrugs, receptors, binding agents, antibodies, small molecules or other drugs, or ribozymes which alter (*e.g.*, increase or decrease) the activity of the polypeptides described herein, or which otherwise interact with the polypeptides herein. For example, such agents can be agents which bind to polypeptides described herein (*e.g.*, binding agent for members of the leukotriene pathway, such as FLAP binding agents); which have a stimulatory or inhibitory effect on, for example, activity of polypeptides of the invention; or which change (*e.g.*, enhance or inhibit) the ability of the polypeptides of the invention to interact with members of the leukotriene pathway binding agents (*e.g.*, receptors or other binding agents); or which alter posttranslational processing of the leukotriene pathway member polypeptide, such as a FLAP polypeptide (*e.g.*, agents that alter proteolytic

processing to direct the polypeptide from where it is normally synthesized to another location in the cell, such as the cell surface; agents that alter proteolytic processing such that more polypeptide is released from the cell, etc.)

5 In one embodiment, the invention provides assays for screening candidate or test agents that bind to or modulate the activity of polypeptides described herein (or biologically active portion(s) thereof), as well as agents identifiable by the assays. Test agents can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or
10 solution phase libraries; synthetic library methods requiring deconvolution; the “one-bead one-compound” library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to polypeptide libraries, while the other four approaches are
15 applicable to polypeptide, non-peptide oligomer or small molecule libraries of compounds (Lam, K.S., *Anticancer Drug Des.* 12:145 (1997)).

 In one embodiment, to identify agents which alter the activity of a FLAP polypeptide, a cell, cell lysate, or solution containing or expressing a FLAP polypeptide (*e.g.*, SEQ ID NO: 2 or another splicing variant encoded
20 by a FLAP nucleic acid, such as a nucleic acid comprising a SNP as shown in Table 3), or a fragment or derivative thereof (as described above), can be contacted with an agent to be tested; alternatively, the polypeptide can be contacted directly with the agent to be tested. The level (amount) of FLAP activity is assessed (*e.g.*, the level (amount) of FLAP activity is measured,
25 either directly or indirectly), and is compared with the level of activity in a control (*i.e.*, the level of activity of the FLAP polypeptide or active fragment or derivative thereof in the absence of the agent to be tested). If the level of the activity in the presence of the agent differs, by an amount that is statistically significant, from the level of the activity in the absence of the
30 agent, then the agent is an agent that alters the activity of a FLAP polypeptide. An increase in the level of FLAP activity in the presence of the

agent relative to the activity in the absence of the agent, indicates that the agent is an agent that enhances FLAP activity. Similarly, a decrease in the level of FLAP activity in the presence of the agent, relative to the activity in the absence of the agent, indicates that the agent is an agent that inhibits FLAP activity. In another embodiment, the level of activity of a FLAP polypeptide or derivative or fragment thereof in the presence of the agent to be tested, is compared with a control level that has previously been established. A statistically significant difference in the level of the activity in the presence of the agent from the control level indicates that the agent alters FLAP activity.

The present invention also relates to an assay for identifying agents which alter the expression of a FLAP nucleic acid (*e.g.*, antisense nucleic acids, fusion proteins, polypeptides, peptidomimetics, prodrugs, receptors, binding agents, antibodies, small molecules or other drugs, or ribozymes; which alter (*e.g.*, increase or decrease) expression (*e.g.*, transcription or translation) of the nucleic acid or which otherwise interact with the nucleic acids described herein, as well as agents identifiable by the assays. For example, a solution containing a nucleic acid encoding a FLAP polypeptide (*e.g.*, a FLAP nucleic acid) can be contacted with an agent to be tested. The solution can comprise, for example, cells containing the nucleic acid or cell lysate containing the nucleic acid; alternatively, the solution can be another solution that comprises elements necessary for transcription/translation of the nucleic acid. Cells not suspended in solution can also be employed, if desired. The level and/or pattern of FLAP expression (*e.g.*, the level and/or pattern of mRNA or of protein expressed, such as the level and/or pattern of different splicing variants) is assessed, and is compared with the level and/or pattern of expression in a control (*i.e.*, the level and/or pattern of the FLAP expression in the absence of the agent to be tested). If the level and/or pattern in the presence of the agent differ, by an amount or in a manner that is statistically significant, from the level and/or pattern in the absence of the agent, then the agent is an agent that alters the expression of the FLAP

nucleic acid. Enhancement of FLAP expression indicates that the agent is an activator of FLAP activity. Similarly, inhibition of FLAP expression indicates that the agent is a repressor of FLAP activity.

5 In another embodiment, the level and/or pattern of FLAP polypeptide(s) (*e.g.*, different splicing variants) in the presence of the agent to be tested, is compared with a control level and/or pattern that have previously been established. A level and/or pattern in the presence of the agent that differs from the control level and/or pattern by an amount or in a manner that is statistically significant indicates that the agent alters FLAP
10 expression.

In another embodiment of the invention, agents which alter the expression of a FLAP nucleic acid or which otherwise interact with the nucleic acids described herein, can be identified using a cell, cell lysate, or solution containing a nucleic acid encoding the promoter region of the FLAP
15 nucleic acid operably linked to a reporter gene. After contact with an agent to be tested, the level of expression of the reporter gene (*e.g.*, the level of mRNA or of protein expressed) is assessed, and is compared with the level of expression in a control (*i.e.*, the level of the expression of the reporter gene in the absence of the agent to be tested). If the level in the presence of
20 the agent differs, by an amount or in a manner that is statistically significant, from the level in the absence of the agent, then the agent is an agent that alters the expression of the FLAP nucleic acid, as indicated by its ability to alter expression of a nucleic acid that is operably linked to the FLAP nucleic acid promoter.

25 Enhancement of the expression of the reporter indicates that the agent is an activator of FLAP expression. Similarly, inhibition of the expression of the reporter indicates that the agent is a repressor of FLAP expression. In another embodiment, the level of expression of the reporter in the presence of the test agent, is compared with a control level that has previously been
30 established. A level in the presence of the agent that differs from the control

level by an amount or in a manner that is statistically significant indicates that the agent alters expression.

Agents which alter the amounts of different splicing variants encoded by a FLAP nucleic acid (*e.g.*, an agent which enhances expression of a first splicing variant, and which inhibits expression of a second splicing variant),
5 as well as agents which stimulate activity of a first splicing variant and inhibit activity of a second splicing variant, can easily be identified using these methods described above.

In other embodiments of the invention, assays can be used to assess
10 the impact of a test agent on the activity of a polypeptide relative to a FLAP binding agent. For example, a cell that expresses a compound that interacts with a FLAP nucleic acid (herein referred to as a "FLAP binding agent", which can be a polypeptide or other molecule that interacts with a FLAP nucleic acid, such as a receptor, or another molecule, such as 5-LO) is
15 contacted with a FLAP in the presence of a test agent, and the ability of the test agent to alter the interaction between the FLAP and the FLAP binding agent is determined. Alternatively, a cell lysate or a solution containing the FLAP binding agent, can be used. An agent which binds to the FLAP or the FLAP binding agent can alter the interaction by interfering with, or
20 enhancing the ability of the FLAP to bind to, associate with, or otherwise interact with the FLAP binding agent. Determining the ability of the test agent to bind to a FLAP nucleic acid or a FLAP nucleic acid binding agent can be accomplished, for example, by coupling the test agent with a radioisotope or enzymatic label such that binding of the test agent to the
25 polypeptide can be determined by detecting the labeled with ^{125}I , ^{35}S , ^{14}C or ^3H , either directly or indirectly, and the radioisotope detected by direct counting of radioemmission or by scintillation counting. Alternatively, test agents can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label
30 detected by determination of conversion of an appropriate substrate to product. It is also within the scope of this invention to determine the ability

of a test agent to interact with the polypeptide without the labeling of any of the interactants. For example, a microphysiometer can be used to detect the interaction of a test agent with a FLAP or a FLAP binding agent without the labeling of either the test agent, FLAP, or the FLAP binding agent.

5 McConnell, H.M. *et al.*, *Science* 257:1906-1912 (1992). As used herein, a “microphysiometer” (*e.g.*, Cytosensor™) is an analytical instrument that measures the rate at which a cell acidifies its environment using a light-addressable potentiometric sensor (LAPS). Changes in this acidification rate can be used as an indicator of the interaction between ligand and
10 polypeptide.

Thus, these receptors can be used to screen for compounds that are agonists for use in treating a disease or condition associated with FLAP or a susceptibility to a disease or condition associated with FLAP, or antagonists for studying a susceptibility to a disease or condition associated with FLAP
15 (*e.g.*, MI, ACS, stroke or PAOD). Drugs can be designed to regulate FLAP activation, that in turn can be used to regulate signaling pathways and transcription events of genes downstream or of proteins or polypeptides interacting with FLAP (*e.g.*, 5-LO).

In another embodiment of the invention, assays can be used to
20 identify polypeptides that interact with one or more FLAP polypeptides, as described herein. For example, a yeast two-hybrid system such as that described by Fields and Song (Fields, S. and Song, O., *Nature* 340:245-246 (1989)) can be used to identify polypeptides that interact with one or more FLAP
25 polypeptides. In such a yeast two-hybrid system, vectors are constructed based on the flexibility of a transcription factor that has two functional domains (a DNA binding domain and a transcription activation domain). If the two domains are separated but fused to two different proteins that interact with one another, transcriptional activation can be achieved, and
30 transcription of specific markers (*e.g.*, nutritional markers such as His and Ade, or color markers such as lacZ) can be used to identify the presence of

interaction and transcriptional activation. For example, in the methods of the invention, a first vector is used which includes a nucleic acid encoding a DNA binding domain and also a FLAP polypeptide, splicing variant, or fragment or derivative thereof, and a second vector is used which includes a nucleic acid encoding a transcription activation domain and also a nucleic acid encoding a polypeptide which potentially may interact with the FLAP polypeptide, splicing variant, or fragment or derivative thereof (*e.g.*, a FLAP polypeptide binding agent or receptor). Incubation of yeast containing the first vector and the second vector under appropriate conditions (*e.g.*, mating conditions such as used in the Matchmaker™ system from Clontech (Palo Alto, California, USA)) allows identification of colonies that express the markers of interest. These colonies can be examined to identify the polypeptide(s) that interact with the FLAP polypeptide or fragment or derivative thereof. Such polypeptides may be useful as agents that alter the activity of expression of a FLAP polypeptide, as described above.

In more than one embodiment of the above assay methods of the present invention, it may be desirable to immobilize either the FLAP, the FLAP binding agent, or other components of the assay on a solid support, in order to facilitate separation of complexed from uncomplexed forms of one or both of the polypeptides, as well as to accommodate automation of the assay. Binding of a test agent to the polypeptide, or interaction of the polypeptide with a binding agent in the presence and absence of a test agent, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtitre plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein (*e.g.*, a glutathione-S-transferase fusion protein) can be provided which adds a domain that allows a FLAP nucleic acid or a FLAP binding agent to be bound to a matrix or other solid support.

In another embodiment, modulators of expression of nucleic acid molecules of the invention are identified in a method wherein a cell, cell lysate, or solution containing a nucleic acid encoding a FLAP nucleic acid is

contacted with a test agent and the expression of appropriate mRNA or polypeptide (*e.g.*, splicing variant(s)) in the cell, cell lysate, or solution, is determined. The level of expression of appropriate mRNA or polypeptide(s) in the presence of the test agent is compared to the level of expression of mRNA or polypeptide(s) in the absence of the test agent. The test agent can then be identified as a modulator of expression based on this comparison. For example, when expression of mRNA or polypeptide is greater (statistically significantly greater) in the presence of the test agent than in its absence, the test agent is identified as a stimulator or enhancer of the mRNA or polypeptide expression. Alternatively, when expression of the mRNA or polypeptide is less (statistically significantly less) in the presence of the test agent than in its absence, the test agent is identified as an inhibitor of the mRNA or polypeptide expression. The level of mRNA or polypeptide expression in the cells can be determined by methods described herein for detecting mRNA or polypeptide.

In yet another embodiment, the invention provides methods for identifying agents (*e.g.*, fusion proteins, polypeptides, peptidomimetics, prodrugs, receptors, binding agents, antibodies, small molecules or other drugs, or ribozymes) which alter (*e.g.*, increase or decrease) the activity of a member of leukotriene pathway binding agent, such as a FLAP binding agent (*e.g.*, 5-LO), as described herein. For example, such agents can be agents which have a stimulatory or inhibitory effect on, for example, the activity of a member of leukotriene pathway binding agent, such as a FLAP binding agent; which change (*e.g.*, enhance or inhibit) the ability a member of leukotriene pathway binding agents, (*e.g.*, receptors or other binding agents) to interact with the polypeptides of the invention; or which alter posttranslational processing of the member of leukotriene pathway binding agent, (*e.g.*, agents that alter proteolytic processing to direct the member of the leukotriene pathway binding agent from where it is normally synthesized to another location in the cell, such as the cell surface; agents that alter

proteolytic processing such that more active binding agent is released from the cell, etc.).

For example, the invention provides assays for screening candidate or test agents that bind to or modulate the activity of a member of the leukotriene pathway (or enzymatically active portion(s) thereof), as well as agents identifiable by the assays. As described above, test agents can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the “one-bead one-compound” library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to polypeptide libraries, while the other four approaches are applicable to polypeptide, non-peptide oligomer or small molecule libraries of compounds (Lam, K.S. *Anticancer Drug Des.*, 12:145 (1997)).

In one embodiment, to identify agents which alter the activity of a member of the leukotriene pathway (such as a FLAP binding agent, or an agent which binds to a member of the leukotriene pathway (a “binding agent”)), a cell, cell lysate, or solution containing or expressing a binding agent (*e.g.*, 5-LO, or a leukotriene pathway member receptor, or other binding agent), or a fragment (*e.g.*, an enzymatically active fragment) or derivative thereof, can be contacted with an agent to be tested; alternatively, the binding agent (or fragment or derivative thereof) can be contacted directly with the agent to be tested. The level (amount) of binding agent activity is assessed (either directly or indirectly), and is compared with the level of activity in a control (*i.e.*, the level of activity in the absence of the agent to be tested). If the level of the activity in the presence of the agent differs, by an amount that is statistically significant, from the level of the activity in the absence of the agent, then the agent is an agent that alters the activity of the member of the leukotriene pathway. An increase in the level of the activity relative to a control, indicates that the agent is an agent that

enhances (is an agonist of) the activity. Similarly, a decrease in the level of activity relative to a control, indicates that the agent is an agent that inhibits (is an antagonist of) the activity. In another embodiment, the level of activity in the presence of the agent to be tested, is compared with a control level that has previously been established. A level of the activity in the presence of the agent that differs from the control level by an amount that is statistically significant indicates that the agent alters the activity.

This invention further pertains to novel agents identified by the above-described screening assays. Accordingly, it is within the scope of this invention to further use an agent identified as described herein in an appropriate animal model. For example, an agent identified as described herein (*e.g.*, a test agent that is a modulating agent, an antisense nucleic acid molecule, a specific antibody, or a polypeptide-binding agent) can be used in an animal model to determine the efficacy, toxicity, or side effects of treatment with such an agent. Alternatively, an agent identified as described herein can be used in an animal model to determine the mechanism of action of such an agent.

Furthermore, this invention pertains to uses of novel agents identified by the above-described screening assays for treatments as described herein. In addition, an agent identified as described herein can be used to alter activity of a polypeptide encoded by a FLAP nucleic acid, or to alter expression of a FLAP nucleic acid, by contacting the polypeptide or the nucleic acid (or contacting a cell comprising the polypeptide or the nucleic acid) with the agent identified as described herein.

25

The present invention is now illustrated by the following Examples, which are not intended to be limiting in any way. The teachings of all references cited are incorporated herein in their entirety.

EXAMPLE 1: IDENTIFICATION OF GENE AND HAPLOTYPES ASSOCIATED WITH MI

SUBJECTS AND METHODS

5 *Study population*

Patients entering the study were defined from an infarction registry that includes all MIs (over 8,000 patients) in Iceland 1981-2000. This registry is a part of the World Health Organization MONICA Project (The World Health Organization MONICA Project (monitoring trends and determinants in cardiovascular disease): a major international collaboration. (WHO MONICA Project Principal Investigators. *J Clin. Epidemiol.* 1988; 41:105-14). Diagnosis of all patients in the registry follow strict diagnostic rules based on symptoms, electrocardiograms, cardiac enzymes, and necropsy findings.

15 Blood samples from 570 female MI patients and 1380 male patients, both cases with a family history and sporadic cases were collected. For each patient that participated, blood was collected from 2 relatives (unaffected or affected). Their genotypes were used to help with construction of haplotypes.

Linkage analysis

20 One hundred and sixty female MI patients were clustered into large extended families such that each patient is related to at least one other patient within and including six meiotic events (*e.g.*, 6 meiotic events separate second cousins). The information regarding the relatedness of patients was obtained from an encrypted genealogy database that covers the entire Icelandic nation (Gulcher *et al.*, *Eur. J. Hum. Genet.* 8: 739-742 (2000)). A
25 genomewide scan was performed using a framework map of 1000 microsatellite markers, using protocols described elsewhere (Gretarsdottir S., *et al. Am. J. Hum. Genet.*, 70: 593-603, 2002)). The marker order and positions were obtained from deCODE genetics' high resolution genetic map
30 (Kong A, *et al.*, *Nat. genet.*, 31: 241-247 (2002)). The population-based

allelic frequencies were constructed from a cohort of more than 30,000 Icelanders who have participated in genetic studies of various disease projects. Additional markers were genotyped within the highest linkage peak on chromosome 13 to increase the information on identity by descent within the families. For those markers at least 180 Icelandic controls were genotyped to derive the population allele frequencies.

For statistical analysis, multipoint, affected-only allele-sharing methods were used to assess evidence for linkage. All results, both the LOD and the non-parametric linkage (NPL) score, were obtained using the program ALLEGRO (Gudbjartsson D.F., *et al.*, *Nat Genet.*, 25: 12-13(2000)). The baseline linkage analysis (Gretarsdottir S., *et al.*, *Am. J. Hum. Genet.* 70: 593-603, (2002)) uses the Spairs scoring function (Whittemore AS, and Haplern J A., *Biometrics* 50: 118-127 (1994)) and Kruglyak *et al.*, *Am. J. Hum. Genet.*, 58:1347-1363 (1996)) the exponential allele-sharing model (Kong A., and Cox N.J., *Am. J. Hum. Genet.* 61:1179-1188 (1997)), and a family weighting scheme which is halfway, on the log-scale, between weighing each affected pairs equally and weighing each family equally.

Ultra-fine mapping and haplotype analysis:

A candidate susceptibility locus was defined as the region under the LOD score curve where the score was one lod lower than the highest lod score. This region (approx. 12Mb) was ultra-finemapped with microsatellite markers with an average spacing between markers of less than 100Kb. All usable microsatellite markers found in public databases and mapped within that region were used. In addition, microsatellite markers identified within the deCODE genetics sequence assembly of the human genome were used.

Haplotype analysis.

The frequencies of haplotypes were estimated in the patient and the control groups using an expectation-maximization algorithm (Dempster A.P.

et al., *J. R. Stat. Soc. B.* 39: 1-389 (1977)). An implementation of this algorithm that can handle missing genotypes and uncertainty with the phase was used. Under the null hypothesis, the patients and the controls are assumed to have identical frequencies. Using a likelihood approach, an
5 alternative hypothesis where a candidate at-risk-haplotype is allowed to have a higher frequency in patients than controls, while the ratios of the frequencies of other haplotypes are assumed to be the same in both groups was tested. Likelihoods are maximized separately under both hypothesis and a corresponding 1-df likelihood ratio statistic is used to evaluate the statistic
10 significance.

To look for at-risk-haplotypes in the 1-lod drop, association of all possible combinations of genotyped markers was studied, provided those markers spanned a region of size less than 1000 Kb. Due to a certain amount of testing, the p -values were adjusted using simulations. The combined
15 patient and control groups were randomly divided into two sets, equal in size to the original group of patients and controls. The haplotype analysis was then repeated and the most significant p -value registered was observed. This randomization scheme was repeated over 100 times to construct an empirical distribution of p -values.

Results and Discussion

In a genome wide search for susceptibility genes for MI, a locus was mapped to a location on chromosome 13q12. FIG. 1 shows the multipoint non-parametric LOD scores a linkage scan for a framework marker map on
25 chromosome 13. A LOD score suggestive of linkage of 2.5 was found centered at marker D13S289. The marker map for chromosome 13 that was used in the linkage analysis is shown in Table 1. The LOD score at this location remained with increased number of microsatellite markers which increased information content of the linkage (FIG. 2).

30 A very large number of microsatellite markers were then added within the central 12 megabase (Mb) segment under the LOD score defined

by the drop in one LOD from the peak marker. FIG. 3.1 shows the results from a haplotype association case-control analysis of 437 female MI patients versus 721 controls using combinations of 4 and 5 microsatellite markers to define the test haplotypes. The most significant microsatellite marker haplotype association across this entire 12 Mb segment was found using markers DG13S1103, DG13S166, DG13S1287, DG13S1061 and DG13S301, with alleles 4, 0, 2, 14 and 3, respectively (p -value of 1.02×10^{-7}). Carrier frequency of this haplotype is 7.3% in female MI patients and 0.3% in controls. There are several other haplotypes that show great association to MI that overlap the first haplotype. The 80Kb segment that is defined by two markers (DG13S166 and D13S1238) common to all the haplotypes shown in the figure includes only one gene, FLAP (ALOX5AP). A two marker haplotype involving alleles 0 and -2 for markers DG13S166 and D13S1238, respectively, is found in excess in patients. Carrier frequency of this haplotype was estimated to be 27% in female MI patients and 15.4% in controls (p -value 1×10^{-3}). This was our first evidence that variation in the FLAP gene might contribute to MI risk.

To confirm this observation, the FLAP gene was sequenced in its entirety and numerous SNPs were defined. Many of these were used to genotype 437 female MI patients, 1049 male MI patients, and 811 controls. In a case-control study of the MI patients using these data, several haplotypes were found, that were significantly over-represented in the female MI patients compared to controls (see Table 6). These haplotypes were highly correlated to each other. Table 7 shows two haplotypes that are representative of these female MI risk haplotypes. They have relative risks of 2.4 and 4 and are carried by 23% and 13% of female MI patients, respectively. Table 8 shows that these same haplotypes show association to male MI although with lower relative risks.

In an effort to identify haplotypes involving only SNP markers that associate with MI, more SNPs were identified by sequencing the FLAP gene and the region flanking the gene. Currently, a total number of 45 SNPs have

been genotyped on 1343 patients and 624 unrelated controls. Two correlated series of SNP haplotypes were observed in excess in patients, denoted as A and B in Table 9. The length of the haplotypes varies between 33 and 69 Kb, and the haplotypes cover one or two blocks of linkage disequilibrium. Both series of haplotypes contain the common allele G of the SNP SG13S25. All haplotypes in the A series contain the SNP DG00AAHID, while all haplotypes in the B series contain the SNP DG00AAHII. In the B series, the haplotypes B4, B5, and B6 have a relative risk (RR) greater than 2 and with allelic frequencies above 10%. The haplotypes in A series have slightly lower RR and lower p-values, but higher frequency (15-16%). The haplotypes in series B and A are strongly correlated, i.e. the haplotypes in B define a subset of the haplotypes in A. Hence, haplotypes B are more specific than A. Haplotypes A are however more sensitive, i.e. they capture more individuals with the putative mutation, as is observed in the population attributable risk which is less for B than for A. Furthermore, these haplotypes show similar risk ratios and allelic frequency for early-onset patients (defined as onset of first MI before the age of 55) and for both gender. In addition, analyzing various groups of patients with known risk factors, such as hypertension, high cholesterol, smoking and diabetes, did not reveal any significant correlation with these haplotypes, indicating that the haplotypes in the FLAP gene represent an independent genetic susceptibility factor for MI.

The FLAP gene encodes for a protein that is required for leukotriene synthesis (LTA4, LTB4, LTC4, LTD4, LTE4). Inhibitors of its function impede translocation of 5-lipoxygenase from the cytoplasm to the cell membrane and inhibit activation of 5-lipoxygenase. The leukotrienes are potent inflammatory lipid mediators derived from arachidonic acid that can potentially contribute to development of atherosclerosis and destabilization of atherosclerotic plaques through lipid oxidation and/or proinflammatory effects. Allen *et al.*, (*Circulation*. 97: 2406-2413(1998)) described a novel mechanism in which atherosclerosis is associated with the appearance of a

leukotriene receptor(s) capable of inducing hyperreactivity of human epicardial coronary arteries in response to LTC₄ and LTD₄. Allen *et al.* show a photomicrograph of a section of human atherosclerotic coronary artery a positive staining of a number of members of the leukotriene pathway, including FLAP. Mehrabian *et al.* described the identification of 5-Lipoxygenase (5-LO) as a major gene contributing to atherosclerosis susceptibility in mice. Mehrabian *et al.* described that heterozygous deficiency for the enzyme in a knockout model decreased the atherosclerotic lesion size in LDL^{-/-} mice by about 95%. Mehrabian *et al.* show that the enzyme is expressed abundantly in macrophage-rich regions of atherosclerotic lesions, and suggested that 5-LO and/or its products might act locally to promote lesion development (Mehrabian *et al.*, *Circulation Research*. 91:120 (2002)). Studies of FLAP inhibition in animal models of atherosclerosis are scarce. However, in a rabbit model of acute MI assessed 72 hours after coronary artery ligation the FLAP-inhibitor BAYx1005 markedly reduced mortality, from 65% to 25%, and blocked the increase in CPK and neutrophil accumulation as well as the ECG-changes observed in sham treated animals (*J. Pharmacol. Exp. Ther.*, 276:332 (1996)).

Mutations and /or polymorphisms within the FLAP nucleic acid, and other members of the same pathway (*e.g.*, 5-lipoxygenase, LTA₄ Hydrolase, LTB₄ receptors, LTC₄ Synthase, and CysLT₂ receptor), that show association with the disease, can be used as a diagnostic test. The members of the 5-LO pathway in particular are valuable therapeutic targets for myocardial infarction.

Table 1 The marker map for chromosome 13 used in the linkage analysis.

Location (cM)	Marker	Location (cM)	Marker
6	D13S175	63.9	D13S170
9.8	D13S1243	68.7	D13S265
13.5	D13S1304	73	D13S167
17.2	D13S217	76.3	D13S1241
21.5	D13S289	79.5	D13S1298
25.1	D13S171	81.6	D13S1267
28.9	D13S219	84.7	D13S1256
32.9	D13S218	85.1	D13S158
38.3	D13S263	87	D13S274
42.8	D13S326	93.5	D13S173
45.6	D13S153	96.7	D13S778
49.4	D13S1320	102.7	D13S1315
52.6	D13S1296	110.6	D13S285
55.9	D13S156	115	D13S293
59.8	D13S1306		

Table 2 Marker Map for the second step of Linkage Analysis

Location (cM)	Marker	Location (cM)	Marker
1.758	D13S175	42.585	D13S1248
9.235	D13S787	44.288	D13S1233
11.565	D13S1243	44.377	D13S263
16.898	D13S221	45.535	D13S325
17.454	D13S1304	45.536	D13S1270
18.011	D13S1254	45.537	D13S1276
18.59	D13S625	49.149	D13S326
19.308	D13S1244	49.532	D13S1272
19.768	D13S243	52.421	D13S168
22.234	D13S1250	52.674	D13S287
22.642	D13S1242	60.536	D13S1320
22.879	D13S217	64.272	D13S1296
25.013	D13S1299	71.287	D13S156
28.136	D13S289	76.828	D13S1306
28.678	D13S290	77.86	D13S170
29.134	D13S1287	82.828	D13S265
30.073	D13S260	91.199	D13S1241
31.98	D13S171	93.863	D13S1298
32.859	D13S267	97.735	D13S779
33.069	D13S1293	100.547	D13S1256
33.07	D13S620	102.277	D13S274
34.131	D13S220	111.885	D13S173
36.427	D13S219	112.198	D13S796
39.458	D13S1808	115.619	D13S778
40.441	D13S218	119.036	D13S1315
41.113	D13S1288	126.898	D13S285
41.996	D13S1253	131.962	D13S293

Table 3 shows the exons with positions that encode the FLAP protein; markers, polymorphisms and SNPs identified within the genomic sequence by the methods described herein:

Table 3

NCBI build34; start chr. (bp)	NCBI build34; on stop 13 chr. (bp)	13 SNP/marker/ exon name	alias1	alias2	public SNP	Variation
28932432	28932432	SG13S421		DG00AAFQR	rs1556428	A/G
28960356	28960356	SG13S417		SNP13B_R1028729	rs1028729	C/T
28965803	28965803	SG13S418		SNP13B_Y1323898	rs1323898	A/G
28974627	28974627	SG13S44				A/G
28975101	28975101	SG13S45				C/G
28975315	28975315	SG13S46				A/G
28975353	28975353	SG13S50				C/T
28975774	28975774	SG13S52				A/G
28985244	28985244	SG13S53			rs1408167	A/C
28985303	28985303	SG13S55			rs1408169	A/G
28985423	28985423	SG13S56				G/T
28985734	28985734	SG13S57			rs6490471	C/T
28985902	28985902	SG13S58			rs6490472	A/G
29003869	29003869	SG13S59				C/G
29004696	29004696	SG13S60				A/G
29007670	29007670	SG13S419		SNP13B_K912392	rs912392	C/T
29015410	29015410	SG13S61				C/T
29025792	29025792	SG13S62				C/T
29026202	29026202	SG13S63			rs7997114	A/G
29026668	29026668	SG13S64				A/G
29038707	29038707	SG13S65				A/G
29042180	29042180	SG13S420		DG00AAFIV	rs2248564	A/T
29049355	29049355	SG13S66				A/G
29049446	29049446	SG13S67				C/T
29050416	29050416	SG13S69				A/C
29059348	29059348	SG13S70				A/G
29059383	29059383	SG13S71				A/G
29059402	29059402	SG13S72				G/T
29063702	29063949	D13S289				
29064359	29064753	DG13S166				
29066272	29066272	SG13S73				A/G
29070551	29070551	SG13S99	SNP_13_Y1323892	DG00AAFIU	rs1323892	C/T
29081983	29081983	SG13S382	FLA267479			A/G
29082200	29082200	SG13S383	FLA267696			A/G
29082357	29082357	SG13S384	FLA267853			A/G
29083350	29083350	SG13S381	FLA268846	DG00AAJER		C/G
29083518	29083518	SG13S366	FLA269014	DG00AAJES	rs4312166	A/G
29085102	29085102	SG13S385	FLA270742			C/T
29085190	29085190	SG13S386	FLA270830			A/G
29086224	29086224	SG13S1	FLA271864			G/T
29087473	29087473	SG13S2	FLA273371			A/G
29088090	29088090	SG13S367	FLA273988	DG00AAJEU	rs4474551	A/G
29088186	29088186	SG13S388	FLA274084			A/G
29088473	29088473	SG13S10	FLA274371			A/T
29089044	29089044	SG13S3	FLA274942			C/T
29089886	29089886	SG13S368	FLA275784	DG00AAJEV		C/T
29090025	29090025	SG13S369	FLA275923	DG00AAJEV		G/T
29090054	29090054	SG13S370	FLA275952	DG00AAJEX		A/G
29090997	29090997	SG13S4	FLA276895			G/C
29091307	29091307	SG13S5	FLA277205		rs4238133	G/T
29091580	29091580	SG13S389	FLA277478			A/G

29091780	29091780	SG13S90	FLA277678			
29092287	29092287	SG13S390	FLA278185			A/C
29092536	29092536	SG13S6	FLA278434		rs5004913	A/G
29092594	29092594	SG13S391	FLA278492			A/G
29092947	29092947	SG13S392	FLA278845			A/G
29093964	29093964	SG13S371	FLA279888			G/T
29094259	29094259	SG13S372	FLA280183	DG00AAJEY	rs4409939	A/G
29094999	29094999	SG13S393	FLA280923	DG00AAJEZ		A/G
29096688	29096688	SG13S373	FLA282612			A/T
29096813	29096813	SG13S374	FLA282737	DG00AAJFA		A/G
29096874	29096874	SG13S375	FLA282798	DG00AAJFB		A/G
29096962	29096962	SG13S376	FLA282886	DG00AAJFC		C/T
29097476	29097476	SG13S394	FLA283400	DG00AAJFD		A/G
29097553	29097553	SG13S25	FLA283477			C/G
29098486	29098486	SG13S395	FLA284410			A/G
29098891	29098891	SG13S396	FLA284815			A/G
29098979	29098979	SG13S397	FLA284903			A/C
29101965	29101965	SG13S377	FLA287889	DG00AAJFF		C/T
29103909	29103909	SG13S189	FLA289833			A/G
29104271	29104271	SG13S100	FLA290195	DG00AAHIK	rs4073259	C/G
29104629	29104629	SG13S398	FLA290553			A/G
29104646	29104646	SG13S94	FLA290570			C/G
29105099	29105099	SG13S101	FLA291023		rs4073261	C/T
29106329	29106329	SG13S95	FLA292253		rs4075474	C/T
29106652	29106652	SG13S102	FLA292576			G/T
29107138	29107138	SG13S103	FLA293062			A/T
29107404	29107404	SG13S104	FLA293328			C/T
29107668	29107812	EXON1				A/G
29107830	29107830	SG13S191	FLA293754	DG00AAFJT	rs4769055	A/C
29108398	29108398	SG13S105	FLA294322			A/G
29108579	29108579	SG13S106	FLA294503	DG00AAHII		A/G
29108919	29108919	SG13S107	FLA294843		rs4075131	A/G
29108972	29108972	SG13S108	FLA294896		rs4075132	C/T
29109112	29109112	SG13S109	FLA295036			A/G
29109182	29109182	SG13S110	FLA295106			A/G
29109344	29109344	SG13S111	FLA295268		rs4597169	C/T
29109557	29109557	SG13S112	FLA295481			C/T
29109773	29109773	SG13S113	FLA295697		rs4293222	C/G
29110096	29110096	SG13S114	FLA296020	DG00AAHID		A/T
29110178	29110178	SG13S115	FLA296102			A/T
29110508	29110508	SG13S116	FLA296432		rs4769871	C/T
29110630	29110630	SG13S117	FLA296554		rs4769872	A/G
29110689	29110689	SG13S118	FLA296613		rs4769873	C/T
29110862	29110862	SG13S119	FLA296786			A/G
29111889	29111889	SG13S120	FLA297813			C/T
29112174	29112174	SG13S121	FLA298098	DG00AAHIJ	rs4503649	A/G
29112264	29112264	SG13S122	FLA298188	DG00AAHIH		A/G
29112306	29112306	SG13S123	FLA298230			C/T
29112455	29112455	SG13S43	FLA298379		rs3885907	A/C
29112583	29112583	SG13S399	FLA298507			A/C
29112680	29112680	SG13S124	FLA298604		rs3922435	C/T
29113139	29113139	SG13S125	FLA299063			A/G
29114056	29114056	SG13S400	FLA299980			A/G
29114738	29114738	SG13S126	FLA300662			A/G
29114940	29114940	SG13S127	FLA300864			A/G
29115878	29115878	SG13S128	FLA302094		rs4254165	A/G

29116020	29116020	SG13S129	FLA302236		rs4360791	A/G
29116068	29116068	SG13S130	FLA302284			G/T
29116196	29116296	EXON2				
29116249	29116249	SG13S190	FLA302465			C/T
29116308	29116308	SG13S192	FLA302524	B_SNP_302524	rs3803277	A/C
29116344	29116344	SG13S193	FLA302560			A/G
29116401	29116401	SG13S88	FLA302617	B_SNP_302617	rs3803278	C/T
29116688	29116688	SG13S131	FLA302904			C/T
29117133	29117133	SG13S132	FLA303349			A/C
29117546	29117546	SG13S133	FLA303762		rs4356336	C/T
29117553	29117553	SG13S38	FLA303769		rs4584668	A/T
29117580	29117580	SG13S134	FLA303796			C/T
29117741	29117741	SG13S135	FLA303957		rs4238137	C/T
29117954	29117954	SG13S136	FLA304170		rs4147063	C/T
29118118	29118118	SG13S137	FLA304334	DG00AAHIG	rs4147064	C/T
29118815	29118815	SG13S86	FLA305031			A/G
29118873	29118873	SG13S87	FLA305089	DG00AAHOJ		A/G
29119069	29119069	SG13S138	FLA305285			C/T
29119138	29119138	SG13S139	FLA305354			C/G
29119289	29119289	SG13S140	FLA305505			A/G/T
29119462	29119462	SG13S141	FLA305678			C/T
29119740	29119740	SG13S39	FLA305956			G/T
29120939	29120939	SG13S142	FLA307155		rs4387455	C/T
29120949	29120949	SG13S143	FLA307165		rs4254166	C/T
29121342	29121342	SG13S144	FLA307558		rs4075692	A/G
29121572	29121572	SG13S145	FLA307788			C/G
29121988	29121988	SG13S146	FLA308204			C/T
29122253	29122253	SG13S26	FLA308469			C/T
29122283	29122283	SG13S27	FLA308499			A/G
29122294	29122294	SG13S147	FLA308510			C/T
29122298	29122298	SG13S28	FLA308514			G/T
29122311	29122311	SG13S148	FLA308527			G/T
29123370	29123370	SG13S98	FLA309586			G/T
29123635	29123635	SG13S149	FLA309851			A/G
29123643	29123643	SG13S29	FLA309859			A/C
29124188	29124259	EXON3				
29124441	29124441	SG13S89	FLA310657	B_SNP_310657	rs4769874	A/G
29124906	29124906	SG13S96	FLA311122		rs4072653	A/G
29125032	29125032	SG13S150	FLA311248			C/G
29125521	29125521	SG13S401	FLA311737			C/T
29125822	29125822	SG13S151	FLA312038			C/T
29125840	29125840	SG13S30	FLA312056			G/T
29127301	29127301	SG13S31	FLA313550			C/T
29128080	29128162	EXON4				
29128284	29128284	SG13S152	FLA314500			C/G
29128316	29128316	SG13S402	FLA314532		rs4468448	C/T
29128798	29128798	SG13S403	FLA315014		rs4399410	A/G
29129016	29129016	SG13S153	FLA315232			A/T
29129139	29129139	SG13S97	FLA315355			A/G
29129154	29129154	SG13S154	FLA315370			C/T
29129395	29129395	SG13S40	FLA315611			G/T
29129915	29129915	SG13S155	FLA316131		rs4769875	A/G
29130192	29130192	SG13S156	FLA316408			A/C
29130256	29130256	SG13S157	FLA316472			A/G
29130299	29130299	SG13S158	FLA316515			A/C
29130353	29130353	SG13S159	FLA316569			G/T

29130391	29130391	SG13S160	FLA316607		C/T
29130547	29130547	SG13S32	FLA316763		A/C
29131280	29131280	SG13S161	FLA317496		A/G
29131403	29131403	SG13S162	FLA317619		A/G
29131404	29131404	SG13S163	FLA317620		C/T
29131431	29131431	SG13S164	FLA317647	rs4769058	C/T
29131517	29131517	SG13S165	FLA317733		A/T
29131528	29131528	SG13S166	FLA317744	rs4769059	C/T
29131599	29131599	SG13S167	FLA317815	rs4769876	A/G
29132003	29132003	SG13S168	FLA318219		A/C
29133753	29133753	SG13S33	FLA319969		G/T
29134045	29134045	SG13S41	FLA320261		A/G
29134177	29134177	SG13S169	FLA320393		A/G
29134379	29134379	SG13S404	FLA320595	rs4427651	G/T
29135558	29135558	SG13S170	FLA321774	rs3935645	C/T
29135640	29135640	SG13S171	FLA321856	rs3935644	A/G
29135750	29135750	SG13S172	FLA321966		A/G
29135809	29135809	SG13S173	FLA322025		A/T
29135877	29135877	SG13S42	FLA322093	rs4769060	A/G
29136080	29136556	EXON5			
29136290	29136290	SG13S194	FLA322506		C/T
29136462	29136462	SG13S195	FLA322678	rs1132340	A/G
29136797	29136797	SG13S174	FLA323013		A/G
29137100	29137100	SG13S34	FLA323316		G/T
29137150	29137150	SG13S175	FLA323366		A/G
29137607	29137607	SG13S176	FLA323823		A/G
29137651	29137651	SG13S177	FLA323867		C/T
29137905	29137905	SG13S178	FLA324121		C/G
29138117	29138117	SG13S35	FLA324333		A/G
29138375	29138375	SG13S179	FLA324591		A/G
29138385	29138385	SG13S180	FLA324601		C/T
29138633	29138633	SG13S181	FLA324849	DG00AAHIF	rs4420371
29139153	29139153	SG13S182	FLA325369		C/T
29139277	29139277	SG13S183	FLA325493		rs4466940
29139435	29139435	SG13S184	FLA325651	DG00AAHOI	rs4445746
29139971	29139971	SG13S185	FLA326187		A/G
29140441	29140441	SG13S405	FLA326657		A/G
29140649	29140649	SG13S91	FLA326865		A/G
29140695	29140695	SG13S186	FLA326911	rs4769877	A/T
29140703	29140703	SG13S187	FLA326919		A/G
29140805	29140805	SG13S188	FLA327021	DG00AAJFE	A/G
29141049	29141049	SG13S406	FLA327265		C/T
29142392	29142392	SG13S92	FLA328644	rs4429158	C/T
29142397	29142397	SG13S93	FLA328649		A/G
29142712	29142712	SG13S36	FLA328964		C/T
29144013	29144013	SG13S407	FLA330265		C/T
29144203	29144203	SG13S408	FLA330455		C/T
29144234	29144589	D13S1238			
29144255	29144255	SG13S7	FLA330507		C/T
29144877	29144877	SG13S37	FLA331129		A/G
29144982	29144982	SG13S409	FLA331234		A/G
29144983	29144983	SG13S8	FLA331235	rs4491352	A/C
29145122	29145122	SG13S410	FLA331374	rs4319601	C/T
29145143	29145143	SG13S411	FLA331395		A/G
29145171	29145171	SG13S9	FLA331423		C/T
29145221	29145221	SG13S412	FLA331473	rs4769062	A/G
29145265	29145265	SG13S413	FLA331517	rs4238138	C/T

minor allele	minor allele frequenc y (%)	start position in sequence xx	end position in sequence xx
G	10.32	432	432
G	30.46	28356	28356
T	37.38	33803	33803
G	0.545	42627	42627
G	1.111	43101	43101
G	0.328	43315	43315
C	0.495	43353	43353
A	6.993	43774	43774
C	30.876	53244	53244
G	6.731	53303	53303
T	0.353	53423	53423
C	31.356	53734	53734
A	30.935	53902	53902
G	5.492	71869	71869
A	1.812	72696	72696
G	35.00	75670	75670
C	1.314	83410	83410
T	3.521	93792	93792
A	30.031	94202	94202
A	1.724	94668	94668
A	0.369	106707	106707
A	13.66	110180	110180
A	20.779	117355	117355
T	5.965	117446	117446
A	16.923	118416	118416
A	34.364	127348	127348
A	8.537	127383	127383
T	25.536	127402	127402
		131702	131949
		132359	132753
A	37.302	134272	134272
C	6.25	138551	138551
A	0.49	149983	149983
A	14.08	150200	150200
G	0.62	150357	150357
G	14.01	151350	151350
T	0.58	151518	151518
C	30.21	153102	153102
A	10.95	153190	153190
G	30.00	154224	154224
A	27.95	155473	155473
G	2.41	156090	156090
A	0.39	156186	156186
T	10.23	156473	156473
T	15.17	157044	157044
T	13.60	157886	157886
G	12.44	158025	158025
A	13.45	158054	158054
G	14.59	158997	158997
T	26.84	159307	159307
A	12.73	159580	159580

C	43.67	159780	159780
A	12.18	160287	160287
A	8.38	160536	160536
G	0.62	160594	160594
T	12.34	160947	160947
G	25.34	161964	161964
C	0.24	162259	162259
T	25.66	162999	162999
A	14.84	164688	164688
G	12.37	164813	164813
C	14.55	164874	164874
G	11.99	164962	164962
C	14.66	165476	165476
A	12.21	165553	165553
A	0.79	166486	166486
C	10.15	166891	166891
C	3.53	166979	166979
A	12.45	169965	169965
C	0.62	171909	171909
G	31.55	172271	172271
G	4.94	172629	172629
C	15.51	172646	172646
T	27.91	173099	173099
G	14.74	174329	174329
T	1.17	174652	174652
T	1.28	175138	175138
A	2.17	175404	175404
		175668	175812
A	30.11	175830	175830
G	0.66	176398	176398
A	28.31	176579	176579
G	14.85	176919	176919
C	1.21	176972	176972
A	1.04	177112	177112
G	0.88	177182	177182
C	1.14	177344	177344
T	7.10	177557	177557
C	22.52	177773	177773
A	20.86	178096	178096
T	13.83	178178	178178
T	4.05	178508	178508
A	4.07	178630	178630
T	4.07	178689	178689
A	1.06	178862	178862
C	16.00	179889	179889
G	49.36	180174	180174
A	29.75	180264	180264
T	5.06	180306	180306
C	46.23	180455	180455
C	1.59	180583	180583
T	1.45	180680	180680
G	11.32	181139	181139
A	3.25	182056	182056
A	34.12	182738	182738
G	29.63	182940	182940
A	45.68	183878	183878

G	36.65	184020	184020
G	8.07	184068	184068
		184196	184296
T	1.02	184249	184249
A	49.57	184308	184308
A	0.58	184344	184344
C	24.71	184401	184401
T	7.19	184688	184688
A	1.10	185133	185133
T	37.65	185546	185546
A	45.50	185553	185553
T	1.22	185580	185580
T	0.89	185741	185741
T	36.69	185954	185954
T	29.11	186118	186118
A	30.19	186815	186815
G	3.29	186873	186873
T	36.96	187069	187069
G	36.63	187138	187138
T	37.34	187289	187289
C	1.15	187462	187462
T	9.91	187740	187740
C	3.36	188939	188939
T	36.24	188949	188949
A	31.58	189342	189342
G	0.45	189572	189572
T	1.14	189988	189988
T	46.57	190253	190253
A	10.34	190283	190283
T	8.00	190294	190294
T	33.71	190298	190298
T	2.29	190311	190311
G	1.19	191370	191370
A	1.01	191635	191635
A	47.88	191643	191643
		192188	192259
A	4.68	192441	192441
G	29.72	192906	192906
C	8.22	193032	193032
C	21.10	193521	193521
T	8.57	193822	193822
T	23.23	193840	193840
T	24.20	195301	195301
		196080	196162
C	23.89	196284	196284
T	19.33	196316	196316
G	11.50	196798	196798
T	3.08	197016	197016
A	9.72	197139	197139
T	0.98	197154	197154
T	2.24	197395	197395
A	1.43	197915	197915
A	1.80	198192	198192
G	2.38	198256	198256
A	0.61	198299	198299
G	2.55	198353	198353

T	0.83	198391	198391
C	48.50	198547	198547
G	2.44	199280	199280
G	2.45	199403	199403
C	2.45	199404	199404
C	2.55	199431	199431
T	20.00	199517	199517
T	2.46	199528	199528
A	3.50	199599	199599
C	8.39	200003	200003
T	8.99	201753	201753
G	5.41	202045	202045
G	4.12	202177	202177
G	38.33	202379	202379
C	32.77	203558	203558
G	48.03	203640	203640
G	1.67	203750	203750
A	0.68	203809	203809
G	42.44	203877	203877
		204080	204556
T	0.30	204290	204290
G	2.46	204462	204462
G	0.56	204797	204797
G	30.23	205100	205100
A	2.40	205150	205150
A	2.24	205607	205607
T	1.64	205651	205651
C	1.40	205905	205905
A	9.52	206117	206117
A	48.14	206375	206375
T	2.50	206385	206385
C	49.41	206633	206633
T	2.36	207153	207153
T	12.07	207277	207277
A	16.67	207435	207435
G	7.66	207971	207971
A	9.66	208441	208441
A	7.78	208649	208649
A	25.71	208695	208695
A	1.43	208703	208703
G	4.71	208805	208805
T	0.56	209049	209049
T	8.33	210392	210392
A	7.23	210397	210397
C	15.88	210712	210712
T	3.29	212013	212013
T	0.30	212203	212203
		212234	212589
T	16.28	212255	212255
G	16.70	212877	212877
A	1.93	212982	212982
C	30.64	212983	212983
T	20.57	213122	213122
A	1.54	213143	213143
C	16.37	213171	213171
A	7.42	213221	213221
T	1.91	213265	213265

Significant 4 microsatellite marker haplotypes. Length=length of haplotype in Mb. P-val=p-value. RR=Relative risk. N af=Number of patients. P al=allelic frequency of haplotype. P ca =carrier frequency of haplotype. N ct= number of controls. Alleles= alleles in the haplotype. Markers= markers in the haplotype.

4 markers :		pos.rr-frqgt1perc											
Length	p-val	RR	N_af	P_al	P_ca	N_ct	P_al	P_ca	Alleles				Markers
0.88	4.71E-06	6.23	428	0.065	0.125	721	0.011	0.022	0	-12	-6	0	DG13S80 DG13S83 DG13S110 DG13S163
0.82	8.60E-06	INF	438	0.032	0.062	720	0	0	0	4	2	14	DG13S111 1 DG13S1103 D13S1287 DG13S1061
0.67	6.98E-06	19.91	435	0.03	0.059	721	0.002	0.003	8	6	0	8	DG13S1103 DG13S163 D13S290 DG13S1061
0.767	4.85E-06	26.72	436	0.048	0.094	721	0.002	0.004	0	0	2	12	DG13S1101 DG13S166 D13S1287 DG13S1061
0.515	1.93E-06	INF	422	0.048	0.094	721	0	0	2	0	0	6	DG13S166 DG13S163 D13S290 DG13S1061
0.864	1.68E-06	INF	424	0.024	0.048	717	0	0	0	2	0	-16	DG13S166 DG13S163 DG13S1061 DG13S293
0.927	5.38E-06	INF	435	0.034	0.067	720	0	0	4	2	14	3	DG13S1103 D13S1287 DG13S1061 DG13S301

Alleles #'s: For SNP alleles A = 0, C = 1, G = 2, T = 3; for microsatellite alleles: the CEPH sample (Centre d'Etudes du Polymorphisme Humain, genomics repository) is used as a reference, the lower allele of each microsatellite in this sample is set at 0 and all other alleles in other samples are numbered according in relation to this reference. Thus allele1 is 1 bp longer than the lower allele in the CEPH sample, allele 2 is 2 bp longer than the lower allele in the CEPH sample, allele 3 is 3 bp longer than the lower allele in the CEPH sample, allele 4 is 4 bp longer than the lower allele in the CEPH sample, allele -1 is 1 bp shorter than the lower allele in the CEPH sample, allele -2 is 2 bp shorter than the lower allele in the CEPH sample, and so on.

Table 5

Significant 5 microsatellite marker haplotypes. Length=length of haplotype in Mb. P-val=p-value. RR=Relative risk. N af=Number of patients. P al=allelic frequency of haplotype. P ca =carrier frequency of haplotype. N ct= number of controls. Alleles= alleles in the haplotype. Markers= markers in the haplotype

5markers	Length	p-val	RR	N af	P al	P ca	N ct	P al	P ca	Alleles	Markers
	0.851	7.45E-06	15.43	413	0.034	0.067	715	0.002	0.005	0 18 0 0 0	DG13S79 D13S1299 DG13S87 D13S1246 DG13S166
	0.964	8.07E-06	INF	437	0.023	0.045	721	0	0	0 -12 6 8 6	DG13S79 DG13S83 DG13S1104 DG13S1103 DG13S163
	0.964	2.38E-06	INF	437	0.026	0.052	720	0	0	0 6 0 8 6	DG13S79 DG13S1104 DG13S172 DG13S1103 DG13S163
	0.931	7.05E-06	5.8	429	0.068	0.131	721	0.012	0.025	0 -6 0 0 -2	DG13S79 DG13S1110 DG13S175 DG13S166 D13S1238
	0.964	8.13E-06	INF	434	0.021	0.041	721	0	0	0 3 8 2 6	DG13S79 DG13S1098 DG13S1103 DG13S166 DG13S163
	0.597	9.78E-06	4.58	428	0.074	0.143	717	0.017	0.034	-6 0 0 0 -2	DG13S1110 DG13S89 DG13S175 DG13S166 D13S1238
	0.896	6.92E-06	INF	428	0.026	0.051	721	0	0	-12 -6 0 -2 2	DG13S83 DG13S1110 DG13S166 D13S1238 D13S290
	0.722	2.18E-06	INF	453	0.026	0.051	738	0	0	-6 0 0 -2 2	DG13S1110 D13S289 DG13S166 D13S1238 D13S290
	0.982	7.88E-06	INF	437	0.028	0.055	721	0	0	0 0 4 2 14	DG13S87 DG13S175 DG13S1103 D13S1287 DG13S1061
	0.841	8.88E-06	INF	438	0.032	0.062	720	0	0	0 0 4 2 14	DG13S89 DG13S1111 DG13S1103 D13S1287 DG13S1061

																	DG13S89 DG13S1103 DG13S163 D13S290 DG13S1061
0.841	9.67E-07	INF	435	0.029	0.057	721	0	0	0	8	6	0	8				
																	DG13S87 DG13S1103 DG13S166 D13S1287 DG13S1061
0.982	7.90E-06	18.63	437	0.026	0.052	721	0.001	0.003	0	4	0	2	14				
																	DG13S89 DG13S1101 DG13S166 D13S1287 DG13S1061
0.841	3.52E-06	28.52	436	0.048	0.094	721	0.002	0.004	0	0	0	2	12				
																	DG13S175 DG13S1103 DG13S163 D13S290 DG13S1061
0.705	5.28E-06	INF	435	0.027	0.053	721	0	0	0	8	6	0	8				
																	DG13S89 DG13S166 DG13S163 D13S290 DG13S1061
0.841	4.21E-06	INF	422	0.048	0.093	721	0	0	0	2	0	0	6				
																	DG13S1101 DG13S175 DG13S166 D13S1287 DG13S1061
0.767	4.02E-06	28.11	436	0.049	0.095	721	0.002	0.004	0	0	0	2	12				
																	DG13S1101 DG13S172 DG13S166 D13S1287 DG13S1061
0.767	1.29E-06	31.07	436	0.047	0.092	721	0.002	0.003	0	0	0	2	12				
																	DG13S175 DG13S166 DG13S163 D13S290 DG13S1061
0.705	4.25E-07	INF	422	0.048	0.093	721	0	0	0	2	0	0	6				
																	DG13S172 DG13S1103 DG13S166 D13S1287 DG13S1061
0.683	6.58E-06	INF	437	0.029	0.056	721	0	0	0	4	0	2	14				
																	DG13S1101 DG13S166 D13S290 D13S1287 DG13S1061
0.767	2.85E-06	32.43	436	0.044	0.087	721	0.001	0.003	0	0	0	2	12				
																	D13S289 DG13S166 DG13S163 D13S1287 DG13S293
0.865	9.58E-06	18.39	451	0.023	0.045	739	0.001	0.003	0	0	2	2	16				
																	D13S289 DG13S166 DG13S163 DG13S1061 DG13S293
0.865	5.08E-06	INF	453	0.019	0.038	739	0	0	0	0	2	0	16				
																	DG13S1103 DG13S166 D13S1287 DG13S1061 DG13S301
0.927	1.02E-07	27.65	437	0.037	0.073	721	0.001	0.003	4	0	2	14	3				

Additional haplotypes were associated with MI, as shown in the following Tables.

5 **Table 6** shows haplotypes in the FLAP region (FLAP and flanking nucleotide sequences) that are significantly associated with female MI.

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DG13S1103	DG00AAFQR	SNP13B_R1028729	SNP13B_Y1323898	SNP13B_K912392	DG00AAFIV	D13S289	DG13S166	DG00AAFJT	DG00AAHII	DG00AAHID	DG00AAHIJ	DG00AAHIH	DG00AAHIE	B_SNP_302524	B_SNP_302617	DG00AAHIG	DG00AAHIF	DG00AAHOI	D13S1238	DG13S2605	DG13S163	p-val	N _{aff}	aff. frq	N _{ctrl}	ctrl. frq	rel _{risk}	PAR	info
		1	3	0			0			3	0			3		2	-2					1.30E-05	455	0.108	811	0.048	2.4	0.122	0.815
		1	3	0			0		3					3		-2	0					7.81E-06	455	0.065	812	0.02	3.45	0.091	0.815
		1	3	0			0		3					3		-2	0					8.82E-06	455	0.065	812	0.02	3.47	0.092	0.802
		1	3	0			0		3	2				3		-2	0					9.31E-06	455	0.065	812	0.02	3.30	0.089	0.811
		1	3	0			0		3					3		-2	0					8.91E-06	455	0.063	812	0.019	3.54	0.09	0.824
		1	0	3	0		0		3					3		-2	0					9.78E-06	455	0.063	812	0.019	3.51	0.089	0.808
		1	3	0			0		3	0				3		-2	0					1.09E-05	455	0.063	811	0.019	3.41	0.090	0.818
		1	3	0			0		3					3	2	-2	0					1.10E-05	455	0.063	812	0.019	3.44	0.087	0.811
		1	3	0			0		2					3		-2	0					1.11E-05	455	0.063	812	0.018	3.58	0.088	0.809
		1	3	0			0		2					3		-2	0					1.22E-05	455	0.063	811	0.018	3.8	0.087	0.577
		1	3	0			0	2						3		-2	0					1.26E-05	455	0.063	812	0.02	3.35	0.089	0.828
		1	3	0			0		0					3		-2	0					8.59E-06	455	0.062	812	0.018	3.53	0.085	0.82
		1	3	0			0		0					3		-2	0					1.20E-05	455	0.062	811	0.019	3.42	0.086	0.817
		1	3	0			0		2					3		-2	0					1.21E-05	455	0.062	811	0.019	3.43	0.086	0.819
	0	1	3	0			0		2					3		-2	0					7.83E-06	455	0.061	811	0.018	3.95	0.088	0.562
	0	1	3	0			0							3		-2	0					1.08E-05	455	0.061	811	0.017	3.85	0.09	0.56
	0	1	3	0			0		3	2				3		-2	0					5.00E-06	455	0.06	811	0.015	4.11	0.087	0.578
	1	0	3	0			0			2				3		-2	0					1.31E-05	455	0.06	811	0.017	3.86	0.085	0.588
	0	1	3	0			0			0				3		-2	0					8.53E-06	455	0.059	811	0.018	3.85	0.085	0.593
	0	1	0	3	0		0							3		2	-2					9.63E-06	455	0.058	811	0.015	4.03	0.085	0.585

25 **Table 7** Two variants of the female MI “at risk” haplotypes

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40 **P-val:** p-value for the association. **N_{aff}:** Number of patients used in the analysis. **Aff. frq:** haplotype frequency in patients. **N_{ctrl}:** number of controls used in the analysis. **Ctrl. frq:** Haplotype frequency in controls. **Rel_{risk}:** Relative risk of the haplotype. **PAR:** population attributable risk. **Info:** information content.

Table 8 The frequencies of the female MI “at risk” haplotypes in male patients vs controls.

10	DG13S1103	DG00AAFQR	SNP13B_R1028729	SNP13B_Y1323898	SNP13B_K912392	DG00AAFIV	D13S289	DG13S166	DG00AAFJT	DG00AAHII	DG00AAHID	DG00AAHIJ	DG00AAHIH	DG00AAHIE	B_SNP_302524	B_SNP_302617	DG00AAHIG	DG00AAHIF	DG00AAHOI	D13S1238	DG13S2605	DG13S163	p-val	N_aff	aff_frq	N_ctrl	ctrl_frq	rel_risk	PAR	info
15	male MI	0	1	3	0	3	0	3	0	3	2	-2	3.37E-01	1087	0.027	809	0.021	1.32	0.013	0.577										
		1	3	0	3	0	3	2	-2	5.39E-01	1067	0.056	809	0.05	1.13	0.013	0.568													

P-val: p-value for the association. N_aff: Number of patients used in the analysis. Aff. frq: haplotype frequency in patients. N_ctrl: number of controls used in the analysis. Ctrl.frq: Haplotype frequency in controls. Rel_risk: Relative risk of the haplotype. PAR: population attributable risk. Info: information content.

Table 9. The selected SNP haplotypes and the corresponding p-values, relative risk (RR), number of patients (#aff), allelic frequency in patients (aff.frq.), carrier frequency in patients (carr.frq.), number of controls (#con), allelic frequency in controls (con.frq.), population attributable risk (PAR). The patients used for this analysis were all unrelated within 4 meioses.

	p-val	RR	#aff	aff.frq.	carr.frq.	#con	con.frq.	PAR	DG00AAFIU	SG13S25	DG00AAJFF	DG00AAHII	DG00AAHID	B_SNP_310657	SG13S30	SG13S32	SG13S42	SG13S35
B4	4.80E-05	2.08	903	0.106	0.2	619	0.054	0.11	2	2	2	2	2	2	2	0	0	
B5	2.40E-05	2.2	910	0.101	0.19	623	0.049	0.11	3	2	2	2	2	2	2	0	0	
B6	1.80E-06	2.22	913	0.131	0.24	623	0.063	0.14	3	2	2	2	2	2	2	0	2	
A4	5.10E-06	1.81	919	0.159	0.29	623	0.095	0.14	2	2	2	3	2	2	2	0		
A5	2.60E-06	1.91	920	0.15	0.28	624	0.085	0.14	3	2	2	3	2	2	2	0		

EXAMPLE 2 RELATIONSHIP BETWEEN MUTATION IN 5-LO
PROMOTER AND MI

A family of mutations in the G-C rich transcription factor binding region of the 5-LO gene has previously been identified. These mutations consist of deletion of one, deletion of two, or addition of one zinc finger (Sp1/Egr-1) binding sites in the region 176 to 147 bp upstream from the ATG translation start site where there are normally 5 Sp1 binding motifs in tandem. These naturally occurring mutations in the human 5-LO gene promoter have been shown to modify transcription factor binding and reporter gene transcription. The capacity of the mutant forms of DNA to promote transcription of CAT reporter constructs have been shown to be significantly less than that of the wild type DNA (*J. Clin. Invest.* Volume 99, Number 5, March 1997, 1130-1137).

To test whether 5-LO is associated with the atherosclerotic diseases, particularly myocardial infarction (MI) in the human population, this promoter polymorphism, consisting of variable number of tandem Sp1/Egr-1 binding sites, was genotyped in 1112 MI patients, 748 patients with PAOD, and 541 stroke patients.

The results, shown in Table 10, demonstrate that the wild type allele (which represents the allele with the most active promoter and thus with the highest expression of the 5-LO mRNA) is significantly associated with MI (RR=1.2, $p<0.05$). The results are consistent with a disease hypothesis that increased expression of the 5-LO plays a role in the pathogenesis of MI.

Table 10

	N_aff	Frq_aff	N_ctrl	Frq_ctrl	Risk Ratio	P-value
MI patients	1112	0.8701	734	0.8501	1.1803	0.048
Independent	969	0.8720	734	0.8501	1.2013	0.037
Males	646	0.8740	734	0.8501	1.2232	0.039
Females	465	0.8645	734	0.8501	1.1249	0.180
Age of onset < 60	522	0.8745	734	0.8501	1.2286	0.046
Males	353	0.8768	734	0.8501	1.2542	0.053
Females	169	0.8698	734	0.8501	1.1779	0.202

EXAMPLE 3: ELEVATED LTE4 BIOSYNTHESIS IN INDIVIDUALS WITH 5 THE FLAP MI-RISK HAPLOTYPE

Based on the known function of the end products of the leukotriene pathway and based on our 5-LO association data, the association of the FLAP haplotype with MI is best explained by increased expression and/or increased function of the FLAP gene. In other words, those individuals that have a “at risk” FLAP haplotype have
10 either, or both, increased amount of FLAP, or more active FLAP. This would lead to increased production of leukotrienes in these individuals.

To demonstrate this theory, LTE4, a downstream leukotriene metabolite, was measured in patient serum samples. A quantitative determination of LTE4 in human serum was performed by liquid chromatography coupled with tandem mass
15 spectrometry. The protocol was performed as follows:

ANALYTICAL METHOD

Table P1 (Protocol 1): List of Abbreviations

5

CAN	Acetonitrile
IS	Internal standard
LC-MS/MS	Liquid chromatography tandem mass spectrometry
LOQ	Limit of quantification
QCs	Quality controls
R ²	Coefficient of determination
SS	Spiking solution

Apparatus and conditions

Table P2 Analytical apparatus and conditions

Instruments / Conditions	Details																												
Analytical column	Zorbax extend C ₁₈ , 3.5µm (50 x 2.1 mm)																												
Column temperature	Ambient																												
Pump and flow	Hewlett Packard Series 1100 Binary pump delivering 0.3 ml/min																												
Mobile phase	A: Buffer: Acetonitrile:H ₂ O (5:95 % v/v). (Containing 10 mM Ammonium Acetate and 0.1% Acetic acid at pH 4.6). B: Buffer: Acetonitrile:H ₂ O (95:5 % v/v). (Containing 10 mM Ammonium Acetate and 0.1% Acetic acid at pH 4.6).																												
Gradient	<table><tr><td>Time</td><td>%A</td><td>%B</td><td>Flow rate</td></tr><tr><td>0.00</td><td>30</td><td>70</td><td>0.3 ml/min</td></tr><tr><td>1.00</td><td>30</td><td>70</td><td>0.3 ml/min</td></tr><tr><td>1.50</td><td>90</td><td>10</td><td>0.3 ml/min</td></tr><tr><td>6.00</td><td>90</td><td>10</td><td>0.3 ml/min</td></tr><tr><td>6.50</td><td>30</td><td>70</td><td>0.3 ml/min</td></tr><tr><td>10.00</td><td>30</td><td>70</td><td>0.3 ml/min</td></tr></table>	Time	%A	%B	Flow rate	0.00	30	70	0.3 ml/min	1.00	30	70	0.3 ml/min	1.50	90	10	0.3 ml/min	6.00	90	10	0.3 ml/min	6.50	30	70	0.3 ml/min	10.00	30	70	0.3 ml/min
Time	%A	%B	Flow rate																										
0.00	30	70	0.3 ml/min																										
1.00	30	70	0.3 ml/min																										
1.50	90	10	0.3 ml/min																										
6.00	90	10	0.3 ml/min																										
6.50	30	70	0.3 ml/min																										
10.00	30	70	0.3 ml/min																										
Sample injection	HTC PAL autosampler 10 µl onto the HPLC column																												
Mass Spectrometric system	Quattro Ultima TM Tandem MS/MS, Micromass. England.																												
Recording and integration	Mass Lynx, version 3.5. All chromatograms and reports are printed out in hardcopy and stored in electronic form on the workstation hard disk drive. Recording time was 10 min.																												
Retentions times	LTE ₄ ~ 3.05 min. LTE ₄ -d ₃ ~ 3.05 min.																												
Ionization mode	Electrospray atmospheric pressure in negative ion mode																												

Scan mode	Multiple reaction monitoring (MRM)		
	Compound	Parent ion	Daughter ion
	LTE ₄	438.2	333.2
	LTE ₄ -d ₃	441.2	336.2

Other instruments

Table P3 The apparatus used for sample treatment and measurements

Apparatus	Brand	Type
Pipette	Eppendorf	Edos 5221
Pipette	Labsystems	Finnpipette 200 µl
Centrifuge	Eppendorf	5417C
Evaporation unit	Porvair	Ultravap
Vibrofix	Ika-Werk	VF-1
	Thermolyne	Maxi-mix III™, 65800
Balance	Sartorius	LA 120 S
Ultra sonic bath	Cole Parmer	8891

Materials

5 Table P4 Reagents for sample treatment and measurements

Reagent	Manufacturer	Quality	Art no.
Acetonitrile (ACN)	Rathburn	HPLC grade	RH 1016
Methanol	Rathburn	HPLC grade	RH 1019
Ammonium acetate	Merck	Pro analysis	1116

Table P5 Reference substances

	Details	Reference
Reference standards	Leukotrine E ₄ from Cayman Chemical, MI, USA	20410
Internal standards	Leukotriene E ₄ -20, 20,20-d ₃ from Biomol, PA, USA	S10120

Stock solutions

A stock solution of LTE₄ was prepared by the supplier at a concentration of 100µg/ml in methanol. The stock solution was diluted to a concentration of 20µg/ml in methanol and this working solution (WS-1) was kept refrigerated at 2-8°C.

An internal standard stock solution (LTE₄-d₃) was prepared by the supplier at concentration of 49.5µg/ml. The stock solution was diluted to a concentration of 1µg/ml in methanol and this working solution was kept refrigerated at 2-8°C.

Preparation of spiking solutions, calibration standards and quality control samples

10 Spiking solutions (SS) in the concentration range of 1 ng/ml to 10000 ng/ml were prepared by dilution of the working Solution.

The following spiking solutions were prepared:

Table P6 Spiking solutions for calibration standards

SS	Concentration (ng/ml)	Preparation
1	10000	500µl of WS-1 (20µg/ml) diluted to 1.0 ml with 70% MeOH/water
2	1000	100µl of SS-1 was diluted to 1.0 ml with 70% MeOH/water
3	100	100µl of SS-2 was diluted to 1.0 ml with 70% MeOH/water
4	30	300µl of SS-3 was diluted to 1.0 ml with 70% MeOH/water
5	20	200µl of SS-3 was diluted to 1.0 ml with 70% MeOH/water

6	16	160µl of SS-3 was diluted to 1.0 ml with 70% MeOH/water
7	12	120µl of SS-3 was diluted to 1.0 ml with 70% MeOH/water
8	8.0	400µl of SS-5 was diluted to 1.0 ml with 70% MeOH/water
9	4.0	200µl of SS-5 was diluted to 1.0 ml with 70% MeOH/water
10	2.0	100µl of SS-5 was diluted to 1.0 ml with 70% MeOH/water
11	1.4	175µl of SS-8 was diluted to 1.0 ml with 70% MeOH/water
12	1.0	125µl of SS-8 was diluted to 1.0 ml with 70% MeOH/water

Table P7 Spiking solutions for quality controls

SS	Concentration (ng/ml)	Preparation
13	14	140µl of SS-3 was diluted to 1.0 ml with 70% MeOH/water
14	6.0	300µl of SS-5 was diluted to 1.0 ml with 70% MeOH/water
15	2.4	120µl of SS-5 was diluted to 1.0 ml with 70% MeOH/water

After preparation, spiking solutions for calibration standards and quality controls were kept refrigerated at 2-8°C.

Preparation of calibration standards and quality controls

Fresh calibration standards and quality controls (QCs) were prepared each day by spiking blank plasma as described in Tables P8 and P9, respectively.

Table P8 Preparation of calibration standards

Concentration (ng/ml)	SS (μl)	Blank Plasma
1500	20 μl of the SS-4 (30ng/ml)	380 μl
1000	20 μl of the SS-5 (20ng/ml)	380 μl
800	20 μl of the SS-6 (16ng/ml)	380 μl
600	20 μl of the SS-7 (12ng/ml)	380 μl
400	20 μl of the SS-8 (8ng/ml)	380 μl
200	20 μl of the SS-9 (4.0ng/ml)	380 μl
100	20 μl of the SS-10 (2.0ng/ml)	380 μl
70	20μl of the SS-11 (1.4ng/ml)	380 μl
50	20μl of the SS-12 (1.0ng/ml)	380 μl

Table P9 Preparation of quality controls

Concentration (ng/ml)	SS (μl)	Blank Plasma
800	20 μl of the SS-13 (14ng/ml)	380 μl
40	20μl of the SS-14 (6.0ng/ml)	380 μl
8.0	20μl of the SS-15 (2.4ng/ml)	380 μl

5

Sample preparation

Aliquots of 400 μl of each study sample, calibration standards, QC samples and control blank are pipetted into an eppendorf vial. All samples apart from blank are then spiked with 20 μl of internal standard working solution and the samples are then vortex-mixed for few seconds. The pH of the plasma samples is adjusted to pH 4.5 using 60 μl of 10% acetic acid and centrifuged for 10 min. at 4100 rpm immediately before the extraction. The solid phase extraction 96-well plate is

conditioned with 1 ml methanol and 1 ml water. Then 400µl of the plasma samples are loaded on the plate. Vacuum is applied, followed by drying the disk for 1 min. After being washed with 2ml water and 1 ml 30% methanol in 2% acetic acid. Next the plate is eluted with 0.6 ml methanol. The plate is then dried for few minutes.

- 5 The methanol eluate is evaporated almost to dryness under a stream of nitrogen at 45°C. The residue is reconstituted in 30 µl mobile phase and vortex-mixed for few min. Subsequently, the solutions are centrifuged for 10 min at 10.000 rpm. and 10 µl are injected by the autosampler into the LC-MS/MS system for quantification.

10 *PERFORMANCE OF MEASUREMENTS*

The samples will be prepared and measured in batches and a typical batch will consist of:

- 15 One set of calibration standards, one extra lowest calibration standard and one blank.
Samples collected from a 16 individuals and one set of control samples (C_L, C_M, C_H)
Samples collected from a 17 individuals and one set of control samples (C_L, C_M, C_H)

QUANTITATIVE DETERMINATION OF ANALYTE IN PLASMA

20 *SAMPLES*

The standard curve is calculated from the peak area ratios ANALYTE/INTERNAL STANDARD of the calibration standards and their nominal ANALYTE concentrations. The unknown samples for LTE₄ were calculated from a quadratic regression equation where a weighted curve, $1/X^2$, is
25 used. The measured peak area of the samples was converted into pictogram of ANALYTE per milliliter (pg/ml) of plasma according to the calculated equation for the standard curve.

The calculation of the regression for the standard curve and the calculations of the concentration of the unknown samples and the control samples are performed
30 with MassLynx Software.

ACCEPTANCE CRITERIA

Calibration standards

- 5 The coefficient of determination (R^2) for the calibration curve must exceed 0.98.

 The calibration curve included the concentration range from 50pg/ml – 1500pg/ml.

- Concentration of the calibration standards must be within $\pm 25\%$ of their nominal
10 value when recalculated from the regression equation. Calibration standards that fail these criteria (at most 3 in each run) are rejected and the calibration performed again with the remaining standards. If the standard curve is not accepted, the samples must be reanalyzed.

Control samples

- 15 At least two thirds of the analysed quality controls must be within $\pm 25\%$ of their nominal value when calculated from regression equation. If more than a third of the controls fail, the samples must be reanalyzed.

RESULTS

- 20 Table 11 (below) shows that the female MI “at risk” haplotype is more significantly associated with female MI patients who have high LTE4 levels (top 50th percentile), than with female MI patients who have low levels of LTE4 (bottom 50th percentile).

- In addition, haplotype analysis, comparing female MI patients with high
25 levels of LTE4 with female patients with low levels, showed that those with high levels had increased prevalence of the “at risk” haplotype by 1.6 fold (see Table 12). The results show clearly that the “at risk” haplotypes are enriched in the MI patient group that has high levels of LTE4. The carrier frequency of the “at risk” haplotypes are 12% and 20%, respectively, in the whole female MI group, but go up
30 to 15% and 24%, respectively, in the female MI group that has high levels of LTE4.

Correspondingly, the carrier frequency of the “at risk” haplotypes decrease to 8% and 18%, respectively, in the group of female MI that has low levels of LTE4 (Note carrier frequencies are twice the disease allele frequency times 1 minus the disease allele frequency plus the square of the disease allele frequency).

- 5 Note that LTE4 may simply reflect the leukotriene synthesis rate of the leukotriene synthetic pathway upstream of the key leukotriene metabolite involved in MI risk. For example, leukotriene B4 is probably more likely than leukotriene E4 to be involved in the inflammatory aspects of MI plaques but since B4 has a short half life, it is difficult to measure reliably in serum samples, while E4 has long term
- 10 stability.

Table 11 Association of the at risk haplotypes for female MI, with female MI who also have high levels of LTE4 (>50pg/ml (roughly the upper 50th percentile). Less significant association between

15 the at risk haplotype for female MI, with female MI who also have low levels of LTE4 (<50pg/ml).

	DG13S1103	DG00AAFOR	SNP13B_R1028729	SNP13B_Y1323898	SNP13B_K912392	DG00AAFV	D13S289	DG13S166	DG00AAFJT	DG00AAHII	DG00AAHID	DG00AAHIJ	DG00AAHIH	DG00AAHIE	B_SNP_302524	B_SNP_302617	DG00AAHIG	DG00AAHIF	DG00AAHOI	D13S1238	DG13S2605	DG13S163	p-val	N _{aff}	aff.frq	N _{ctrl}	ctrl.frq	rel_risk	PAR	info
20																														
25	High LTE4	0	1	3	0			0			3					3			2	-2			3.72E-06	221	0.075	809	0.014	5.51	0.115	0.565
			1	3	0			0											2	-2			2.30E-05	220	0.122	809	0.046	2.89	0.154	0.608
30	Low LTE4	0	1	3	0			0			3					3			2	-2			4.65E-02	185	0.04	809	0.015	2.67	0.048	0.511
			1	3	0			0											2	-2			2.88E-02	182	0.087	809	0.048	1.89	0.08	0.622

P-val: p-value for the association. N_aff: Number of patients used in the analysis. Aff. frq: haplotype frequency in patients. N_ctrl: number of controls used in the analysis. Ctrl.frq: Haplotype frequency in controls. Rel_risk: Relative risk of the

35 haplotype. PAR: population attributable risk. Info: information content.

Table 12 Association between haplotypes that are most significantly associated with female MI, and serum LTE4 levels. Here, the group of affected individuals are defined as female MI patients with high serum LTE4 (higher than 50 pg/ml) and the control group is defined as female MI patients with low serum LTE4 (below 50 pg/ml)

10

	DG13S1103	DG00AAAFQR	SNP13B_R1028729	SNP13B_Y1323888	SNP13B_K912392	DG00AAAFV	D13S289	DG13S166	DG00AAAFJT	DG00AAHII	DG00AAHID	DG00AAHIJ	DG00AAHIH	DG00AAHIE	B_SNP_302524	B_SNP_302617	DG00AAHIG	DG00AAHIF	DG00AAHOI	D13S1238	DG13S2605	DG13S163	p-val	N_eff	aff.frq	N_ctrl	ctrl.frq	rel_risk	PAR	info
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	High vs low LTE4																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
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P-val: p-value for the association. **N_{aff}:** Number of patients used in the analysis. **aff. frq:** haplotype frequency in patients. **N_{ctrl}:** number of controls used in the analysis. **Ctrl.frq:** Haplotype frequency in controls. **Rel_risk:** Relative risk of the haplotype. **PAR:** population attributable risk. **Info:** information content.

EXAMPLE 4 ELEVATED LTE4 CORRELATED WITH ELEVATED C-REACTIVE PROTEIN (CRP)

The relationship between the increased production of leukotrienes and the inflammatory marker CRP, a well established risk factor for MI, was then explored. As shown in FIG. 9, a significant positive correlation was found between serum LTE4 levels and serum CRP levels.

EXAMPLE 5: ASSESSMENT OF LEVEL OF CRP IN PATIENTS WITH AT-RISK HAPLOTYPE

The level of CRP in female patients with female MI at-risk haplotypes was assessed, in order to demonstrate the presence of a raised level of inflammatory marker in the presence of the female MI at-risk haplotype. Results are shown in Table 13. The average CRP was elevated in those patients with the at-risk haplotype versus those without it.

Table 13

All female patients		no	Mean CRP	SE CRP
affecteds:	With haplotype.	155	4.91	8.7
	Not with haplotype.	218	4.35	6.13

5

EXAMPLE 6: ELEVATED SERUM LTE4 LEVELS IN MI PATIENTS VERSUS CONTROLS

The end products of the leukotriene pathway are potent inflammatory lipid mediators that can potentially contribute to development of atherosclerosis and destabilization of atherosclerotic plaques through lipid oxidation and/or proinflammatory effects. Examples one through five show that: 1) MI correlates with genetic variation at FLAP; 2) MI correlates with high expression promoter polymorphism at 5-LO; 3) C-reactive protein levels correlate with serum leukotriene E4; and 4) Patients with MI-risk FLAP haplotypes have higher levels of serum leukotriene E4 and CRP. Based on these data, it was hypothesized that serum leukotriene E4 levels correlate with MI risk.

To test this hypothesis, LTE4, a downstream leukotriene metabolite, was measured in 488 female MI patient and 164 control serum samples. The LTE4 levels for the patients was higher than that for the controls using a one-sided Wilcoxon rank-sum test. The p-value of the difference was 0.0092 thus confirming our hypothesis. Therefore, elevated leukotriene E4 represents a risk factor for MI. Serum or plasma LTE4 levels may be used to profile the MI risk for individuals to aid in deciding which treatment and lifestyle management plan is best for primary or secondary MI prevention. In the same way other leukotriene metabolites may be used to risk profile for MI.

EXAMPLE 7: INCREASED LTB₄ PRODUCTION IN ACTIVATED NEUTROPHILS FROM MI PATIENTS

A principal bioactive product of one of the two branches of the 5-LO pathway is LTB₄. To determine whether the patients with past history of MI have increased activity of the 5-LO pathway compared to controls, we measured the LTB₄ production in isolated blood neutrophils before and after stimulation in vitro with the calcium ionophore, ionomycin. No difference was detected between the LTB₄ production in resting neutrophils from MI patients or controls (results not shown). In contrast, the LTB₄ generation by neutrophils from MI patients stimulated with the ionophore was significantly greater than by neutrophils from controls at 15 and 30 minutes, respectively (FIG. 10a). Moreover, as shown in FIG. 10b, the observed increase in the LTB₄ release was largely accounted for by male carriers of haplotype A4, whose cells produced significantly more LTB₄ than cells from controls (P value = 0.0042) (Table 14). As shown in Table 14 there was also a heightened LTB₄ response in males who do not carry HapA but of borderline significance. This could be explained by additional variants in the FLAP gene that have not been uncovered, or alternatively in other genes belonging to the 5-LO pathway, that may account for upregulation in the LTB₄ response in some of the patients without the FLAP at-risk haplotype. As shown in Table 14, we did not detect differences in LTB₄ response in females. However, due to a small sample size this cannot be considered conclusive. Taken together, the elevated levels of LTB₄ production of stimulated neutrophils from male carriers of the at-risk haplotype suggest that the disease associated variants in the FLAP gene increase FLAP's response to factors that stimulate inflammatory cells, resulting in increased leukotriene production and increased risk for MI.

Methods

Isolation and activation of peripheral blood neutrophils

50ml of blood were drawn into EDTA containing vacutainers from 43 MI
5 patients and 35 age and sex matched controls. All blood was drawn at the same time
in the early morning after 12 hours of fasting. The neutrophils were isolated using
Ficoll-Paque PLUS (Amersham Biosciences).

Briefly, the red cell pellets from the Ficoll gradient were harvested and red
blood cells subsequently lysed in 0.165 M NH_4Cl for 10 minutes on ice. After
10 washing with PBS, neutrophils were counted and plated at 2×10^6 cells/ml in 4ml
cultures of 15% Fetal calf serum (FCS) (GIBCO BRL) in RPMI-1640 (GIBCO
BRL). The cells were then stimulated with maximum effective concentration of
ionomycin ($1 \mu\text{M}$). At 0, 15, 30, 60 minutes post ionomycin addition 600 μl of culture
medium was aspirated and stored at -80°C for the measurement of LTB₄ release as
15 described below. The cells were maintained at 37°C in a humidified atmosphere of
5% CO_2 /95% air. We treated all samples with indomethasine ($1 \mu\text{M}$) to block the
cyclooxygenase enzyme.

Ionomycin-induced release of LTB₄ in neutrophils

20 LTB₄ Immunoassay (R&D systems) was used to quantitate LTB₄
concentration in supernatant from cultured ionomycin stimulated neutrophils. The
assay used is based on the competitive binding technique in which LTB₄ present in
the testing samples (200 μl) competes with a fixed amount of alkaline phosphatase-
labelled LTB₄ for sites on a rabbit polyclonal antibody. During the incubation, the
25 polyclonal Ab becomes bound to a goat anti-rabbit Ab coated onto the microplates.
Following a wash to remove excess conjugate and unbound sample, a substrate
solution is added to the wells to determine the bound-enzyme activity. The color
development is stopped and the absorbance is read at 405 nm. The intensity of the
color is inversely proportional to the concentration of LTB₄ in the sample. Each
30 LTB₄ measurement using the LTB₄ Immunoassay, was done in duplicate.

Table 14 LTB4 levels after ionomycin stimulation of isolated neutrophils^a

Phenotype (n)	After 15 Minutes		After 30 Minutes	
	Mean (SD)	P value	Mean (SD)	P value
Controls (35)	4.53 (1.00)		4.67 (0.88)	
Males (18)	4.61 (1.10)		4.68 (1.07)	
Females (17)	4.51 (0.88)		4.67 (0.62)	
MI (41)	5.18 (1.09)	0.011	5.24 (1.06)	0.016
Carriers (16)	5.26 (1.09)	0.027	5.27 (1.09)	0.051
Non-carriers (24)	5.12 (1.08)	0.040	5.22 (1.03)	0.035
MI males (28)	5.37 (1.10)	0.0033	5.38 (1.09)	0.0076
Carriers (10)	5.66 (1.04)	0.0042	5.58 (1.12)	0.013
Non-carriers (18)	5.20 (1.09)	0.039	5.26 (1.05)	0.041
MI females (13)	4.78 (0.95)	0.46	4.95 (0.92)	0.36
Carriers (6)	4.59 (0.80)	0.90	4.75 (0.82)	0.85
Non-carriers (7)	4.94 (1.04)	0.34	5.12 (0.96)	0.25

^aMean \pm SD of log-transformed values of LTB4 levels of ionomycin-stimulated neutrophils from MI patients and controls. Results are shown for two time points: 15 and 30 minutes. The results for males and females and for MI male and female carriers and non-carriers of the at-risk haplotype HapA are shown separately. Two-sided p values corresponding to a standard two-sample test of the difference in the mean values between the MI patients, their various sub-cohorts and the controls are shown.

15

EXAMPLE 8: HAPLOTYPES ASSOCIATED WITH MI ALSO CONFER RISK OF STROKE AND PAOD.

Because stroke and PAOD are diseases that are closely related to MI (all occur on the basis of atherosclerosis), we examined if the SNP haplotype in the FLAP gene that confers risk to MI also conferred risk of stroke and/or PAOD. The 'at risk' haplotype can be defined by the following 4 SNPs: SG13S25 with allele G,

DG00AAHID with allele T, B_SNP_310657 with allele G, and SG13S32 with allele A.

Table 15 shows that the haplotype (A4) increases the risk of having a stroke to a similar extent as it increases the risk of having an MI. The 'at risk' haplotype is carried by 28% of stroke patients and 17% of controls, meaning that the relative risk of having stroke for the carriers of this haplotype is 1.7 (p-value = 5.8×10^{-6}). Although not as significant, the 'at risk' haplotype also confers risk of having PAOD.

10 Table15.

		p-val	r	#aff	aff.frq.	#con	con.frq.	info	SG13S6	SG13S25	DG00AAJFF	DG00AAFJT	DG00AAHII	DG00AAHID	SG13S26	B_SNP_310657	SG13S30	SG13S32	SG13S41	SG13S42
MI haplotypes																				
All MI patients																				
	A4	5.3E-07	1.80	1407	0.16	614	0.09	0.82	2					3		2		0		
	B4	1.0E-04	1.87	1388	0.10	612	0.06	0.67	2			2					2			0
Males MI																				
	A4	2.5E-08	2.00	864	0.17	614	0.09	0.82	2					3		2		0		
	B4	1.1E-05	2.12	852	0.11	612	0.06	0.67	2			2					2			0
Females MI																				
	A4	1.9E-02	1.44	543	0.13	614	0.09	0.73	2					3		2		0		
	B4	7.9E-02	1.45	536	0.08	612	0.06	0.60	2			2					2			0
Replication in stroke																				
All stroke patients																				
	A4	5.8E-06	1.73	1238	0.15	614	0.09	0.80	2					3		2		0		
	B4	2.3E-04	1.83	1000	0.10	612	0.06	0.71	2			2					2			0
Males stroke																				
	A4	1.1E-06	1.91	710	0.17	614	0.09	0.79	2					3		2		0		
	B4	3.1E-05	2.11	574	0.11	612	0.06	0.72	2			2					2			0
Females stroke																				
	A4	9.9E-03	1.49	528	0.13	614	0.10	0.74	2					3		2		0		
	B4	6.3E-02	1.47	426	0.08	612	0.06	0.70	2			2					2			0
All stroke excluding MI																				
		8.4E-05	1.65	1054	0.15	614	0.09	0.78	2					3		2		0		

Males stroke excluding MI	6.4E-05	1.78	573	0.16	614	0.09	0.75	2	3	2	0
Females stroke excluding MI	1.2E-02	1.49	481	0.14	614	0.10	0.72	2	3	2	0
Cardioembolic stroke	6.6E-04	1.87	248	0.16	614	0.10	0.74	2	3	2	0
Cardioembolic stroke excluding MI	3.8E-02	1.56	191	0.14	614	0.10	0.70	2	3	2	0
Large vessel stroke	8.0E-02	1.47	150	0.13	614	0.09	0.83	2	3	2	0
Large vessel stroke excluding MI	2.9E-01	1.31	114	0.12	614	0.09	0.80	2	3	2	0
Small vessel stroke	7.2E-04	2.05	166	0.18	614	0.09	0.71	2	3	2	0
Small vessel stroke excluding MI	1.0E-04	2.31	152	0.20	614	0.10	0.71	2	3	2	0
Hemorrhagic stroke	4.4E-02	1.73	97	0.15	614	0.09	0.72	2	3	2	0
Hemorrhagic stroke excluding MI	3.9E-02	1.78	92	0.16	614	0.09	0.71	2	3	2	0
Unknown cause stroke	1.3E-04	1.88	335	0.16	614	0.09	0.75	2	3	2	0
Unknown cause stroke excluding MI	6.5E-04	1.82	297	0.16	614	0.09	0.72	2	3	2	0

MI and stroke together**All patients**

<i>Best haplo A4</i>	4.1E-07	1.75	2659	0.15	614	0.09	0.82	2	3	2	0
<i>B4</i>	4.1E-05	1.85	2205	0.10	612	0.06	0.70	2	2	2	0

Males

<i>A4</i>	1.4E-08	1.93	1437	0.17	614	0.09	0.82	2	3	2	0
<i>B4</i>	2.0E-06	2.11	1290	0.11	612	0.06	0.70	2	2	2	0

Females

<i>A4</i>	3.6E-03	1.47	1024	0.13	614	0.09	0.77	2	3	2	0
<i>B4</i>	2.8E-02	1.48	915	0.08	612	0.06	0.66	2	2	2	0

Patients with both MI and stroke

<i>A4</i>	6.1E-05	2.10	184	0.18	614	0.09	0.86	2	3	2	0
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Replication in PAOD

All PAOD patients	3.6E-02	1.31	920	0.12	614	0.10	0.84	2	3	2	0
Males PAOD	1.8E-02	1.40	580	0.13	614	0.10	0.84	2	3	2	0
Females PAOD	3.7E-01	1.17	340	0.11	614	0.10	0.83	2	3	2	0

All PAOD excluding MI	1.1E-01	1.24	750	0.12	614	0.10	0.83	2	3	2	0
Males PAOD excluding MI	8.3E-02	1.30	461	0.12	614	0.10	0.83	2	3	2	0
Males PAOD excluding MI and stroke	8.7E-02	1.32	388	0.12	614	0.10	0.83	2	3	2	0

SUMMARY

In summary, it has been found that: MI correlates with genetic variation at FLAP; MI correlates with high expression promoter polymorphism at 5-LO; patients
5 with female MI at-risk FLAP haplotypes have higher levels of serum LTE4; LTE4 levels correlate with CRP levels in serum; and patients with MI at-risk FLAP haplotypes have elevated CRP. Taken together, these results show that increased leukotriene synthesis is a risk factor for MI, especially but not only in females, and that this risk is driven in part by variants in FLAP and 5-LO genes and are captured in
10 part by measurement of levels of serum LTE4 and CRP. Furthermore, the SNP haplotype in the FLAP gene that confers risk to MI also confers risk of stroke and/or PAOD.

EXAMPLE 9 ADDITIONAL CORRELATION BETWEEN FLAP GENE AND MI, STROKE AND PAOD

15 A genome wide scan of 296 multiplex Icelandic families with 713 MI patients was performed. This genome-wide scan involves more MI phenotypes than described in Example 1. The cohort is a subset of the study population described in Example 1; in this cohort, related individuals were assessed. Through the suggestive
20 linkage to a locus on chromosome 13q12-13 for female MI patients and early onset MI patients, and a new microsatellite marker association analysis (including more microsatellite markers than described in Example 1), the gene encoding the 5-lipoxygenase activating protein (FLAP) was again identified, and a 4-SNP haplotype within the gene was determined to confer a near 2-fold risk of MI and stroke. Male
25 patients showed strongest association to the at-risk haplotype. Independent confirmation of FLAP association to MI was obtained in a British cohort of patients with sporadic MI. These findings support FLAP as the first specific gene isolated that confers substantial risk of the complex traits of MI and stroke.

METHODS

Study population

The study population was the same as used in Example 1.

5 Genotypes from 713 MI patients and 1741 of their first-degree relatives were used in the linkage analysis. For the microsatellite association study of the MI locus, 802 unrelated MI patients (n=233 females, n=624 males and n= 302 early onset) and 837 population-based controls were used. For the SNP association study in and around the FLAP gene 779 unrelated MI patients were genotyped (n=293 females,
10 n=486 males and n=358 early onset). The control group for the SNP association study was population based and comprised of 628 unrelated males and females in the age range of 30-85 years whose medical history was unknown. The stroke and PAOD cohorts used in this study have previously been described (Gretarsdottir, S. *et al. Nat Genet* 35, 131-8 (2003); Gretarsdottir, S. *et al., Am J Hum Genet* 70, 593-603 (2002);
15 Gudmundsson, G. *et al., Am J Hum Genet* 70, 586-92 (2002)). For the stroke linkage analysis, genotypes from 342 male patients with ischemic stroke or TIA that were linked to at least one other male patient within and including 6 meioses in 164 families were used. For the association studies 702 patients with all forms of stroke (n=329 females and n=373 males) and 577 PAOD patients (n=221 females and n=356
20 males) were analysed. Patients with stroke or PAOD that also had MI were excluded. Controls used for the stroke and PAOD association studies were the same as used in the MI SNP association study (n=628).

The study was approved by the Data Protection Commission of Iceland and the National Bioethics Committee of Iceland. Informed consent was obtained from
25 all study participants. Personal identifiers associated with medical information and blood samples were encrypted with a third party encryption system as previously described (Gulcher, J.R., Kristjansson, K., Gudbjartsson, H. & Stefansson, K., *Eur J Hum Genet* 8, 739-42 (2000)).

30 *Statistical analysis*

A genome-wide scan was performed as previously described (Gretarsdottir, S. *et al. Am J Hum Genet* 70, 593-603 (2002)), using a set of 1000 microsatellite markers. Multipoint, affected-only allele-sharing methods (Kong, A. & Cox, N.J., *Am J Hum Genet* 61, 1179-88 (1997)) were used to assess the evidence for linkage. All results were obtained using the program Allegro (Gudbjartsson, D.F., Jonasson, K., Frigge, M.L. & Kong, A. Allegro, *Nat Genet* 25, 12-3 (2000)) and the deCODE genetic map (Kong, A. *et al.*, *Nat Genet* 31, 241-7 (2002)). The S_{pairs} scoring function (Whittemore, A.S. & Halpern, J., *Biometrics* 50, 118-27 (1994); Kruglyak, L., Daly, M.J., Reeve-Daly, M.P. & Lander, E.S., *Am J Hum Genet* 58, 1347-63 (1996)) was used, as was the exponential allele-sharing model (Kong, A. & Cox, N.J. *Am J Hum Genet* 61, 1179-88 (1997)) to generate the relevant 1-df (degree of freedom) statistics. When combining the family scores to obtain an overall score, a weighting scheme was used that is halfway on a log scale between weighting each affected pair equally and weighting each family equally. In the analysis, all genotyped individuals who are not affected are treated as “unknown”. Because of concern with small sample behaviour, corresponding P values were usually computed in two different ways for comparison, and the less significant one was reported. The first P value is computed based on large sample theory; $Z_{lr} = \sqrt{(2 \log_e (10) \text{ LOD})}$ and is distributed approximately as a standard normal distribution under the null hypothesis of no linkage (Kong, A. & Cox, N.J. *Am J Hum Genet* 61, 1179-88 (1997)). A second P value is computed by comparing the observed LOD score to its complete data sampling distribution under the null hypothesis (Gudbjartsson, D.F., Jonasson, K., Frigge, M.L. & Kong, A. Allegro, *Nat Genet* 25, 12-3 (2000)). When a data set consists of more than a handful of families, these two P values tend to be very similar. The information measure that was used (Nicolae, D. University of Chicago (1999)), and is implemented in Allegro, is closely related to a classical measure of information (Dempster, A., Laird, N.M., Rubin, D.B., *J R Stat Soc B* 39, 1-38 (1977) and has a property that is between 0, if the marker genotypes are completely uninformative, and 1, if the genotypes determine the exact amount of allele sharing by descent among the affected relatives.

For single-marker association studies, Fisher's exact test was used to calculate two-sided P values for each allele. All P values were unadjusted for multiple comparisons unless specifically indicated. Allelic rather than carrier frequencies were presented for microsatellites, SNPs and haplotypes. To minimize any bias due to the relatedness of the patients that were recruited as families for the linkage analysis first and second-degree relatives were eliminated from the patient list. For the haplotype analysis, the program NEMO was used (Gretarsdottir, S. *et al.*, *Nat Genet* **35**, 131-8 (2003)), which handles missing genotypes and uncertainty with phase through a likelihood procedure, using the expectation-maximization algorithm as a computational tool to estimate haplotype frequencies. Under the null hypothesis, the affected individuals and controls are assumed to have identical haplotype frequencies. Under the alternative hypotheses, the candidate at-risk haplotype is allowed to have a higher frequency in the affected individuals than in controls, while the ratios of frequencies of all other haplotypes are assumed to be the same in both groups. Likelihoods are maximized separately under both hypotheses, and a corresponding 1-df likelihood ratio statistic used to evaluate statistical significance (*id*). Even though searches were only performed for haplotypes that increase the risk, all reported P values are two-sided unless otherwise stated. To assess the significance of the haplotype association corrected for multiple testing, a randomisation test was carried out using the same genotype data. The cohorts of affected individuals and controls were randomized, and the analysis was repeated. This procedure was repeated up to 1,000 times and the P value presented is the fraction of replications that produced a P value for a haplotype tested that is lower than or equal to the P value observed using the original patient and control cohorts.

For both single-marker and haplotype analysis, relative risk (RR) and population attributable risk was calculated assuming a multiplicative model (Terwilliger, J.D. & Ott, J. A., *Hum Hered* **42**, 337-46 (1992); Falk, C.T. & Rubinstein, P., *Ann Hum Genet* **51** (Pt 3), 227-33 (1987)) in which the risk of the two alleles of haplotypes a person carries multiply. We calculated LD between pairs of SNPs using the standard definition of D' (Lewontin, R.C., *Genetics* **50**, 757-82 (1964)) and R^2 (Hill, W.G. & Robertson, A., *Genetics* **60**, 615-28 (1968)). Using

NEMO, frequencies of the two marker allele combinations are estimated by maximum likelihood, and deviation from linkage equilibrium is evaluated by a likelihood ratio test. When plotting all SNP combinations to elucidate the LD structure in a particular region, D' was plotted in the upper left corner and the P value in the lower right corner. In the LD plots presented, the markers are plotted equidistantly rather than according to their physical positions.

Identification of DNA polymorphisms.

New polymorphic repeats (i.e. dinucleotide or trinucleotide repeats) were identified with the Sputnik program (<http://abajian.net/sputnik/index.html>). The lower allele of the CEPH sample 1347-02 (CEPH genomics repository) was subtracted from the alleles of the microsatellites and used as a reference. Single nucleotide polymorphisms in the gene were detected by PCR sequencing exonic and intronic regions from patients and controls. Public single nucleotide polymorphisms were obtained from the NCBI SNP database (<http://www.ncbi.nlm.nih.gov/SNP/>). SNPs were genotyped using a method for detecting SNPs with fluorescent polarization template-directed dye-terminator incorporation (SNP-FP-TDI assay) (Chen, X., Zehnauer, B., Gnirke, A. & Kwok, P.Y., *Proc Natl Acad Sci US A* 94, 10756-61. (1997)) and TaqMan assays (Applied Biosystems).

20

British study population

The method of recruitment of 3 separate cohorts of British subjects has been described previously (Steeds, R., Adams, M., Smith, P., Channer, K. & Samani, N.J., *Thromb Haemost* 79, 980-4 (1998); Brouillette, S., Singh, R.K., Thompson, J.R., Goodall, A.H. & Samani, N.J., *Arterioscler Thromb Vasc Biol* 23, 842-6 (2003)). In brief, in the first two cohorts a total of 547 patients included those who were admitted to the coronary care units (CCU) of the Leicester Royal Infirmary, Leicester (July 1993–April 1994) and the Royal Hallamshire Hospital, Sheffield (November 1995–March 1997) and satisfied the World Health Organisation criteria for acute MI in terms of symptoms, elevations in cardiac enzymes or electrocardiographic changes (Nomenclature and criteria for diagnosis of ischemic heart disease. Report of the Joint

30

International Society and Federation of Cardiology/World Health Organization task force on standardization of clinical nomenclature. *Circulation* 59, 607-9 (1979)). A total of 530 control subjects were recruited in each hospital from adult visitors to patients with non-cardiovascular disease on general medical, surgical, orthopaedic
5 and obstetric wards to provide subjects likely to be representative of the source population from which the subjects originated. Subjects who reported a history of coronary heart disease were excluded.

In the third cohort, 203 subjects were recruited retrospectively from the registries of 3 coronary care units in Leicester. All had suffered an MI according to
10 WHO criteria before the age of 50 years. At the time of participation, patients were at least 3 months from the acute event. The control cohort comprised 180 subjects with no personal or family history of premature coronary heart disease, matched for age, sex, and current smoking status with the cases. Control subjects were recruited from 3 primary care practices located within the same geographical area. In all cohorts
15 subjects were white of Northern European origin.

RESULTS

Linkage analysis

20 A genome wide scan was performed in search of MI susceptibility genes using a framework set of around 1000 microsatellite markers. The initial linkage analysis included 713 MI patients who fulfilled the WHO MONICA research criteria (The World Health Organization MONICA Project, WHO MONICA Project Principal Investigators,. *J Clin Epidemiol* 41, 105-14 (1988)) and were clustered in 296
25 extended families. The linkage analysis was also repeated for early onset, male and female patients separately. Description of the number of patients and families in each analysis are provided in Table 16, and the corresponding allele sharing LOD scores are shown in FIG. 11.

TABLE 16 Number of patients that cluster into families and the corresponding number of families used in the linkage analysis

Phenotype	Number of patients	Number of families	Number of pairs	Genotyped relatives ^a
All MI patients	713	296	863	1741
Males	575	248	724	1385
Females	140	56	108	366
Early onset	194	93	156	739

^aGenotyped relatives were used to increase the information on IBD sharing among the patients in the linkage analysis

None of these analyses yielded a locus of genome-wide significance.

However, the most promising LOD score (LOD = 2.86) was observed on

5 chromosome 13q12 for female MI patients at the peak marker D13S289 (FIG. 11).

This locus also had the most promising LOD score (LOD = 2.03) for patients with

early onset MI. After increasing the information on identity-by-descent sharing to

over 90% by typing 14 additional microsatellite markers in a 30 centiMorgan (cM)

region around D13S289, the LOD score from the female analysis dropped to 2.48 (P

10 value = 0.00036), while the highest LOD score remained at D13S289 (FIG. 12(a)). In

addition, in an independent linkage study of male patients with ischemic stroke or

transient ischemic attack we observed linkage to the same locus with a LOD score of

1.51 at the same peak marker (FIG. 13), further suggesting that a cardiovascular

susceptibility factor might reside at this locus.

15

Microsatellite association study

The 7.6 Mb region that corresponds to a drop of one in LOD score in the female MI analysis, contains 40 known genes (Table 17).

20 **Table 17** Genes residing within the one LOD drop region of the chromosome 13q12 linkage peak.

LL Symbol	LL gene name
USP12L1	ubiquitin specific protease 12 like 1
RPL21	ribosomal protein L21
GTF3A	general transcription factor IIIA
MTIF3	mitochondrial translational initiation factor 3
PDZRN1	PDZ domain containing ring finger 1

MGC9850	hypothetical protein MGC9850
POLR1D	polymerase (RNA) I polypeptide D, 16kDa
GSH1	GS homeobox 1
IPF1	insulin promoter factor 1, homeodomain transcription factor
CDX2	caudal type homeo box transcription factor 2
FLT3	fms-related tyrosine kinase 3
LOC255967	hypothetical protein LOC255967
FLT1	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)
C13orf12	chromosome 13 open reading frame 12
LOC283537	hypothetical protein LOC283537
KIAA0774	KIAA0774 protein
SLC7A1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1
UBL3	ubiquitin-like 3
MGC2599	hypothetical protein MGC2599 similar to katanin p60 subunit A 1 2599
HMGB1	high-mobility group box 1
D13S106E	highly charged protein
ALOX5AP	arachidonate 5-lipoxygenase-activating protein
FLJ14834	hypothetical protein FLJ14834
MGC40178	hypothetical protein MGC40178
HSPH1	heat shock 105kDa/110kDa protein 1
B3GTL	beta 3-glycosyltransferase-like
GREAT	similar to G protein coupled receptor affecting testicular descent (H. sapiens)
LOC196549	similar to hypothetical protein FLJ20897
13CDNA73	hypothetical protein CG003
BRCA2	breast cancer 2, early onset
CG018	hypothetical gene CG018
PRO0297	PRO0297 protein
LOC88523	CG016
CG012	hypothetical gene CG012
CG030	hypothetical gene CG030
CG005	hypothetical protein from BCRA2 region
APRIN	androgen-induced proliferation inhibitor
KL	Klotho
STARD13	START domain containing 13
RFC3	replication factor C (activator 1) 3, 38kDa

To determine which gene in this region most likely contributes to MI 120 microsatellite markers were typed within this region, and a case-control association study was performed using 802 unrelated MI patients and 837 population-based controls. The association study was also repeated for each of the three phenotypes that were used in the linkage study, i.e. early onset, male and female MI patients. In addition to testing each marker individually, haplotypes constructed out of those markers for association were also tested. To limit the number of haplotypes tested,

only haplotypes that were in excess in the patient cohorts and that spanned less than 300 kb were assessed (see Methods).

As shown in FIG. 12(b), the haplotype that showed association to all MI with the lowest P value (0.00009) covered a region that contains 2 known genes, including
5 the gene encoding arachidonate 5-lipoxygenase-activating protein (FLAP) and a gene with an unknown function called highly charged protein. However, the haplotype association to female MI in this region was less significant (P value = 0.005) than for all MI patients and to our surprise, the most significant haplotype association was observed for male MI patients (P value = 0.000002). This male MI haplotype was the
10 only haplotype that remained significant after adjusting for all haplotypes tested.

In view of the association results described above, FLAP was an attractive candidate and therefore efforts were focused on this gene.

Screening for polymorphisms in FLAP and linkage disequilibrium mapping

15 To determine whether variations within the FLAP gene significantly associate with MI and to search for causal variations, the FLAP gene was sequenced in 93 patients and 93 controls. The sequenced region covers 60 kb containing the FLAP gene, including the 5 known exons and introns and the 26 kb region 5' to the first exon and 7 kb region 3' to the fifth exon. In all, 144 SNPs were identified, of those
20 96 were excluded from further analysis either because of low minor allele frequency or they were completely correlated with other SNPs and thus redundant. FIG. 12(c) shows the distribution of the 48 SNPs, used for genotyping, relative to exons, introns and the 5' and 3' flanking regions of the FLAP gene. Only one SNP was identified within a coding sequence (exon 2). This SNP did not lead to amino acid substitution.
25 The locations of these SNPs in the NCBI human genome assembly, build 34, are listed in Table 18.

Table 18 Locations of all genotyped SNPs in NCBI build 34 of the human genome assembly.

SNP name	Build34 start
SG13S381	29083350
SG13S366	29083518
SG13S1	29086224
SG13S2	29087473
SG13S367	29088090
SG13S10	29088473
SG13S3	29089044
SG13S368	29089886
SG13S4	29090997
SG13S5	29091307
SG13S90	29091780
SG13S6	29092536
SG13S371	29093964
SG13S372	29094259
SG13S373	29096688
SG13S375	29096874
SG13S376	29096962
SG13S25	29097553
SG13S377	29101965
SG13S100	29104271
SG13S95	29106329
SG13S191	29107830
SG13S106	29108579
SG13S114	29110096
SG13S121	29112174
SG13S122	29112264
SG13S43	29112455
SG13S192	29116308
SG13S88	29116401
SG13S137	29118118
SG13S86	29118815
SG13S87	29118873
SG13S39	29119740
SG13S26	29122253
SG13S27	29122283
SG13S29	29123643
SG13S89	29124441
SG13S96	29124906
SG13S30	29125840
SG13S97	29129139

SG13S32	29130547
SG13S41	29134045
SG13S42	29135877
SG13S34	29137100
SG13S35	29138117
SG13S181	29138633
SG13S184	29139435
SG13S188	29140805

In addition to the SNPs, a polymorphism consisting of a monopolymer A repeat that has been described in the FLAP promoter region was typed (Koshino, T. *et al.*, *Mol Cell Biol Res Commun* **2**, 32-5 (1999)).

The linkage disequilibrium (LD) block structure defined by the 48 SNPs that were selected for further genotyping is shown in FIG. 14. A strong LD was detected across the FLAP region, although it appears that at least one recombination may have occurred dividing the region into two strongly correlated LD blocks.

Haplotype association to MI

To perform a case-control association study the 48 selected SNPs and the monopolymer A repeat marker were genotyped in a set of 779 unrelated MI patients and 628 population-based controls. Each of the 49 markers were tested individually for association to the disease. Three SNPs, one located 3 kb upstream of the first exon and the other two 1 and 3 kb downstream of the first exon, showed nominally significant association to MI (Table 19).

Table 19 SNP allelic association in the MI cohort

Phenotype	Marker	Allele	P value	RR	# Pat.	% Pat.	# Ctrl	% Ctrl
All patients	SG13S106	G	0.0044	1.29	681	72.0	530	66.6
	SG13S100	A	0.020	1.29	388	69.6	377	63.9
	SG13S114	T	0.021	1.21	764	70.0	602	65.8
Males	SG13S106	G	0.0037	1.35	422	72.9	530	66.6
	SG13S100	A	0.0099	1.36	292	70.7	377	63.9
	SG13S114	T	0.026	1.24	477	70.4	602	65.8
Early onset	SG13S100	A	0.0440	1.43	99	71.7	377	63.9

Nominally significant SNP association with corresponding number of patients (# Pat.) and controls (#Ctrl). RR refers to relative risk.

- 5 However, after adjusting for the number of markers tested, these results were not significant. A search was then conducted for haplotypes that show association to the disease using the same cohorts. For computational reasons, the search was limited to haplotype combinations constructed out of two, three or four SNPs and only haplotypes that were in excess in the patients were tested. The resulting P values
- 10 were adjusted for all the haplotypes we tested by randomizing the patients and controls (see Methods).

Several haplotypes were found that were significantly associated to the disease with an adjusted P value less than 0.05 (Table 20).

TABLE 20 SNP haplotypes that significantly associate with Icelandic MI patients

SG13S4	SG13S6	SG13S372	SG13S25	SG13S377	SG13S100	SG13S95	SG13S114	SG13S192	SG13S137	SG13S86	SG13S87	SG13S39	SG13S27	SG13S89	SG13S96	SG13S32	SG13S41	SG13S42	SG13S34	SG13S188	P value ^a	P value ^b	Pat.frq	Ctrl.frq	RR	D' ^c
		G					T							G	A						0,0000023	0,005	0,158	0,095	1,80	1,00
		G					T			A					A						0,0000030	0,006	0,158	0,095	1,78	1,00
		G					T								A			T			0,0000032	0,007	0,157	0,094	1,79	1,00
		G	A							A					A						0,0000046	0,012	0,158	0,083	2,07	0,89
		G		T	T										A						0,0000047	0,012	0,154	0,093	1,78	1,00
		G					T			G					A						0,0000055	0,015	0,147	0,087	1,81	1,00
		G	A												A			T			0,0000061	0,017	0,157	0,083	2,07	0,89
		G	A										G		A						0,0000063	0,017	0,157	0,084	2,04	0,89
		G					T								A						0,0000070	0,021	0,157	0,096	1,76	1,00
		G					T								A	A					0,0000075	0,022	0,149	0,089	1,78	1,00
G					T	T									A						0,0000083	0,024	0,208	0,139	1,62	0,99
		G	A							G					A						0,0000084	0,026	0,145	0,074	2,14	0,88
		G					T	A							A						0,0000084	0,026	0,139	0,082	1,82	1,00
		G					T						G		A						0,0000091	0,028	0,156	0,096	1,75	1,00
G							T								A			T			0,0000094	0,028	0,210	0,141	1,61	0,99
G		G					T								A						0,0000100	0,028	0,156	0,096	1,74	1,00
G			A												A			A			0,0000101	0,028	0,215	0,133	1,80	0,81
		G	A												A						0,0000105	0,028	0,157	0,084	2,03	0,89
G			A							A					A						0,0000108	0,029	0,214	0,133	1,78	0,81
		G	A												A	A					0,0000110	0,030	0,146	0,075	2,10	0,88
G							T			A					A						0,0000112	0,030	0,212	0,144	1,60	1,00
		G	A				A											T			0,0000113	0,030	0,151	0,081	2,03	0,78
		G					T					G			A						0,0000118	0,031	0,156	0,096	1,73	1,00
G			A												A			T			0,0000126	0,034	0,212	0,131	1,79	0,79
G							T							G	A						0,0000129	0,035	0,211	0,144	1,59	1,00
		G	A									G			A						0,0000134	0,035	0,156	0,084	2,01	0,89
G							T								A						0,0000136	0,036	0,211	0,143	1,60	1,00
G		G	A												A						0,0000137	0,036	0,156	0,085	2,00	0,89
		G	A				A								A						0,0000148	0,037	0,151	0,081	2,01	0,78
		G					T	A										T			0,0000150	0,037	0,160	0,099	1,73	0,87
		G	A				A								A						0,0000150	0,037	0,130	0,066	2,13	0,90
		G					T	C										T			0,0000154	0,039	0,152	0,094	1,73	0,93
		G					T								A		A				0,0000154	0,040	0,155	0,097	1,70	1,00
		G					T	C							A						0,0000157	0,040	0,141	0,085	1,76	1,00
		G	G	A											A						0,0000158	0,040	0,152	0,084	1,94	0,90
G							T					G			A						0,0000163	0,040	0,210	0,143	1,59	0,99
G							T			G					A						0,0000166	0,041	0,200	0,134	1,61	0,92
G			A										G		A						0,0000168	0,042	0,213	0,133	1,76	0,81

		G	A		G	A	0,0000168	0,042	0,156	0,084	2,000,89	
C	G		A			A	0,0000171	0,042	0,211	0,136	1,700,81	
	G			T	A	A	0,0000183	0,043	0,192	0,128	1,620,85	
	G		A			A	0,0000184	0,043	0,212	0,132	1,770,81	
	G			T		A	T	0,0000193	0,046	0,328	0,251	1,460,99
		G		T		G	T	0,0000194	0,046	0,175	0,115	1,640,98
	G	G		A		A		0,0000202	0,048	0,210	0,136	1,700,81
	G	G	A		A			0,0000209	0,049	0,151	0,082	2,000,76

^a Single test P values. ^b P values adjusted for all the SNP haplotypes tested.

^c Measure of correlation with Haplotype A4 .

The most significant association was observed for a four SNP haplotype spanning 33 kb, including the first four exons of the gene (Fig. 12(c)), with a nominal P value of 0.0000023 and an adjusted P value of 0.005. This haplotype, labelled A4 , has haplotype frequency of 15.8% (carrier frequency 30.3%) in patients versus 9.5% (carrier frequency 17.9%) in controls (Table 21).

Table 21 Association of the A4 haplotype to MI, Stroke and PAOD

Phenotype (n)	Frq. Pat.	RR	PAR	P-value	P-value ^a
<i>MI (779)</i>	0.158	1.80	0.135	0.0000023	0.005
Males (486)	0.169	1.95	0.158	0.00000091	ND ^b
Females (293)	0.138	1.53	0.094	0.0098	ND
Early onset (358)	0.138	1.53	0.094	0.0058	ND
<i>Stroke (702)^c</i>	0.149	1.67	0.116	0.000095	ND
Males (373)	0.156	1.76	0.131	0.00018	ND
Females (329)	0.141	1.55	0.098	0.0074	ND
<i>PAOD (577)^c</i>	0.122	1.31	0.056	0.061	ND
Males (356)	0.126	1.36	0.065	0.057	ND
Females (221)	0.114	1.22	0.041	0.31	ND

^a P value adjusted for the number of haplotypes tested. ^b Not done. ^c Excluding known cases of MI.

Shown is the FLAP A4 haplotype and corresponding number of patients (n), haplotype frequency in patients (Frq. pat.), relative risk (RR), population attributed risk (PAR) and P values. The A4 haplotype is defined by the following SNPs: SG13S25, SG13S114, SG13S89 and SG13S32 (Table 20). The same controls (n=628) are used for the association analysis in MI, stroke and PAOD as well as for the male, female and early onset analysis. The A4 haplotype frequency in the control cohort is 0.095.

10

The relative risk conferred by The A4 haplotype compared to other haplotypes constructed out of the same SNPs, assuming a multiplicative model, was 1.8 and the corresponding population attributable risk (PAR) was 13.5%. As shown in Table 21, The A4 haplotype was observed in higher frequency in male patients (carrier frequency 30.9%) than in female patients (carrier frequency 25.7%). All the

other haplotypes that were significantly associated with an adjusted P value less than 0.05, were highly correlated with The A4 haplotype and should be considered variants of that haplotype (Table 20).

5 *Association of The A4 haplotype to stroke and peripheral arterial occlusive disease*

In view of the linkage observed for stroke in male patients to the FLAP locus and since there is a high degree of co-morbidity among MI, stroke and peripheral arterial occlusive disease (PAOD), with most of these cases occurring on the basis of
10 an atherosclerotic disease, it was determined whether The A4 haplotype also shows association to stroke and/or PAOD and typed the SNPs defining The A4 haplotype on these patient cohorts. First and second degree relatives and all known cases of MI were removed, and 702 stroke patients and 577 PAOD patients were tested for association. The results are also listed in Table 21, above. A significant association
15 of The A4 haplotype to stroke was observed, with a relative risk of 1.67 (P value = 0.000095). In addition, it was determined whether The A4 haplotype was primarily associated with a particular sub-phenotype of stroke, and found that both ischemic and hemorrhagic stroke were significantly associated with The A4 haplotype (Table 22).

20 Table 22 Association of The A4 haplotype to subgroups of stroke

Phenotype (n)	Pat. Frq.	RR	PAR	P-value
Stroke ^a (702)	0.149	1.67	0.116	0.000095
Ischemic (484)	0.148	1.65	0.113	0.00053
TIA (148)	0.137	1.51	0.090	0.058
Hemorrhagic (68)	0.167	1.91	0.153	0.024

^aExcluding known cases of MI.

Finally, although The A4 haplotype was more frequent in the PAOD cohort
25 than in the population controls (Table 21), this was not significant. It should be noted

that similar to the stronger association of The A4 haplotype to male MI compared to female MI, it also shows stronger association to male stroke and PAOD (Table 15).

Haplotype association to FLAP in a British cohort

- 5 In an independent study, it was determined whether variants in the FLAP gene also have impact on risk of MI in a population outside Iceland. The four SNPs, defining The A4 haplotype, were typed in a cohort of 750 patients from the United Kingdom who had sporadic MI, and in 728 British population controls. The patients and controls come from 3 separate study cohorts recruited in Leicester and Sheffield.
- 10 No significant differences were found in the frequency of the haplotype between patients and controls (16.9% versus 15.3%, respectively). However, when we typed additional 9 SNPs, distributed across the FLAP gene, in the British cohort and searched for other haplotypes that might be associated with MI, two SNPs showed association to MI with a nominally significant P value (data not shown). Moreover,
- 15 three and four SNP haplotype combinations increased the risk of MI in the British cohort further and the most significant association was observed for a four SNP haplotype with a nominal P value = 0.00037 (Table 23).

Table 23 Association of the HapB haplotype to British MI patients

Phenotype (n)	Frq. Pat.	RR	PAR	P-value	P-value ^a
MI (750)	0.075	1.95	0.072	0.00037	0.046
Males (546)	0.075	1.97	0.072	0.00093	ND
Females (204)	0.073	1.90	0.068	0.021	ND

^aP value adjusted for the number of haplotypes tested using 1,000 randomization tests. Shown are the results for HapB that shows the strongest association in British MI cohort. HapB is defined by the following SNPs: SG13S377, SG13S114, SG13S41 and SG13S35 (that have the following alleles A, A, A and G, respectively). In all three phenotypes shown the same set of n=728 British controls is used and the frequency of HapB in the control cohort is 0.040. Number of patients (n), haplotype frequency in patients (Frq. pat.), relative risk (RR) and population attributed risk (PAR).

20

This was called haplotype HapB. The haplotype frequency of HapB is 7.5% in the MI patient cohort (carrier frequency 14.4%), compared to 4.0% (carrier frequency 7.8%) in controls, conferring a relative risk of 1.95 (Table 23). This haplotype

remained significant after adjusting for all haplotypes tested, using 1000 randomisation steps, with an adjusted P value = 0.046. No other SNP haplotype had an adjusted P value less than 0.05. The two at-risk haplotypes A4 and HapB appear to be mutually exclusive with no instance where the same chromosome carries both
5 haplotypes.

DISCUSSION:

These results show that variants of the gene encoding FLAP associate with increased risk of MI and stroke. In the Icelandic cohort, a haplotype that spans the
10 FLAP gene is carried by 30% of all MI patients and almost doubles the risk of MI. These findings were subsequently replicated in an independent cohort of stroke patients. In addition, another haplotype that spans the FLAP gene is associated with MI in a British cohort. Suggestive linkage to chromosome 13q12 was observed with several different phenotypes, including female MI, early onset MI of both sexes, and
15 ischemic stroke or TIA in males. However, surprisingly, the strongest haplotype association was observed to males with MI or stroke. Therefore, there may be other variants or haplotypes within the FLAP gene, or in other genes within the linkage region, that also may confer risk to these cardiovascular phenotypes.

These data also show that the at-risk haplotype of the FLAP gene has
20 increased frequency in all subgroups of stroke, including ischemic, TIA, and hemorrhagic stroke. Of interest is that The A4 haplotype confers significantly higher risk of MI and stroke than it does of PAOD. This could be explained by differences in the pathogenesis of these diseases. Unlike PAOD patients who have ischemic legs because of atherosclerotic lesions that are responsible for gradually diminishing blood
25 flow to the legs, the MI and stroke patients have suffered acute events, with disruption of the vessel wall suddenly decreasing blood flow to regions of the heart and the brain.

Association was not found between The A4 haplotype and MI in a British cohort. However, significant association to MI was found with a different variant
30 over the FLAP gene. The fact that different haplotypes of the gene are found conferring risk to MI in a second population is not surprising. A common disease like

MI associates with many different mutations or sequence variations, and the frequencies of these disease associated variants may differ between populations. Furthermore, the same mutations may be seen arising on different haplotypic backgrounds.

MARKERS UTILIZED HEREIN

Table 24: Position (Mb) of microsatellite markers sequence assembly (SA5), primers and size of the markers.

5

mb	Marker	Forward	Reverse	size
25.0920 42	DG13S2101	ACGGTGATGACGCCTACATT (SEQ ID NO: 4)	TCACATGGACCAATTACCTAGA A(SEQ ID NO: 5)	188
25.0920 42	DG13S48	CAAATTTTCAGATGTGCCAACC (SEQ ID NO: 6)	ACGGTGATGACGCCTACATT(S EQ ID NO: 7)	214
25.3965 04	D13S1304	ACCAGCCTTTGCTTAGGA(SEQ ID NO: 8)	ACATTCTAGTGCTACAGGGTAC TC(SEQ ID NO: 9)	133
25.3965 35	DG13S2105	TGTTCTGCACACGAACATTCT(SEQ ID NO: 10)	TCCTGAGTCCTCTCCACCTG(S EQ ID NO: 11)	104
25.4455 11	DG13S2106	TGGGAATTAATGAAGAACAACAA A(SEQ ID NO: 12)	CATGTTTCGAAGAACTCAAGAG G(SEQ ID NO: 13)	428
25.5449 20	D13S1254	AAATTACTTCATCTTGACGATAAC A(SEQ ID NO: 14)	CTATTGGGGACTGCAGAGAG (SEQ ID NO: 15)	218
25.5449 25	DG13S2107	GGGACTGCAGAGAGCAGAAG (SEQ ID NO: 16)	CAAGAAGGGAATTCCTACGC (SEQ ID NO: 17)	95
25.5659 56	DG13S55	AGCCAGTGTCCACAAGGAAG (SEQ ID NO: 18)	GAGGGTGAGACACATCTCTGG (SEQ ID NO: 19)	283
25.6057 93	DG13S54	AATCGTGCCTCAGTTCCATC (SEQ ID NO: 20)	CCACCAGGAACAACACACAC (SEQ ID NO: 21)	156
25.6196 93	D13S625	TTGCTCTCCAGCCTGGGC (SEQ ID NO: 22)	TTCTCTGGCTGCCTGCG (SEQ ID NO: 23)	185
25.6874 22	DG13S1479	TTTGATTCCGTGGTCCATTA (SEQ ID NO: 24)	TTATTTGGTCGGTGACCTTT (SEQ ID NO: 25)	339
25.7493 44	DG13S1440	GGTAGGTTGAAATGGGCTAACA (SEQ ID NO: 26)	TCATGACAAGGTGTTGGATTT (SEQ ID NO: 27)	153
25.9012 12	DG13S1890	CCTCCTCTGCCATGAAGCTA (SEQ ID NO: 28)	CTATTTGGTCTGCGGGTTGT (SEQ ID NO: 29)	418
25.9280 81	DG13S1879	TTTGAGCCCAGATCTAAGCAA (SEQ ID NO: 30)	AAATGTTAATGTCACCGACAAA (SEQ ID NO: 31)	443
25.9326 09	DG13S1540	TACTGGGTTATCGCCTGACC (SEQ ID NO: 32)	CCAATGGACCTCTTGGACAT (SEQ ID NO: 33)	152
25.9467 43	DG13S1889	TTTGAATGTTTCATATTTGTGGT G (SEQ ID NO: 34)	CCCTCGTAATGAAACCTATTTG A (SEQ ID NO: 35)	222
25.9486 79	DG13S59	TTTCGGCACAGTCCTCAATA (SEQ ID NO: 36)	CAGGGTGTGGTGACAT (SEQ ID NO: 37)	228
25.9523 47	DG13S1894	TGTTTCTTTCTTCTCTCTCTTT C (SEQ ID NO: 38)	AAATGAGTTCAATGAGTTGTGG TT (SEQ ID NO: 39)	209
25.9883 60	DG13S1545	CAGAGAGGAACAGGCAGAGG (SEQ ID NO: 40)	AGTGGCTGGGAAGCCTTATT (SEQ ID NO: 41)	394
26.0718 66	DG13S1524	AGGTGAGAGAACAACCTGTCTT (SEQ ID NO: 42)	GCCTTCCTTCTAAGGCCAAC (SEQ ID NO: 43)	115
26.1834 92	DG13S1491	TGTTATACATTTCAATTTACCTC A (SEQ ID NO: 44)	GTAATCCAGCCGGGCAAC (SEQ ID NO: 45)	286
26.2362 89	DG13S62	TTGTTTCAGTGCTCTATAGTTACAA AGT (SEQ ID NO: 46)	GGTCACAAAGCTATGCGATTA (SEQ ID NO: 47)	158
26.2734 63	D13S1244	TCAACAAGTGGATTAAGAAACTG TG (SEQ ID NO: 48)	CTGTTTATGGCTGAGAAGTATG C (SEQ ID NO: 49)	86

26.2869	35	DG13S64	TAGCAGGGTGCAGTCTA (SEQ ID NO:50)	ACCATACCACCACCACCATC (SEQ ID NO: 51)	247
26.3145	01	D13S243	ACTGTACTTCTGCCTGGGC (SEQ ID NO: 52)	TTTTGTAATGCCTCAACCATG (SEQ ID NO: 53)	147
26.3271	84	DG13S1529	CTGTAGACTTTATCCCTGACTTAC TG (SEQ ID NO: 54)	CAATGAATGATGAAGATTCCAC TC (SEQ ID NO: 55)	132
26.3387	67	DG13S1908	TGACACCATGTCTTACTGTTTGC (SEQ ID NO: 56)	GAGGATACAATGAGAACCAAAT CTC (SEQ ID NO: 57)	224
26.3880	34	DG13S1546	CCACAGAATGCTCCAAAGGT (SEQ ID NO: 58)	GAGTTCAAGTGATGGATGACG A (SEQ ID NO:59)	357
26.4358	11	DG13S1444	CAGATAGATGAATAGGTGGATGG A (SEQ ID NO: 60)	CACTGTTCCAAGTGCTTTGC (SEQ ID NO: 61)	193
26.4866	57	DG13S1458	GCAGGGCAAACCTGCCTTAT (SEQ ID NO:62)	TTTGGTGAAATGTCTGTTTATG G (SEQ ID NO: 63)	402
26.5045	45	D13S252	CTCAACCTGGCTTCTACT (SEQ ID NO: 64)	TACTCCTTAATAAACTCCCC (SEQ ID NO: 65)	338
26.5082	31	DG13S66	TATGCGTTGTGTGTGTG (SEQ ID NO:66)	GGGCCTTAGATTCTTGTAGTG G (SEQ ID NO: 67)	217
27.1151	20	DG13S1554	CTCGCATCTCGCTTCTCACT (SEQ ID NO: 68)	CTCAAGGGTCCAGTGGTTTG (SEQ ID NO: 69)	420
27.1406	75	DG13S1907	TGTCCAGACTGCCTCCTACA (SEQ ID NO:70)	TGCAACACCTGGTTCACAAT (SEQ ID NO: 71)	131
27.1458	42	D13S802	CACAGTGAGACTCTATCTCAAAA A (SEQ ID NO: 72)	TCAGACTGGCTTAGACTGTGG (SEQ ID NO: 73)	150
27.2406	16	DG13S1892	AAATTCCAAAGGCCAGGTG (SEQ ID NO: 74)	CCATACAGTTTCCTAGGTTCTG G (SEQ ID NO: 75)	373
27.2534	52	DG13S1849	CACCTGGCCAAATGTTTGTT (SEQ ID NO: 76)	TGCTTGAATCCAGAGACTGC (SEQ ID NO: 77)	190
27.2738	60	DG13S68	TTTGCGAGTCCTTGTGGAGT (SEQ ID NO: 78)	ACAGTCCGCTCCCTCCTAAT (SEQ ID NO: 79)	238
27.2804	61	DG13S69	ATGCTTGGCCCTCAGTTT (SEQ ID NO: 80)	TTGGCAACCCAAGCTAATATG (SEQ ID NO:81)	296
27.4837	99	D13S1250	CTCCACAGTGACAGTGAGG (SEQ ID NO:82)	GAGAGGTTCCCAATCCC (SEQ ID NO: 83)	160
27.6104	06	D13S1448	CATCAACCTCCCCACCAC (SEQ ID NO: 84)	TATTTTTCAGTCCCACAGTTA GC (SEQ ID NO:85)	227
27.6158	14	DG13S574	CAGCTCCTGGCCATATTTCT (SEQ ID NO: 86)	GAGCCATTCTCTGGGTCTG (SEQ ID NO:87)	153
27.6412	11	DG13S73	GGTCCGTGTCAACCCTTAGA (SEQ ID NO: 88)	CAGGTTGATGGGAGGGAAA (SEQ ID NO: 89)	198
27.6615	07	DG13S1532	CGGGAAATGACAGTGAGACC (SEQ ID NO: 90)	TGCCTAGATTCTCCCGTAAG (SEQ ID NO: 91)	163
27.7053	47	D13S1242	GTGCCCAGCCAGATTC (SEQ ID NO: 92)	GCCCCCAGTCAGGTTT (SEQ ID NO: 93)	198
27.8838	72	DG13S576	TTTCTCTCTCCACGGAATGAA (SEQ ID NO:94)	AACCCATTCTCACAGGGTGTA (SEQ ID NO: 95)	199
27.8973	65	DG13S1917	AGGAGTGTGGCAGCTTTGAG (SEQ ID NO: 96)	TGGATTCCCGTGAGTACCAG (SEQ ID NO: 97)	165
27.9321	54	D13S217	ATGCTGGGATCACAGGC (SEQ ID NO: 98)	AACCTGGTGGACTTTTGCT (SEQ ID NO: 99)	170
28.0806	32	DG13S581	AGCATTTCCAATGGTGCTTT (SEQ ID NO: 100)	CATGTTGATATGCCTGAAGGA (SEQ ID NO:101)	367
28.1653	48	DG13S1471	CACTGTCTGCTGCCACTCAT (SEQ ID NO:102)	AGAGATTATGTGATGTACCCTC TCTAT (SEQ ID NO:103)	267

28.3032	52	DG13S583	CAAGCCTGGGACACAGAAAT (SEQ ID NO: 104)	TTTGCAGACACCACAACACA (SEQ ID NO: 105)	264
28.3032	56	D13S120	ATGACCTAGAAATGATACTGGC (SEQ ID NO: 106)	CAGACACCACAACACACATT (SEQ ID NO: 107)	175
28.3855	66	D13S1486	TGGTTTAAAAACCTCATGCC (SEQ ID NO: 108)	ATCCCAAACCTCTGTACTTATGT AGG (SEQ ID NO: 109)	151
28.4155	30	DG13S1024	TTTGCACATACACATAAGCGAAC (SEQ ID NO: 110)	CACAAATCCCGTGCACTAAA (SEQ ID NO: 111)	139
28.4155	30	DG13S1510	ATTCCTGGGCTCATGGTACA (SEQ ID NO: 112)	TGCCGTCATCTGCTTTAGAA (SEQ ID NO: 113)	390
28.4303	08	DG13S1495	CCTTGGCTGTTGTGACTGGT (SEQ ID NO: 114)	CACTCAGGTGGGAGGATCAC (SEQ ID NO: 115)	285
28.5175	41	DG13S1482	GCTGTTTCCTTGGCTTCTTCT (SEQ ID NO: 116)	CCCATACTTGAGATGACCATGA (SEQ ID NO: 117)	291
28.5510	60	DG13S1845	CACTTTGCCAGTAGCCTTGA (SEQ ID NO: 118)	TTGGGAAAGTTAACCAGAGA (SEQ ID NO: 119)	284
28.6349	03	DG13S1030	TTTGGGAAGAGCCATGAGAC (SEQ ID NO: 120)	CTCTGGGCATTGGAGGATTA (SEQ ID NO: 121)	354
28.6349	03	DG13S1467	TTTGGGAAGAGCCATGAGAC (SEQ ID NO: 122)	AATGCCCATGTGCACTGTAG (SEQ ID NO: 123)	231
28.6866	07	DG13S584	GGGAGACAAGTCAGGTGAGG (SEQ ID NO: 124)	CTGAGTATGGAGTCTTCATCAT TATC (SEQ ID NO: 125)	151
28.7940	32	DG13S1519	TCGTCTCGAAGAAAGAAAGA (SEQ ID NO: 126)	CACCATGGGTAAATTGCACA (SEQ ID NO: 127)	286
28.8761	56	DG13S77	TGACGTGGGTTTCAGGTTGTA (SEQ ID NO: 128)	AGTGCATTGGTGCCTTCTCT (SEQ ID NO: 129)	220
28.9707	23	DG13S586	GGACTGCCAATTCTACAGCA (SEQ ID NO: 130)	TTTCCATGGGAAATTGATC (SEQ ID NO: 131)	151
28.9756	41	DG13S79	TGCTACTAGATTTGACCAACCA (SEQ ID NO: 132)	GACTTGTAAGGATTTAGTGAT TTCG (SEQ ID NO: 133)	128
29.0593	94	DG13S80	GTGGAAGGCCTCTCTTG (SEQ ID NO: 134)	TGCTTCTTGAGGGAAAGCAT (SEQ ID NO: 135)	233
29.1261	52	DG13S82	CACGTGGTTCACCTCTCTAGG (SEQ ID NO: 136)	TTGGCCACTTATTTGTG (SEQ ID NO: 137)	302
29.1546	91	D13S1299	CGATGAGTGACAGGGCT (SEQ ID NO: 138)	CCTCGTGGGTGGAATAA (SEQ ID NO: 139)	225
29.1547	37	DG13S85	TTGGCCATTAGCAATTAGCA (SEQ ID NO: 140)	CGTGGGTGGAATAAATCAGG (SEQ ID NO: 141)	153
29.1584	62	D13S629	GTTGAGGCAAGAGAATCACT (SEQ ID NO: 142)	GCACATTTACACCAGGGTG (SEQ ID NO: 143)	145
29.2240	60	DG13S1934	CCTTCAGAGGATTTCCCTTTC (SEQ ID NO: 144)	CTGGTTTGACTCCAGCTTCA (SEQ ID NO: 145)	431
29.2454	62	DG13S1098	TGTTCAAACCTAAGGTGCTTCA (SEQ ID NO: 146)	GAAACAACAACAACAACAA CA (SEQ ID NO: 147)	416
29.2598	40	DG13S1104	CCTGGCACGGAATAGACACT (SEQ ID NO: 148)	GGCCTCCTTTGCTCTGAAG (SEQ ID NO: 149)	378
29.2944	36	DG13S1097	CATCCCTGTGGCTGATTAAGA (SEQ ID NO: 150)	AACAGTTCAGCCCGTTCTA (SEQ ID NO: 151)	162
29.3097	00	DG13S1110	TTTCAAAGGAATATCCAAGTGC (SEQ ID NO: 152)	TGGCGTACCATATAAACAGTTC TC (SEQ ID NO: 153)	265
29.3099	09	DG13S86	TTTCAAAGGAATATCCAAGTGC (SEQ ID NO: 154)	AAACGTGACACTTCCACACA (SEQ ID NO: 155)	177
29.3599	61	DG13S87	TTCAATGAAGGTGCCGAAGT (SEQ ID NO: 156)	TGTCTATCCCAAAGCAA (SEQ ID NO: 157)	218

29.5224	43	DG13S1111	GCAAGACTCTGTTGAAGAAGAAG A (SEQ ID NO: 158)	TCCCTCTGTTTGAGTTTCTCG (SEQ ID NO: 159)	110
29.5746	65	DG13S1101	AGGCACAGTCGCTCATGTC (SEQ ID NO: 160)	AAACTTTAGCTAATGGTGGTCA AA (SEQ ID NO: 161)	333
29.6227	55	DG13S1106	TGTGATTCCAGGGAGCTATCA. (SEQ ID NO: 162)	TAGGTGTGTGGAGGACAGCA (SEQ ID NO: 163)	416
29.6589	10	DG13S172	CCAGTTTCAGTTAGCCAAGTCTG (SEQ ID NO: 164)	GAGAGGGAATGAATGCAGGA (SEQ ID NO: 165)	267
29.6657	09	D13S1246	GAGCATGTGTGACTTTCATATTC AG (SEQ ID NO: 166)	AGTGGCTATTTCATTGCTACAGG (SEQ ID NO: 167)	177
29.6725	61	DG13S1103	TTGCTGGATGCTGGTTTCTA (SEQ ID NO: 168)	AAAGAGAGAGAGAAAGAGAAA GAAAGA (SEQ ID NO: 169)	264
29.8259	75	D13S289	CTGGTTGAGCGGCATT (SEQ ID NO: 170)	TGCAGCCTGGATGACA (SEQ ID NO: 171)	260
29.8266	31	DG13S166	CCTATGGAAGCATAGGGAAGAA (SEQ ID NO: 172)	CCCACTTCTGAGTCTCCTGAT (SEQ ID NO: 173)	395
29.9066	89	DG13S164	GGGATGCAGAAAGGATGTGT (SE Q ID NO: 174)	AAGAATGCTGGCCAACGTAA (S EQ ID NO: 177)	218
29.9067	00	D13S1238	CTCTCAGCAGGCATCCA (SEQ ID NO: 178)	GCCAACGTAATTGACACCA (SE Q ID NO: 179)	129
30.0313	78	D13S290	CCTTAGGCCCCATAATCT (SEQ ID NO: 180)	CAAATTCCTCAATTGCAAAAT (S EQ ID NO: 181)	176
30.0863	03	D13S1229	GGTCATTCAGGGAGCCATTC (SE Q ID NO: 182)	CCATTATATTTACCAAGAGGC TGC (SEQ ID NO: 183)	119
30.1928	47	DG13S1460	TGCCTGGTCATCTACCCATT (SEQ ID NO: 184)	TCTACTGCAGCGCTGATCTT (S EQ ID NO: 185)	264
30.2176	70	DG13S1933	CATTTATGAATGGAGGTGAAGC (S EQ ID NO: 186)	ATGGGAGCTCAAAGGGAAAT (S EQ ID NO: 187)	186
30.3032	13	DG13S1448	CAGCAGGAAGATGGACAGGT (SE Q ID NO: 188)	CACACTGCATCACACATACCC (SEQ ID NO: 189)	136
30.3178	71	D13S1287	TATGCCAGTATGCCTGCT (SEQ ID NO: 190)	GTACATCAGTCCATTTGC (SE Q ID NO: 191)	232
30.3421	02	DG13S1061	CCAAAGCAAGTAACCTCCTCA (SE Q ID NO: 192)	AAACAATCACTGCCCTCTGG (S EQ ID NO: 193)	227
30.5718	37	DG13S1904	TGATGAAATTGCCTAGTGATGC (S EQ ID NO: 194)	GGATCCAATCGTACGCTACC (S EQ ID NO: 195)	136
30.6434	38	DG13S882	CGAATGGGTGACTAACAGCA (SE Q ID NO: 196)	CTGGAGTGCAGGGACATGA (SE Q ID NO: 197)	378
30.6659	37	DG13S295	AAAGAAATATTCCAAGAAGAAAG AAA (SEQ ID NO: 198)	TTGCACAACTTTGTGTAGAGCA T (SEQ ID NO: 199)	279
30.6744	68	D13S1226	GGGTATGTCTTTATTCTCGGCAG TA (SEQ ID NO: 200)	GTGCATTCACAGACCAGTCATT (SEQ ID NO: 201)	219
30.6909	59	DG13S293	GGGCTTGAAGGCACTAAATGT (S EQ ID NO: 202)	CCAAGCAGTAATTCCTTCCTCA (SEQ ID NO: 203)	313
30.7124	68	DG13S1490	ACCTAAACACCACGGAAGTGG (SE Q ID NO: 204)	CAGGTATCGACATTCTTCCAAA (SEQ ID NO: 205)	418
30.8244	83	DG13S93	TGGGAAGCCAGTAAAGTAGGAA (SEQ ID NO: 206)	AAAGAGACTCCACACATCCATT T (SEQ ID NO: 207)	190
30.8248	59	DG13S94	AGGGCTATTCCTCAAGGTGTT (SE Q ID NO: 208)	TGCTAACACTACCCTCGCAAT (SEQ ID NO: 209)	332
30.9284	29	DG13S1534	GGGCAGGAATCTCTGAAGTG (SEQ ID NO: 210)	CTCCACTGAGAAGCCAAGGA (S EQ ID NO: 211)	382
30.9403	69	DG13S95	AGGCCAAGCTGGTCCATAG (SEQ ID NO: 212)	TCTCTCAAAGCCTCGCTCTC (S EQ ID NO: 213)	126

30.9702 38	DG13S96	CCTTTGAGGCTGGATCTGTT(SEQ ID NO: 214)	TTTCCTTATCATTCCCTCA (SEQ ID NO: 215)	218
31.0388 74	D13S260	AGATATTGTCTCCGTTCCATGA(S EQ ID NO: 216)	CCCAGATATAAGGACCTGGCT A(SEQ ID NO: 217)	163
31.0922 94	DG13S17	TTTAAGCCCTGTGGAATGTATTT(SEQ ID NO: 218)	GACATTGCAGGTCAAGTAGGG(SEQ ID NO: 219)	157
31.2078 44	DG13S306	TGCATAAGGCTGGAGACAGA(SEQ ID NO: 220)	CACAGCAGATGGGAGCAAA(SEQ ID NO: 221)	158
31.2605 21	DG13S18	GTGCATGTGCATACCAGACC(SEQ ID NO: 222)	GGCAAGATGACCTCTGGAAA(S EQ ID NO: 223)	319
31.2997 20	DG13S1905	GTCCACTGCAGCACACAGAG(SEQ ID NO: 224)	GCACTGGTAGATACATGCTAAC G(SEQ ID NO: 225)	383
31.3532 30	DG13S307	GGGTATCTTGGCCAGGTGT(SEQ ID NO: 226)	TGGCTAAGCACAATCCCTTT(S EQ ID NO: 227)	403
31.3551 35	DG13S1062	TTTGTGTTCCAGGTGAGAATTG(S EQ ID NO: 228)	GAACCATATCCAAGGCACT(S EQ ID NO: 229)	120
31.4143 29	DG13S1874	AACCCAAATCAACAAACCAGA(SEQ ID NO: 230)	AATGAATTCTGGGTCACATGC(SEQ ID NO: 231)	404
31.4295 62	DG13S1093	TTGTTCCACATTCTTCTACA(S EQ ID NO: 232)	TTAAACTCGTGGCAAAGACG(S EQ ID NO: 233)	273
31.6265 02	DG13S1059	CACCATGCCTGGCTCTTT(SEQ ID NO: 234)	AACTTCTCCAGTTGTGTGGTTG (SEQ ID NO: 235)	330
31.7237 49	DG13S1086	AGCTGAGCTCATGCCACT(SEQ ID NO: 236)	CAAGACCTTGTGCATTTGGA(S EQ ID NO: 237)	155
31.7460 74	DG13S1515	AGCCAGACATGGTAGTGTGC(SEQ ID NO: 238)	GCAATAACTCACATCAGCAA (SEQ ID NO: 239)	417
31.8557 32	D13S171	CCTACCATTGACACTCTCAG(SEQ ID NO: 240)	TAGGGCCATCCATTCT(SEQ ID NO: 241)	231
31.9173 32	DG13S1092	ACCAAGATATGAAGGCCAAA(SEQ ID NO: 242)	CCTCCAGCTAGAACAATGTGAA (SEQ ID NO: 243)	176
32.0028 52	DG13S1449	TGTCCATAGCTGTAGCCCTGT(SEQ ID NO: 244)	CTCAATGGGCATCTTTAGGC(S EQ ID NO: 245)	279
32.0729 57	DG13S1489	TGTAATTCAACGACTGGTGTCC(S EQ ID NO: 246)	AGCTTCTGATGTTGCTGGT(S EQ ID NO: 247)	130
32.0839 89	DG13S312	CAAACAAACAAACAAGCAAACC(S EQ ID NO: 248)	TGGACGTTTCTTTCAGTGAGG(SEQ ID NO: 249)	349
32.1251 77	DG13S1511	TGATAACTTACCAGCATGTGAGC(SEQ ID NO: 250)	TCACCTCACCTAAGGATCTGC(SEQ ID NO: 251)	314
32.1835 47	DG13S314	CATGCAATTGCCAATAGAG(SEQ ID NO: 252)	TTGGGCTTGTCTACCTAGTTCA (SEQ ID NO: 253)	335
32.1953 58	DG13S1090	TGGGTTCCCTCATACTGGAGTG(S EQ ID NO: 254)	GCCTGAGCTCCAAGCTCTTT(S EQ ID NO: 255)	169
32.2510 38	DG13S1071	GCTGCACGTATTTGTTGGTG(SEQ ID NO: 256)	AAACAGCAGAAATGGGAACC(S EQ ID NO: 257)	239
32.3568 95	DG13S1068	CCGTGGGCTATCAATTTCTG(SEQ ID NO: 258)	AAGATGCAATCTGGTTTCCAA(SEQ ID NO: 259)	238
32.3730 40	DG13S1077	CCCAAGACTGAGGAGGTCAA(SEQ ID NO: 260)	GCTGACGGAGAGGAAAGAGA(SEQ ID NO: 261)	374
32.4227 80	DG13S1906	TGACAAGGGTGTGGTTATGG (SEQ ID NO: 262)	CCGCACTTCTCTTCTGGAC (SEQ ID NO: 263)	425
32.5115 90	DG13S316	TGAGAAGCCTGGGCATTAAG (SEQ ID NO: 264)	ACAAGCTCATCCAGGGAAAG (SEQ ID NO: 265)	243
32.6105 17	DG13S317	TTGGAAAGGAAGAAAGGAAGG (SEQ ID NO: 266)	TTGAAACCTAAATGCCACCTG (SEQ ID NO: 267)	215

32.6107 13	D13S1493	ACCTGTTGTATGGCAGCAGT (SEQ ID NO: 268)	GGTTGACTCTTTCCCAACT (SEQ ID NO: 269)	248
32.7898 94	DG13S1558	AGAGCTGATCTGGCCGAAG (SEQ ID NO:270)	GGTGGACACAGAATCCCACT (SEQ ID NO: 271)	399
32.8659 50	D13S267	GGCCTGAAAGGTATCCTC (SEQ ID NO:272)	TCCCACCATAAGCACAAG (SEQ ID NO: 273)	160
32.9614 10	DG13S1478	TCAACCTAGGATTGGCATTACA (SEQ ID NO: 274)	TCTAGGATTTGTGCCTTTCCA (SEQ ID NO: 275)	387
33.0099 22	DG13S1513	GACGTCTTAGGATTGACTTCTGC (SEQ ID NO: 276)	CCAAATACACATTCTTAAAGGG AAA (SEQ ID NO: 277)	173
33.1256 96	DG13S1461	GACTGCAGATCGTGGGACTT (SEQ ID NO: 278)	TTCTCCAGAGAAACCAACCA (SEQ ID NO: 279)	148
33.1684 68	DG13S1551	ATTCGTGCAGCTGTTTCTGC (SEQ ID NO: 280)	GCATGACATTGTAAATGGAGG A (SEQ ID NO:281)	263
33.2549 89	DG13S1884	GGTGGGAATGTGTACTGAA (SEQ ID NO: 282)	CCAGGTACAACATTCTCCTGAT (SEQ ID NO:283)	123
33.3401 24	D13S1293	TGCAGGTGGGAGTCAA (SEQ ID NO. 284)	AAATAACAAGAAGTGACCTTCC TA (SEQ ID NO: 285)	129
33.3469 08	DG13S326	TGTTCTCCTCACCTGCTCT (SEQ ID NO: 286)	TTTCAGGCTAGGAAGATCCTTT (SEQ ID NO: 287)	261
33.3926 29	DG13S1518	AAAGGATGCATTCGGTTAGAG (SEQ ID NO: 288)	ACTGTCCTGTGCCTGTGCTT (SEQ ID NO: 289)	375
33.4055 27	DG13S23	CCTGAATAGGTGGAATTAAGATC AA (SEQ ID NO: 290)	TCAAGGAGCATACACACACAC A (SEQ ID NO: 291)	107
33.4315 36	D13S620	GTCCACCTAATGGCTCATTC (SEQ ID NO: 292)	CAAGAAGCACTCATGTTTGTG (SEQ ID NO: 293)	185
33.4370 92	DG13S1866	AGCCTGTGATTGGCTGAGA (SEQ ID NO: 294)	GGCTTACAGCTGCCTCCTTT (SEQ ID NO: 295)	410
33.4957 18	DG13S1927	CCCACAGAGCACTTTGTTAGA (SEQ ID NO: 296)	GCCTCCCTTAAGCTGTTATGC (SEQ ID NO: 297)	401
33.5034 40	DG13S1503	CACTCTTACTGCCAATCACTCC (SEQ ID NO:298)	GCCGTGTGGGTGTATGAAT (SEQ ID NO: 299)	226
33.5681 00	DG13S332	TTGTACCAGGAACCAAAGACAA (SEQ ID NO: 300)	CACAGACAGAGGCACATTGA (SEQ ID NO: 301)	176
33.6758 41	DG13S333	GCTCTGGTCACTCCTGCTGT (SEQ ID NO: 302)	CATGCCTGGCTGATTGTTT (SEQ ID NO: 303)	446
33.7713 89	D13S220	CCAACATCGGGAAGT (SEQ ID NO: 304)	TGCATTCTTTAAGTCCATGTC (SEQ ID NO: 305)	191
33.8180 41	DG13S1919	CAGCAACTGACAATCATCCA (SEQ ID NO: 306)	CCTCAATCCTCAGCTCCAAC (SEQ ID NO.307)	255
33.8736 14	DG13S1439	TCCTTCACAGCTTCAAACCTCA (SEQ ID NO: 308)	AGTGAGAAGCTTCCATACTGGT (SEQ ID NO: 309)	239
33.9060 65	DG13S335	GCCAACCGTTAGACAAATGA (SEQ ID NO: 310)	CTACATGTGCACCACAACACC (SEQ ID NO: 311)	201
33.9286 53	DG13S340	AGTTTATTGCCGCCGAGAG (SEQ ID NO. 312)	ACCCACCACATTCACAAGC (SEQ ID NO: 313)	373
34.0194 55	DG13S1496	CGATTGCCATGTCTCTTTGA (SEQ ID NO: 314)	GAGATCTGGCCTGGATTTGT (SEQ ID NO: 315)	155
34.0340 89	DG13S342	TGAGGCCAGCCTTACCTCTAT (SEQ ID NO: 316)	CCAGACATGGTGGCTTGT (SEQ ID NO: 317)	366
34.0617 77	DG13S344	GAAGGAAGGAAGGAAGGAA (SEQ ID NOv 318)	AAGGATGAGAAGAGTCCATGC (SEQ ID NO: 319)	292
34.0672 39	DG13S345	AAATACCCTTTGAACAGACACAC (SEQ ID NO: 320)	TAGCTGAGCATGGTGGTACG (SEQ ID NO: 321)	201

34.0778 74	DG13S346	AAAGACAAGACAGCAATCCAAA (SEQ ID NO: 322)	GCAGAACCCAGGCTACAGAT (SEQ ID NO: 323)	152
34.0841 38	DG13S347	TCATTGTCAGCACAGAATGAACT (SEQ ID NO: 324)	GGAGGGAGGGGAAGAAAGAGA (SEQ ID NO: 325)	338
34.0843 26	D13S624	GCAACACAGTGAAAGCCCA(SEQ ID NO: 326)	ACAGGAGCATGCCACCATG(SE Q ID NO: 327)	191
34.1560 75	DG13S339	GGGAAGAGGAGATTGACTTGTT (SEQ ID NO: 328)	GGAACACCATCATTTCCAACC(S EQ ID NO: 329)	232
34.1924 78	DG13S1926	TACAAGCTCCACCGTCCTTC(SEQ ID NO: 330)	TGAGTTGCTGCCTCTTCAAA(S EQ ID NO: 331)	261
34.2202 27	DG13S1469	TGCTAATGGGCCAAGGAATA(SE Q ID NO: 332)	GCTAAATGTCTCATGAATAGC C(SEQ ID NO: 333)	382
34.3014 48	DG13S351	TGTCCTGCAGACAGATGGTC(SE Q ID NO: 334)	CCTCCGGAGTAGCTGGATTA(S EQ ID NO: 335)	294
34.3878 83	DG13S26	GAGACTGGCCCTCATTCTTG(SE Q ID NO: 336)	AAGAAGCCAGAGACAAAGAAA TACA(SEQ ID NO: 337)	330
34.5354 41	DG13S30	CATCTATCTTTGGATTCAGTGGT G(SEQ ID NO: 338)	TGCTCCCAACATCTTACCAG(S EQ ID NO: 339)	388
34.5655 94	DG13S1435	TGTCCTCTGGTCATTTCTATGGT (SEQ ID NO: 340)	CATGAATGAGAAGTGATGAATG G(SEQ ID NO: 341)	235
34.6598 58	DG13S1446	AACACGGGAAATTCCAACAG(SE Q ID NO: 342)	TGAAGAAGTAAATTGCCAGTA A(SEQ ID NO: 343)	379
34.7122 60	DG13S356	CAGACACTGTAAACTGGCTTCG (SEQ ID NO: 344)	GCCACATTGCTATCAGCGTA(S EQ ID NO: 345)	212
34.7387 56	DG13S357	TGTCATAGGCTTGCGGTATTT(SE Q ID NO: 346)	TTGGTAGGGTCCTTTCCTTT(SE Q ID NO: 347)	202
34.7705 71	DG13S1032	GCCTGCTCACTGTTGTTTGA(SEQ ID NO: 348)	CGGTTATCAGAGACTGGTGGT (SEQ ID NO: 349)	211
34.7996 79	DG13S1557	GGCTTATTTTCATGTACGGCTA(SE Q ID NO: 350)	GGTTAACTCTACTTAGTCCTG ATGC(SEQ ID NO: 351)	158
34.8829 34	DG13S1925	GAAGCTCTGCAGGCACCTCTT(SE Q ID NO: 352)	CCTGAAGCGCTTGTAAGTAA(S EQ ID NO: 353)	456
34.9326 90	DG13S1484	TGTTGCGTACTCAGCCATA (SEQ ID NO: 354)	GACAGGTGTCAAACGGGTCT(S EQ ID NO: 355)	246
34.9425 47	DG13S360	TTGGCTTCTCGCTCTTTCTT(SEQ ID NO: 356)	AGCCATCAGTCACATGCAAA (SEQ ID NO: 357)	350
34.9989 79	DG13S1522	AGATCTCCAGGGCAGAGGAC(SE Q ID NO: 358)	CCTTCCTCCCTCCTTCTCTC(SE Q ID NO: 359)	355
35.0749 62	DG13S1517	CGTCATTGATCCCAATCATCT(SE Q ID NO: 360)	GGCTGATAGCCTCCCTTGTA (SEQ ID NO: 361)	235
35.0749 62	DG13S1521	GAGAGAGAGCAGCTTGCATGT(S EQ ID NO: 362)	GGCTGATAGCCTCCCTTGTA(S EQ ID NO: 363)	172
35.1268 82	DG13S364	ACCTTTCAAGCTTCCGGTTT(SEQ ID NO: 364)	TTCCATCCGTCCATCTATCC(SE Q ID NO: 365)	172
35.3286 63	DG13S1036	TTAAAGTCACTTGTCTGTGGTCA (SEQ ID NO: 366)	TTTGTAGGAATCAAGTCAAATA ATGTA(SEQ ID NO: 367)	216
35.3353 64	DG13S367	CAAACATCACACTGGGCAAA(SE Q ID NO: 368)	TGCTTTGGAATCTTTCTTGCT(S EQ ID NO: 369)	301
35.3719 57	DG13S1901	CTGCCAGGATGTCAGCATT(SEQ ID NO: 370)	TCCACACTTTCTCATCACCTAA A(SEQ ID NO: 371)	440
35.4202 95	DG13S1037	CTTTCGGAAGCTTGAGCCTA(SE Q ID NO: 372)	CCCAAGACCACTGCCATATT(S EQ ID NO: 373)	269
35.4258 41	DG13S1854	TGACAGGTTTGGGTATATTGGA(S EQ ID NO: 374)	TGCTTAATGTAGTGGCAGCA(S EQ ID NO: 375)	124

35.5060 53	DG13S1038	TCCTGCCTTTGTGAATTCCT(SEQ ID NO: 376)	GTTGAATGAGGTGGGCATTA(S EQ ID NO: 377)	334
35.5472 10	DG13S1039	CCATTTAATCCTCCAGCCATT(SE Q ID NO: 378)	GCTCCACCTTGTTACCCTGA(S EQ ID NO: 379)	167
35.6092 52	DG13S1840	ACAACCCTGGAATCTGGACT(SE Q ID NO: 380)	GAAGGAAAGGAAAGGAAAGAA A(SEQ ID NO: 381)	217
35.6192 86	DG13S369	TGACAAGACTGAACTTCATCAG(SEQ ID NO: 382)	GATGCTTGCTTTGGGAGGTA(S EQ ID NO: 383)	257
35.6279 11	D13S305	TTGAGGACCTGTCGTTACG (SEQ ID NO: 384)	TTATAGAGCAGTTAAGGCACA (SEQ ID NO: 385)	394
35.6566 59	DG13S375	TGAGGGTGGTAAGCCCTTATT(SE Q ID NO: 386)	GGAGTTGTGGCCTCTCTCTCT(SEQ ID NO: 387)	192
35.7603 68	D13S219	AAGCAAATATGCAAAATTGC(SEQ ID NO: 388)	TCCTTCTGTTTCTTGACTTAAC A (SEQ ID NO: 389)	125
35.8258 52	DG13S378	TGCTAAGAGGGCAGATCTCA(SE Q ID NO: 390)	GGCTCATAGCCAATTTCTCC (SEQ ID NO: 391)	324
35.8321 27	DG13S32	CGGCATTCTCAATAACCTCAA (SEQ ID NO: 392)	TCTTTGATGAGGATCAATTAGT GG (SEQ ID NO: 393)	214
35.8729 36	DG13S1549	ACGCACACACACACACACAC (SEQ ID NO: 394)	TGCCTCTGTAATCCTGTGTAGC (SEQ ID NO: 395)	260
35.9123 21	DG13S1473	GCTCTAAGGTGGGTCCCAATA (SEQ ID NO: 396)	GGAATGACAAGATCAGTTTAC C (SEQ ID NO: 397)	163

All references cited herein are incorporated by reference in their entirety. While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that various changes in form and details may be made therein without departing from the scope of the invention encompassed by the appended claims.

CLAIMS

- 5 1. A method of treatment for myocardial infarction, stroke or PAOD or susceptibility to myocardial infarction, stroke or PAOD in an individual, comprising administering a leukotriene synthesis inhibitor to the individual in need thereof, in a therapeutically effective amount.
- 10 2. The method of Claim 1, wherein the individual has at least one risk factor selected from the group consisting of: an at-risk haplotype for myocardial infarction, stroke or PAOD; an at-risk haplotype in the FLAP gene; a polymorphism in a FLAP nucleic acid; and an at-risk polymorphism in the 5-LO gene promoter.
- 15 3. The method of Claim 1, wherein the individual has at least one risk factor selected from the group consisting of: diabetes; hypertension; hypercholesterolemia; elevated triglycerides; elevated lp(a); obesity; ankle/brachial index (ABI) less than 0.9; and past or current smoker.
- 20 4. The method of Claim 1, wherein the individual has at least one risk factor selected from the group consisting of: a transient ischemic attack; transient monocular blindness; carotid endarterectomy; and asymptomatic carotid stenosis.
- 25 5. The method of Claim 1, wherein the individual has at least one risk factor selected from the group consisting of: claudication, limb ischemia leading to gangrene, ulceration or amputation; and a revascularization procedure.
- 30

6. The method of Claim 1, wherein the individual has an elevated inflammatory marker.
- 5 7. The method of Claim 6, wherein the inflammatory marker is selected from the group consisting of: C-reactive protein (CRP), serum amyloid A, fibrinogen, a leukotriene, a leukotriene metabolite, interleukin-6, tissue necrosis factor-alpha, a soluble vascular cell adhesion molecule (sVCAM), a soluble intervascular adhesion molecule (sICAM), E-selectin, matrix metalloprotease type-1, matrix
10 metalloprotease type-2, matrix metalloprotease type-3, matrix metalloprotease type-9, myeloperoxidase (MPO) and N-tyrosine.
8. The method of Claim 1, wherein the individual has increased LDL cholesterol and/or decreased HDL cholesterol.
- 15 9. The method of Claim 1, wherein the individual has increased leukotriene synthesis.
- 20 10. The method of Claim 1, wherein the individual has had at least one previous myocardial infarction or ACS event, or has stable angina.
- 25 11. The method of Claim 1, wherein the individual has had at least one previous transient ischemic attack, transient monocular blindness, or stroke.
12. The method of Claim 1, wherein the individual has asymptomatic carotid stenosis or has had a carotid endarterectomy.
- 30 13. The method of Claim 1, wherein the individual has had a revascularization procedure.

14. The method of Claim 1, wherein the individual has atherosclerosis or who requires treatment (*e.g.*, angioplasty, stents, revascularization procedure) to restore blood flow in arteries.
- 5 15. The method of Claim 1, wherein the leukotriene synthesis inhibitor is selected from the group consisting of: 1-((4-chlorophenyl)methyl)-3-((1,1-dimethylethyl)thio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)-1H-Indole-2-propanoic acid otherwise known as MK-0591, (R)-(+)-alpha-cyclopentyl-4-(2-quinolinylmethoxy)-
10 Benzeneacetic acid otherwise known as BAY-x-1005, 3-(3-(1,1-dimethylethylthio-5-(quinoline-2-ylmethoxy)-1-(4-chloromethylphenyl)indole-2-yl)-2,2-dimethylpropionaldehyde oxime-0-2-acetic acid otherwise known as A-81834, optically pure enantiomers, salts, chemical derivatives, and analogues.
- 15 16. The method of Claim 1, wherein the leukotriene synthesis inhibitor is selected from the group consisting of: zileuton, atreleuton, 6-((3-fluoro-5-(tetrahydro-4-methoxy-2H-pyran-4yl)phenoxy)methyl)-1-methyl-2(1H)-quinolinone otherwise known as ZD-2138, 1-((4-
20 chlorophenyl)methyl)-3-((1,1 dimethylethyl)thio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)-1H-Indole-2-propanoic acid otherwise known as MK-886, 4-(3-(4-(2-Methyl-imidazol-1-yl)-phenylsulfanyl)-phenyl)-tetrahydro-pyran-4-carboxylic acid amide otherwise known as CJ-13610, their optically pure enantiomers, salts,
25 chemical derivatives, and analogues.
17. The method of Claim 1, wherein the leukotriene synthesis inhibitor is a FLAP inhibitor or antagonist.
- 30 18. The method of Claim 1, wherein the leukotriene synthesis inhibitor is a 5-LO inhibitor or antagonist.

19. The method of Claim 1, wherein the leukotriene synthesis inhibitor is a leukotriene inhibitor or antagonist, or an antibody to a leukotriene.
- 5 20. The method of Claim 1, wherein the leukotriene synthesis inhibitor is a leukotriene receptor inhibitor or antagonist.
21. The method of Claim 20, wherein the leukotriene receptor inhibitor or antagonist is an agent that inhibits or antagonizes a receptor selected
10 from the group consisting of: BLT1, BLT2, CysLTR1, and CysLTR2.
22. The method of Claim 1, wherein the leukotriene synthesis inhibitor is an inhibitor of a member of the leukotriene biosynthesis pathway.
- 15 23. The method of Claim 22, wherein the member of the leukotriene biosynthesis pathway is selected from the group consisting of: FLAP, 5-LO, LTC4S, LTA4H, and LTB4DH.
24. A method of treatment for acute coronary syndrome in an individual,
20 comprising administering leukotriene synthesis inhibitor to the individual, in a therapeutically effective amount.
25. The method of Claim 24, wherein the acute coronary syndrome is selected from the group consisting of: unstable angina, non-ST-
25 elevation myocardial infarction (NSTEMI) and ST-elevation myocardial infarction (STEMI).
26. The method of Claim 24, wherein the individual has at least one risk factor selected from the group consisting of: an at-risk haplotype for
30 myocardial infarction; an at-risk haplotype in the FLAP gene; a

polymorphism in a FLAP nucleic acid; and an at-risk polymorphism in the 5-LO gene promoter.

- 5 27. The method of Claim 24, wherein the individual has at least one risk factor selected from the group consisting of: diabetes; hypertension; hypercholesterolemia; elevated triglycerides; elevated lp(a); obesity; ankle/brachial index (ABI) less than 0.9; and past or current smoker.
- 10 28. The method of Claim 24, wherein the individual has an elevated inflammatory marker.
- 15 29. The method of Claim 28, wherein the inflammatory marker is selected from the group consisting of: C-reactive protein (CRP), serum amyloid A, fibrinogen, a leukotriene, a leukotriene metabolite, interleukin-6, tissue necrosis factor-alpha, a soluble vascular cell adhesion molecule (sVCAM), a soluble intervascular adhesion molecule (sICAM), E-selectin, matrix metalloprotease type-1, matrix metalloprotease type-2, matrix metalloprotease type-3, matrix metalloprotease type-9, myeloperoxidase (MPO) and N-tyrosine.
- 20 30. The method of Claim 24, wherein the individual has increased LDL cholesterol and/or decreased HDL cholesterol.
- 25 31. The method of Claim 24, wherein the individual has increased leukotriene synthesis.
32. The method of Claim 24, wherein the individual has had at least one previous myocardial infarction or ACS event, or has stable angina.

33. The method of Claim 24, wherein the individual has atherosclerosis or who requires treatment (e.g., angioplasty, stents, revascularization procedure) to restore blood flow in arteries.
- 5 34. The method of Claim 24, wherein the leukotriene synthesis inhibitor is selected from the group consisting of: 1-((4-chlorophenyl)methyl)-3-((1,1-dimethylethyl)thio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)-1H-Indole-2-propanoic acid otherwise known as MK-0591, (R)-(+)-alpha-cyclopentyl-4-(2-quinolinylmethoxy)-
10 Benzeneacetic acid otherwise known as BAY-x-1005, 3-(3-(1,1-dimethylethylthio-5-(quinoline-2-ylmethoxy)-1-(4-chloromethylphenyl)indole-2-yl)-2,2-dimethylpropionaldehyde oxime-0-2-acetic acid otherwise known as A-81834, optically pure enantiomers, salts, chemical derivatives, and analogues.
- 15 35. The method of Claim 24, wherein the leukotriene synthesis inhibitor is selected from the group consisting of: zileuton, atreleuton, 6-((3-fluoro-5-(tetrahydro-4-methoxy-2H-pyran-4yl)phenoxy)methyl)-1-methyl-2(1H)-quinolinone otherwise known as ZD-2138, 1-((4-
20 chlorophenyl)methyl)-3-((1,1 dimethylethyl)thio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)-1H-Indole-2-propanoic acid otherwise known as MK-886, 4-(3-(4-(2-Methyl-imidazol-1-yl)-phenylsulfanyl)-phenyl)-tetrahydro-pyran-4-carboxylic acid amide otherwise known as CJ-13610, their optically pure enantiomers, salts,
25 chemical derivatives, and analogues.
36. The method of Claim 24, wherein the leukotriene synthesis inhibitor is a FLAP inhibitor or antagonist.
- 30 37. The method of Claim 24, wherein the leukotriene synthesis inhibitor is a 5-LO inhibitor or antagonist.

38. The method of Claim 24, wherein the leukotriene synthesis inhibitor is a leukotriene inhibitor or antagonist, or an antibody to a leukotriene.
- 5 39. The method of Claim 24, wherein the leukotriene synthesis inhibitor is a leukotriene receptor inhibitor or antagonist.
40. The method of Claim 39, wherein the leukotriene receptor inhibitor or antagonist is an agent that inhibits or antagonizes a receptor selected from the group consisting of: BLT1, BLT2, CysLTR1, and CysLTR2.
- 10 41. The method of Claim 24, wherein the leukotriene synthesis inhibitor is an inhibitor of a member of the leukotriene biosynthesis pathway.
- 15 42. The method of Claim 41, wherein the member of the leukotriene biosynthesis pathway is selected from the group consisting of: FLAP, 5-LO, LTC4S, LTA4H, and LTB4DH.
- 20 43. A method of treatment for transient ischemic attack, transient monocular blindness or stroke in an individual, comprising administering leukotriene synthesis inhibitor to the individual, in a therapeutically effective amount.
- 25 44. The method of Claim 43, wherein the individual has at least one risk factor selected from the group consisting of: an at-risk haplotype for stroke; an at-risk haplotype in the FLAP gene; a polymorphism in a FLAP nucleic acid; and an at-risk polymorphism in the 5-LO gene promoter.
- 30 45. The method of Claim 43, wherein the individual has at least one risk factor selected from the group consisting of: diabetes; hypertension;

hypercholesterolemia; elevated triglycerides; elevated lp(a); obesity; ankle/brachial index (ABI) less than 0.9; and past or current smoker.

- 5 46. The method of Claim 43, wherein the individual has an elevated inflammatory marker.
- 10 47. The method of Claim 46, wherein the inflammatory marker is selected from the group consisting of: C-reactive protein (CRP), serum amyloid A, fibrinogen, a leukotriene, a leukotriene metabolite, interleukin-6, tissue necrosis factor-alpha, a soluble vascular cell adhesion molecule (sVCAM), a soluble intervascular adhesion molecule (sICAM), E-selectin, matrix metalloprotease type-1, matrix metalloprotease type-2, matrix metalloprotease type-3, matrix metalloprotease type-9, myeloperoxidase (MPO) and N-tyrosine.
- 15 48. The method of Claim 43, wherein the individual has increased LDL cholesterol and/or decreased HDL cholesterol.
- 20 49. The method of Claim 43, wherein the individual has increased leukotriene synthesis.
- 25 50. The method of Claim 43, wherein the individual has had at least one previous transient ischemic attack, transient monocular blindness or stroke.
51. The method of Claim 43, wherein the individual has asymptomatic carotid stenosis or has had a carotid endarterectomy.
- 30 52. The method of Claim 43, wherein the leukotriene synthesis inhibitor is selected from the group consisting of: 1-((4-chlorophenyl)methyl)-3-((1,1-dimethylethyl)thio)-alpha,alpha-dimethyl-5-(2-

- quinolinylmethoxy)- 1H-Indole-2-propanoic acid otherwise known as MK-0591, (R)-(+)-alpha-cyclopentyl-4-(2-quinolinylmethoxy)-Benzeneacetic acid otherwise known as BAY-x-1005, 3-(3-(1,1-dimethylethylthio-5-(quinoline-2-ylmethoxy)-1-(4-chloromethylphenyl)indole-2-yl)-2,2-dimethylpropionaldehyde oxime-0-2-acetic acid otherwise known as A-81834, optically pure enantiomers, salts, chemical derivatives, and analogues.
53. The method of Claim 43, wherein the leukotriene synthesis inhibitor is selected from the group consisting of: zileuton, atreleuton, 6-((3-fluoro-5-(tetrahydro-4-methoxy-2H-pyran-4yl)phenoxy)methyl)-1-methyl-2(1H)-quinolinone otherwise known as ZD-2138, 1-((4-chlorophenyl)methyl)-3-((1,1 dimethylethyl)thio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)-1H-Indole-2-propanoic acid otherwise known as MK-886, 4-(3-(4-(2-Methyl-imidazol-1-yl)-phenylsulfanyl)-phenyl)-tetrahydro-pyran-4-carboxylic acid amide otherwise known as CJ-13610, their optically pure enantiomers, salts, chemical derivatives, and analogues.
54. The method of Claim 43, wherein the leukotriene synthesis inhibitor is a FLAP inhibitor or antagonist.
55. The method of Claim 43, wherein the leukotriene synthesis inhibitor is a 5-LO inhibitor or antagonist.
56. The method of Claim 43, wherein the leukotriene synthesis inhibitor is a leukotriene inhibitor or antagonist, or an antibody to a leukotriene.
57. The method of Claim 43, wherein the leukotriene synthesis inhibitor is a leukotriene receptor inhibitor or antagonist.

58. The method of Claim 58, wherein the leukotriene receptor inhibitor or antagonist is an agent that inhibits or antagonizes a receptor selected from the group consisting of: BLT1, BLT2, CysLTR1, and CysLTR2.
- 5 59. The method of Claim 43, wherein the leukotriene synthesis inhibitor is an inhibitor of a member of the leukotriene biosynthesis pathway.
60. The method of Claim 59, wherein the member of the leukotriene biosynthesis pathway is selected from the group consisting of: FLAP,
10 5-LO, LTC4S, LTA4H, and LTB4DH.
61. A method of treatment of PAOD or claudication, comprising administering leukotriene synthesis inhibitor to the individual, in a therapeutically effective amount.
- 15 62. The method of Claim 61, wherein the individual has at least one risk factor selected from the group consisting of: an at-risk haplotype for PAOD; an at-risk haplotype in the FLAP gene; a polymorphism in a FLAP nucleic acid; and an at-risk polymorphism in the 5-LO gene promoter.
- 20 63. The method of Claim 61, wherein the individual has at least one risk factor selected from the group consisting of: diabetes; hypertension; hypercholesterolemia; elevated triglycerides; elevated lp(a); obesity; ankle/brachial index (ABI) less than 0.9; and past or current smoker.
- 25 64. The method of Claim 61, wherein the individual has an elevated inflammatory marker.
- 30 65. The method of Claim 64, wherein the inflammatory marker is selected from the group consisting of: C-reactive protein (CRP), serum

- amyloid A, fibrinogen, a leukotriene, a leukotriene metabolite, interleukin-6, tissue necrosis factor-alpha, a soluble vascular cell adhesion molecule (sVCAM), a soluble intervascular adhesion molecule (sICAM), E-selectin, matrix metalloprotease type-1, matrix metalloprotease type-2, matrix metalloprotease type-3, matrix metalloprotease type-9, myeloperoxidase (MPO) and N-tyrosine.
66. The method of Claim 61, wherein the individual has increased LDL cholesterol and/or decreased HDL cholesterol.
67. The method of Claim 61, wherein the individual has increased leukotriene synthesis.
68. The method of Claim 61, wherein the individual has been diagnosed previously with a condition selected from the group consisting of: PAOD, claudication, and limb ischemia leading to gangrene, ulceration or amputation.
69. The method of Claim 61, wherein the individual has had a vascular or peripheral artery revascularization graft.
70. The method of Claim 61, wherein the leukotriene synthesis inhibitor is selected from the group consisting of: 1-((4-chlorophenyl)methyl)-3-((1,1-dimethylethyl)thio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)-1H-Indole-2-propanoic acid otherwise known as MK-0591, (R)-(+)-alpha-cyclopentyl-4-(2-quinolinylmethoxy)-Benzeneacetic acid otherwise known as BAY-x-1005, 3-(3-(1,1-dimethylethylthio)-5-(quinoline-2-ylmethoxy)-1-(4-chloromethylphenyl)indole-2-yl)-2,2-dimethylpropionaldehyde oxime-0-2-acetic acid otherwise known as A-81834, optically pure enantiomers, salts, chemical derivatives, and analogues.

71. The method of Claim 61, wherein the leukotriene synthesis inhibitor is selected from the group consisting of: zileuton, atreleuton, 6-((3-fluoro-5-(tetrahydro-4-methoxy-2H-pyran-4yl)phenoxy)methyl)-1-methyl-2(1H)-quinolinone otherwise known as ZD-2138, 1-((4-chlorophenyl)methyl)-3-((1,1dimethylethyl)thio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)-1H-Indole-2-propanoic acid otherwise known as MK-886, 4-(3-(4-(2-Methyl-imidazol-1-yl)-phenylsulfanyl)-phenyl)-tetrahydro-pyran-4-carboxylic acid amide otherwise known as CJ-13610, their optically pure enantiomers, salts, chemical derivatives, and analogues.
72. The method of Claim 61, wherein the leukotriene synthesis inhibitor is a FLAP inhibitor or antagonist.
73. The method of Claim 61, wherein the leukotriene synthesis inhibitor is a 5-LO inhibitor or antagonist.
74. The method of Claim 61, wherein the leukotriene synthesis inhibitor is a leukotriene inhibitor or antagonist, or an antibody to a leukotriene.
75. The method of Claim 61, wherein the leukotriene synthesis inhibitor is a leukotriene receptor inhibitor or antagonist.
76. The method of Claim 75, wherein the leukotriene receptor inhibitor or antagonist is an agent that inhibits or antagonizes a receptor selected from the group consisting of: BLT1, BLT2, CysLTR1, and CysLTR2.
77. The method of Claim 61, wherein the leukotriene synthesis inhibitor is an inhibitor of a member of the leukotriene biosynthesis pathway.

78. The method of Claim 77, wherein the member of the leukotriene biosynthesis pathway is selected from the group consisting of: FLAP, 5-LO, LTC4S, LTA4H, and LTB4DH.
- 5 79. A method of decreasing risk of a subsequent myocardial infarction or stroke in an individual who has had at least one myocardial infarction or stroke, comprising administering a leukotriene synthesis inhibitor to the individual, in a therapeutically effective amount.
- 10 80. The method of Claim 79, wherein the individual has at least one risk factor selected from the group consisting of: an at-risk haplotype for myocardial infarction or stroke; an at-risk haplotype in the FLAP gene; a polymorphism in a FLAP nucleic acid; and an at-risk polymorphism in the 5-LO gene promoter.
- 15 81. The method of Claim 79, wherein the individual has at least one risk factor selected from the group consisting of: diabetes; hypertension; hypercholesterolemia; elevated triglycerides; elevated lp(a); obesity; ankle/brachial index (ABI) less than 0.9; and past or current smoker.
- 20 82. The method of Claim 79, wherein the individual has at least one risk factor selected from the group consisting of: a transient ischemic attack; transient monocular blindness; carotid endarterectomy; and asymptomatic carotid stenosis.
- 25 83. The method of Claim 79, wherein the individual has an elevated inflammatory marker.
- 30 84. The method of Claim 83, wherein the inflammatory marker is selected from the group consisting of: C-reactive protein (CRP), serum amyloid A, fibrinogen, a leukotriene, a leukotriene metabolite,

- interleukin-6, tissue necrosis factor-alpha, a soluble vascular cell adhesion molecule (sVCAM), a soluble intervascular adhesion molecule (sICAM), E-selectin, matrix metalloprotease type-1, matrix metalloprotease type-2, matrix metalloprotease type-3, matrix metalloprotease type-9, myeloperoxidase (MPO) and N-tyrosine.
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85. The method of Claim 79, wherein the individual has increased LDL cholesterol and/or decreased HDL cholesterol.
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86. The method of Claim 79, wherein the individual has increased leukotriene synthesis.
87. The method of Claim 79, wherein the individual has had at least one previous myocardial infarction or ACS event, or has stable angina.
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88. The method of Claim 79, wherein the individual has had at least one previous transient ischemic attack, transient monocular blindness or stroke.
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89. The method of Claim 79, wherein the individual has asymptomatic carotid stenosis or has had a carotid endarterectomy.
90. The method of Claim 79, wherein the individual has atherosclerosis or who requires treatment (e.g., angioplasty, stents, revascularization procedure) to restore blood flow in arteries.
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91. The method of Claim 79, wherein the leukotriene synthesis inhibitor is selected from the group consisting of: 1-((4-chlorophenyl)methyl)-3-((1,1-dimethylethyl)thio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)-1H-Indole-2-propanoic acid otherwise known as MK-0591, (R)-(+)-alpha-cyclopentyl-4-(2-quinolinylmethoxy)-
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- 5 Benzeneacetic acid otherwise known as BAY-x-1005, 3-(3-(1,1-dimethylethylthio-5-(quinoline-2-ylmethoxy)-1-(4-chloromethylphenyl)indole-2-yl)-2,2-dimethylpropionaldehyde oxime-0-2-acetic acid otherwise known as A-81834, optically pure enantiomers, salts, chemical derivatives, and analogues.
92. The method of Claim 79, wherein the leukotriene synthesis inhibitor is selected from the group consisting of: zileuton, atreleuton, 6-((3-fluoro-5-(tetrahydro-4-methoxy-2H-pyran-4yl)phenoxy)methyl)-1-methyl-2(1H)-quinolinone otherwise known as ZD-2138, 1-((4-chlorophenyl)methyl)-3-((1,1dimethylethyl)thio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)-1H-Indole-2-propanoic acid otherwise known as MK-886, 4-(3-(4-(2-Methyl-imidazol-1-yl)-phenylsulfanyl)-phenyl)-tetrahydro-pyran-4-carboxylic acid amide otherwise known as CJ-13610, their optically pure enantiomers, salts, chemical derivatives, and analogues.
93. The method of Claim 79, wherein the leukotriene synthesis inhibitor is a FLAP inhibitor or antagonist.
94. The method of Claim 79, wherein the leukotriene synthesis inhibitor is a 5-LO inhibitor or antagonist.
95. The method of Claim 79, wherein the leukotriene synthesis inhibitor is a leukotriene inhibitor or antagonist, or an antibody to a leukotriene.
96. The method of Claim 79, wherein the leukotriene synthesis inhibitor is a leukotriene receptor inhibitor or antagonist.

97. The method of Claim 96, wherein the leukotriene receptor inhibitor or antagonist is an agent that inhibits or antagonizes a receptor selected from the group consisting of: BLT1, BLT2, CysLTR1, and CysLTR2.
- 5 98. The method of Claim 79, wherein the leukotriene synthesis inhibitor is an inhibitor of a member of the leukotriene biosynthesis pathway.
99. The method of Claim 98, wherein the member of the leukotriene biosynthesis pathway is selected from the group consisting of: FLAP,
10 5-LO, LTC4S, LTA4H, and LTB4DH.
100. A method of treatment for atherosclerosis or PAOD in an individual, comprising administering a leukotriene synthesis inhibitor to the individual, in a therapeutically effective amount.
- 15 101. The method of Claim 100, wherein the individual is concurrently treated to restore blood flow in coronary, carotid or peripheral arteries.
102. The method of Claim 100, wherein the individual has at least one risk factor selected from the group consisting of: an at-risk haplotype for PAOD; an at-risk haplotype in the FLAP gene; a polymorphism in a
20 FLAP nucleic acid; and an at-risk polymorphism in the 5-LO gene promoter.
- 25 103. The method of Claim 100, wherein the individual has at least one risk factor selected from the group consisting of: diabetes; hypertension; hypercholesterolemia; elevated triglycerides; elevated lp(a); obesity; ankle/brachial index (ABI) less than 0.9; and past or current smoker.
- 30 104. The method of Claim 100, wherein the individual has at least one risk factor selected from the group consisting of: claudication, limb

ischemia leading to gangrene, ulceration or amputation; and a vascular or peripheral artery revascularization graft.

- 5 105. The method of Claim 100, wherein the individual has an elevated inflammatory marker.
- 10 106. The method of Claim 105, wherein the inflammatory marker is selected from the group consisting of: C-reactive protein (CRP), serum amyloid A, fibrinogen, a leukotriene, a leukotriene metabolite, interleukin-6, tissue necrosis factor-alpha, a soluble vascular cell adhesion molecule (sVCAM), a soluble intervascular adhesion molecule (sICAM), E-selectin, matrix metalloprotease type-1, matrix metalloprotease type-2, matrix metalloprotease type-3, matrix metalloprotease type-9, myeloperoxidase (MPO) and N-tyrosine.
- 15 107. The method of Claim 100, wherein the individual has increased LDL cholesterol and/or decreased HDL cholesterol.
- 20 108. The method of Claim 100, wherein the individual has increased leukotriene synthesis.
- 25 109. The method of Claim 100, wherein the individual has been diagnosed previously with a condition selected from the group consisting of: claudication, and limb ischemia leading to gangrene, ulceration or amputation.
110. The method of Claim 100, wherein the individual has had a vascular or peripheral artery revascularization graft.

111. The method of Claim 100, wherein the individual has atherosclerosis or who requires treatment (*e.g.*, angioplasty, stents, revascularization procedure) to restore blood flow in arteries.
- 5 112. The method of Claim 100, wherein the leukotriene synthesis inhibitor is selected from the group consisting of: 1-((4-chlorophenyl)methyl)-3-((1,1-dimethylethyl)thio)- α,α -dimethyl-5-(2-quinolinylmethoxy)-1H-Indole-2-propanoic acid otherwise known as MK-0591, (R)-(+)- α -cyclopentyl-4-(2-quinolinylmethoxy)-Benzeneacetic acid otherwise known as BAY-x-1005, 3-(3-(1,1-dimethylethylthio-5-(quinoline-2-ylmethoxy)-1-(4-chloromethylphenyl)indole-2-yl)-2,2-dimethylpropionaldehyde oxime-10 0-2-acetic acid otherwise known as A-81834, optically pure enantiomers, salts, chemical derivatives, and analogues.
- 15 113. The method of Claim 100, wherein the leukotriene synthesis inhibitor is selected from the group consisting of: zileuton, atreleuton, 6-((3-fluoro-5-(tetrahydro-4-methoxy-2H-pyran-4yl)phenoxy)methyl)-1-methyl-2(1H)-quinolinone otherwise known as ZD-2138, 1-((4-chlorophenyl)methyl)-3-((1,1-dimethylethyl)thio)- α,α -dimethyl-5-(2-quinolinylmethoxy)-1H-Indole-2-propanoic acid otherwise known as MK-886, 4-(3-(4-(2-Methyl-imidazol-1-yl)-phenylsulfanyl)-phenyl)-tetrahydro-pyran-4-carboxylic acid amide otherwise known as CJ-13610, their optically pure enantiomers, salts, 20 chemical derivatives, and analogues.
- 25 114. The method of Claim 100, wherein the leukotriene synthesis inhibitor is a FLAP inhibitor or antagonist.
- 30 115. The method of Claim 100, wherein the leukotriene synthesis inhibitor is a 5-LO inhibitor or antagonist.

116. The method of Claim 100, wherein the leukotriene synthesis inhibitor is a leukotriene inhibitor or antagonist, or an antibody to a leukotriene.
- 5 117. The method of Claim 100, wherein the leukotriene synthesis inhibitor is a leukotriene receptor inhibitor or antagonist.
118. The method of Claim 117, wherein the leukotriene receptor inhibitor or antagonist is an agent that inhibits or antagonizes a receptor selected from the group consisting of: BLT1, BLT2, CysLTR1, and CysLTR2.
- 10 119. The method of Claim 100, wherein the leukotriene synthesis inhibitor is an inhibitor of a member of the leukotriene biosynthesis pathway.
- 15 120. The method of Claim 119, wherein the member of the leukotriene biosynthesis pathway is selected from the group consisting of: FLAP, 5-LO, LTC4S, LTA4H, and LTB4DH.
- 20 121. A method of reducing leukotriene synthesis in an individual, comprising administering a leukotriene synthesis inhibitor to the individual in a therapeutically effective amount.
122. The method of Claim 121, wherein the individual is concurrently treated to restore blood flow in coronary, carotid or peripheral arteries.
- 25 123. The method of Claim 121, wherein the individual has at least one risk factor selected from the group consisting of: an at-risk haplotype for myocardial infarction, stroke or PAOD; an at-risk haplotype in the FLAP gene; a polymorphism in a FLAP nucleic acid; and an at-risk polymorphism in the 5-LO gene promoter.
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124. The method of Claim 121, wherein the individual has at least one risk factor selected from the group consisting of: diabetes; hypertension; hypercholesterolemia; elevated triglycerides; elevated lp(a); obesity; ankle/brachial index (ABI) less than 0.9; and past or current smoker.
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125. The method of Claim 121, wherein the individual has at least one risk factor selected from the group consisting of: a transient ischemic attack; transient monocular blindness; carotid endarterectomy; and asymptomatic carotid stenosis.
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126. The method of Claim 121, wherein the individual has at least one risk factor selected from the group consisting of: claudication, limb ischemia leading to gangrene, ulceration or amputation; and a vascular or peripheral artery revascularization graft.
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127. The method of Claim 121, wherein the individual has an elevated inflammatory marker.
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128. The method of Claim 127, wherein the inflammatory marker is selected from the group consisting of: C-reactive protein (CRP), serum amyloid A, fibrinogen, a leukotriene, a leukotriene metabolite, interleukin-6, tissue necrosis factor-alpha, a soluble vascular cell adhesion molecule (sVCAM), a soluble intervascular adhesion molecule (sICAM), E-selectin, matrix metalloprotease type-1, matrix metalloprotease type-2, matrix metalloprotease type-3, matrix metalloprotease type-9, myeloperoxidase (MPO) and N-tyrosine.
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129. The method of Claim 121, wherein the individual has increased LDL cholesterol and/or decreased HDL cholesterol.
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130. The method of Claim 121, wherein the individual has increased leukotriene synthesis.
- 5 131. The method of Claim 121, wherein the individual has had at least one previous myocardial infarction or ACS event, or has stable angina.
132. The method of Claim 121, wherein the individual has had at least one previous transient ischemic attack, transient monocular blindness or stroke.
- 10 133. The method of Claim 121, wherein the individual has asymptomatic carotid stenosis or has had a carotid endarterectomy.
134. The method of Claim 121, wherein the individual has had a vascular or peripheral artery revascularization graft.
- 15 135. The method of Claim 121, wherein the individual has atherosclerosis or who requires treatment (*e.g.*, angioplasty, stents, revascularization procedure) to restore blood flow in arteries.
- 20 136. The method of Claim 121, wherein the leukotriene synthesis inhibitor is selected from the group consisting of: 1-((4-chlorophenyl)methyl)-3-((1,1-dimethylethyl)thio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)-1H-Indole-2-propanoic acid otherwise known as MK-0591, (R)-(+)-alpha-cyclopentyl-4-(2-quinolinylmethoxy)-Benzeneacetic acid otherwise known as BAY-x-1005, 3-(3-(1,1-dimethylethylthio-5-(quinoline-2-ylmethoxy)-1-(4-chloromethylphenyl)indole-2-yl)-2,2-dimethylpropionaldehyde oxime-0-2-acetic acid otherwise known as A-81834, optically pure enantiomers, salts, chemical derivatives, and analogues.
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137. The method of Claim 121, wherein the leukotriene synthesis inhibitor is selected from the group consisting of: zileuton, atreleuton, 6-((3-fluoro-5-(tetrahydro-4-methoxy-2H-pyran-4yl)phenoxy)methyl)-1-methyl-2(1H)-quinolinone otherwise known as ZD-2138, 1-((4-chlorophenyl)methyl)-3-((1,1dimethylethyl)thio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)-1H-Indole-2-propanoic acid otherwise known as MK-886, 4-(3-(4-(2-Methyl-imidazol-1-yl)-phenylsulfanyl)-phenyl)-tetrahydro-pyran-4-carboxylic acid amide otherwise known as CJ-13610, their optically pure enantiomers, salts, chemical derivatives, and analogues.
138. The method of Claim 121, wherein the leukotriene synthesis inhibitor is a FLAP inhibitor or antagonist.
139. The method of Claim 121, wherein the leukotriene synthesis inhibitor is a 5-LO inhibitor or antagonist.
140. The method of Claim 121, wherein the leukotriene synthesis inhibitor is a leukotriene inhibitor or antagonist, or an antibody to a leukotriene.
141. The method of Claim 121, wherein the leukotriene synthesis inhibitor is a leukotriene receptor inhibitor or antagonist.
142. The method of Claim 141, wherein the leukotriene receptor inhibitor or antagonist is an agent that inhibits or antagonizes a receptor selected from the group consisting of: BLT1, BLT2, CysLTR1, and CysLTR2.
143. The method of Claim 121, wherein the leukotriene synthesis inhibitor is an inhibitor of a member of the leukotriene biosynthesis pathway.

144. The method of Claim 143, wherein the member of the leukotriene biosynthesis pathway is selected from the group consisting of: FLAP, 5-LO, LTC4S, LTA4H, and LTB4DH.
- 5 145. The method of any one of Claims 1-144, wherein the leukotriene synthesis inhibitor is an agent set forth in the Agent Table.
- 10 146. The method of any one of Claims 1-144, wherein the leukotriene synthesis inhibitor is an agent selected from the group consisting of: a complement of a nucleic acid encoding a member of the leukotriene pathway; a binding agent of a member of the leukotriene pathway; an agent that alters expression of a nucleic acid encoding a member of the leukotriene pathway; an agent that alters posttranslational processing of a member of the leukotriene pathway; an agent that alters activity of a polypeptide member of the leukotriene pathway; an agent that alters activity of a leukotriene; an antibody to a leukotriene; and an agent that alters interaction among two or more members of the leukotriene pathway.
- 15 147. The method of any one of Claims 1-144, wherein the leukotriene synthesis inhibitor is an agent selected from the group consisting of: a FLAP nucleic acid binding agent; a 5-lipoxygenase binding agent; a leukotriene synthetase binding agent; a FLAP nucleic acid binding agent; a 5-lipoxygenase nucleic acid binding agent; a leukotriene synthetase nucleic acid binding agent; a peptidomimetic; a fusion protein; a prodrug; an antibody; an agent that alters FLAP nucleic acid expression; an agent that alters activity of a polypeptide encoded by a FLAP nucleic acid, a 5-lipoxygenase nucleic acid, or a leukotriene synthetase nucleic acid; an agent that alters posttranscriptional processing of a polypeptide encoded by a FLAP nucleic acid, a 5-lipoxygenase nucleic acid or a leukotriene synthetase nucleic acid; an
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agent that alters interaction of a FLAP nucleic acid with a FLAP nucleic acid binding agent; an agent that alters interaction of a 5-lipoxygenase nucleic acid with a 5-lipoxygenase nucleic acid binding agent; an agent that alters interaction of a leukotriene synthetase nucleic acid with a leukotriene synthetase nucleic acid binding agent; an agent that alters transcription of splicing variants encoded by a FLAP nucleic acid, a 5-lipoxygenase nucleic acid, or a leukotriene synthetase nucleic acid; and ribozymes.

- 10 148. A method of assessing an individual for an increased risk of MI, comprising assessing the level of a leukotriene metabolite in the individual, wherein an increased level of leukotriene metabolite is indicative of an increased risk of MI.
- 15 149. The method of Claim 148, wherein the leukotriene metabolite is selected from the group consisting of: LTE4, LTD4, and LTB4.
150. The method of Claim 148, wherein the level of the leukotriene metabolite is measured in blood, serum, plasma or urine.
- 20 151. A method of assessing an individual for an increased risk of ACS, comprising assessing the levels of leukotriene metabolites in the individual, wherein an increased level of leukotriene metabolites is indicative of an increased risk of ACS.
- 25 152. The method of Claim 151, wherein the leukotriene metabolite is selected from the group consisting of: LTE4, LTD4 and LTB4.
- 30 153. The method of Claim 151, wherein the level of the leukotriene metabolite is measured in blood, serum, plasma or urine.

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154. A method of assessing an individual for an increased risk of atherosclerosis, comprising assessing the levels of leukotriene metabolites in the individual, wherein an increased level of leukotriene metabolites is indicative of an increased risk of atherosclerosis.
155. The method of Claim 154, wherein the leukotriene metabolite is selected from the group consisting of: LTE4, LTD4 and LTB4.
- 10 156. The method of Claim 154, wherein the level of the leukotriene metabolite is measured in blood, serum, plasma or urine.
- 15 157. A method of assessing an individual for an increased risk of stroke, transient ischemic attack, transient monocular blindness or asymptomatic carotid stenosis, comprising assessing the level of a leukotriene metabolite in the individual, wherein an increased level of leukotriene metabolites is indicative of an increased risk of stroke, transient ischemic attack, transient monocular blindness or asymptomatic carotid stenosis.
- 20 158. The method of Claim 157, wherein the leukotriene metabolite is selected from the group consisting of: LTE4, LTD4 and LTB4.
159. The method of Claim 157, wherein the level of the leukotriene metabolite is measured in blood, serum, plasma or urine.
- 25 160. A method of assessing an individual for an increased risk of PAOD, claudication, or limb ischemia, comprising assessing the level of a leukotriene metabolite in the individual, wherein an increased level of leukotriene metabolites is indicative of an increased risk of PAOD, claudication, or limb ischemia.
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161. The method of Claim 160, wherein the leukotriene metabolite is selected from the group consisting of: LTE₄, LTD₄ and LTB₄.
- 5 162. The method of Claim 160, wherein the level of the leukotriene metabolite is measured in blood, serum, plasma or urine.
163. A method of assessing an individual for an increased risk of MI, comprising:
- 10 i. stimulating production of a leukotriene or a leukotriene metabolite in a test sample from the individual, using a calcium ionophore;
- ii. comparing the level of production of the leukotriene or leukotriene metabolite with a control level,
- 15 wherein a level of production of the leukotriene or leukotriene metabolite that is significantly greater than the control level, is indicative of an increased risk of MI.
164. The method of Claim 163, wherein a level of a leukotriene metabolite is compared, and the leukotriene metabolite is selected from the group consisting of: LTE₄, LTD₄, and LTB₄.
- 20 165. The method of Claim 163, wherein the test sample comprises neutrophils.
- 25 166. A method of assessing an individual for an increased risk of ACS, comprising:
- i. stimulating production of a leukotriene or a leukotriene metabolite in a test sample from the individual, using a calcium ionophore;
- 30 ii. comparing the level of production of the leukotriene or leukotriene metabolite with a control level,

wherein a level of production of the leukotriene or leukotriene metabolite that is significantly greater than the control level, is indicative of an increased risk of ACS.

- 5 167. The method of Claim 166, wherein a level of a leukotriene metabolite is compared, and the leukotriene metabolite is selected from the group consisting of: LTE4, LTD4 and LTB4.
- 10 168. The method of Claim 166, wherein test sample comprises neutrophils.
- 15 169. A method of assessing an individual for an increased risk of atherosclerosis, comprising:
- i. stimulating production of a leukotriene or a leukotriene metabolite in a test sample from the individual, using a calcium ionophore;
 - ii. comparing the level of production of the leukotriene or leukotriene metabolite with a control level,
- 20 wherein a level of production of the leukotriene or leukotriene metabolite that is significantly greater than the control level, is indicative of an increased risk of atherosclerosis.
- 25 170. The method of Claim 169, wherein a level of a leukotriene metabolite is compared, and the leukotriene metabolite is selected from the group consisting of: LTE4, LTD4 and LTB4.
- 30 171. The method of Claim 169, wherein the test sample comprises neutrophils.
172. A method of assessing an individual for an increased risk of stroke, transient ischemic attack, transient monocular blindness or asymptomatic carotid stenosis, comprising:

- i. stimulating production of a leukotriene or a leukotriene metabolite in a test sample from the individual, using a calcium ionophore;
- ii. comparing the level of production of the leukotriene or a leukotriene metabolite with a control level,
- wherein a level of production of the leukotriene or leukotriene metabolite that is significantly greater than the control level, is indicative of an increased risk of stroke, transient ischemic attack, transient monocular blindness or asymptomatic carotid stenosis.
173. The method of Claim 172, wherein a level of a leukotriene metabolite is compared, and the leukotriene metabolite is selected from the group consisting of: LTE₄, LTD₄ and LTB₄.
174. The method of Claim 172, wherein test sample comprises neutrophils.
175. A method of assessing an individual for an increased risk of PAOD, claudication, or limb ischemia, comprising:
- i. stimulating production of a leukotriene or a leukotriene metabolite in a test sample from the individual, using a calcium ionophore;
- ii. comparing the level of production of the leukotriene or leukotriene metabolite with a control level,
- wherein a level of production of the leukotriene or leukotriene metabolite that is significantly greater than the control level, is indicative of an increased risk of PAOD, claudication, or limb ischemia.
176. The method of Claim 175, wherein a level of a leukotriene metabolite is compared, and the leukotriene metabolite is selected from the group consisting of: LTE₄, LTD₄ and LTB₄.

177. The method of Claim 175, wherein test sample comprises neutrophils.
178. A method of assessing response to treatment with a leukotriene
5 synthesis inhibitor by an individual in a target population, comprising:
a) assessing the level of a leukotriene or leukotriene metabolite in
the individual before treatment with a leukotriene synthesis
inhibitor;
b) assessing the level of the leukotriene or leukotriene metabolite
10 in the individual during or after treatment with the leukotriene
synthesis inhibitor;
c) comparing the level of the leukotriene or leukotriene metabolite
before treatment with the level of the leukotriene or leukotriene
metabolite during or after treatment,
15 wherein a level of the leukotriene or leukotriene metabolite during or
after treatment that is significantly lower than the level of the
leukotriene or leukotriene metabolite before treatment, is indicative of
efficacy of treatment with the leukotriene synthesis inhibitor.
- 20 179. The method of Claim 106, wherein the level of the leukotriene in steps
(a) and (b) is assessed by measurement of *ex vivo* production of the
leukotriene in a sample from the individual.
180. A method of assessing response to treatment with a leukotriene
25 synthesis inhibitor by an individual in a target population, comprising:
a) stimulating production of a leukotriene or a leukotriene
metabolite in a first test sample from the individual, using a
calcium ionophore, before treatment with a leukotriene
synthesis inhibitor;
30 b) stimulating production of a leukotriene or a leukotriene
metabolite in a second test sample from the individual, using a

calcium ionophore, during or after treatment with the leukotriene synthesis inhibitor;

- c) comparing the level of production the leukotriene or leukotriene metabolite in the first test sample with the level of production of the leukotriene or leukotriene metabolite in the second test sample,

wherein a level of the leukotriene or leukotriene metabolite in the second test sample that is significantly lower than the level of the leukotriene or leukotriene metabolite in the first test sample, is indicative of efficacy of treatment with the leukotriene synthesis inhibitor.

181. A method of assessing response to treatment with a leukotriene synthesis inhibitor, by an individual in a target population, comprising:

- a) assessing the level of an inflammatory marker in the individual before treatment with a leukotriene synthesis inhibitor;
- b) assessing the level of the inflammatory marker in the individual during or after treatment with the leukotriene synthesis inhibitor;
- c) comparing the level of the inflammatory marker before treatment with the level of the inflammatory marker during or after treatment,

wherein a level of the inflammatory marker during or after treatment that is significantly lower than the level of inflammatory marker before treatment, is indicative of efficacy of treatment with the leukotriene synthesis inhibitor.

182. The method of Claim 181, wherein the inflammatory marker is selected from the group consisting of: C-reactive protein (CRP), serum amyloid A, fibrinogen, a leukotriene, a leukotriene metabolite (*e.g.*, cysteinyl leukotriene 1), interleukin-6, tissue necrosis factor-alpha, soluble vascular cell adhesion molecules (sVCAM), soluble

intervascular adhesion molecules (sICAM), E-selectin, matrix metalloprotease type-1, matrix metalloprotease type-2, matrix metalloprotease type-3, matrix metalloprotease type-9, myeloperoxidase (MPO) and N-tyrosine.

5

183. A method of preventing MI, stroke or PAOD, in an individual with an ankle/brachial index less than 0.9, comprising: administering a leukotriene synthesis inhibitor to the individual in need thereof, in a therapeutically effective amount.

10

184. The method of Claim 183, wherein the individual has at least one risk factor selected from the group consisting of: an at-risk haplotype for myocardial infarction, stroke or PAOD; an at-risk haplotype in the FLAP gene; a polymorphism in a FLAP nucleic acid; and an at-risk polymorphism in the 5-LO gene promoter.

15

185. The method of Claim 183, wherein the individual has at least one risk factor selected from the group consisting of: diabetes; hypertension; hypercholesterolemia; elevated triglycerides; elevated lp(a); obesity; ankle/brachial index (ABI) less than 0.9; and past or current smoker.

20

186. The method of Claim 183, wherein the individual has at least one risk factor selected from the group consisting of: a transient ischemic attack; transient monocular blindness; carotid endarterectomy; and asymptomatic carotid stenosis.

25

187. The method of Claim 183, wherein the individual has at least one risk factor selected from the group consisting of: claudication, limb ischemia leading to gangrene, ulceration or amputation; and a revascularization procedure.

30

188. The method of Claim 183, wherein the individual has an elevated inflammatory marker.
- 5 189. The method of Claim 188, wherein the inflammatory marker is selected from the group consisting of: C-reactive protein (CRP), serum amyloid A, fibrinogen, a leukotriene, a leukotriene metabolite, interleukin-6, tissue necrosis factor-alpha, a soluble vascular cell adhesion molecule (sVCAM), a soluble intervascular adhesion molecule (sICAM), E-selectin, matrix metalloprotease type-1, matrix metalloprotease type-2, matrix metalloprotease type-3, matrix metalloprotease type-9, myeloperoxidase (MPO) and N-tyrosine.
- 10 190. The method of Claim 183, wherein the individual has increased LDL cholesterol and/or decreased HDL cholesterol.
- 15 191. The method of Claim 183, wherein the individual has increased leukotriene synthesis.
- 20 192. The method of Claim 183, wherein the individual has had at least one previous myocardial infarction or ACS event, or has stable angina.
- 25 193. The method of Claim 183, wherein the individual has had at least one previous transient ischemic attack, transient monocular blindness, or stroke.
194. The method of Claim 183, wherein the individual has asymptomatic carotid stenosis or has had a carotid endarterectomy.
- 30 195. The method of Claim 183, wherein the individual has had a revascularization procedure.

196. The method of Claim 183, wherein the individual has atherosclerosis or who requires treatment (*e.g.*, angioplasty, stents, revascularization procedure) to restore blood flow in arteries.
- 5 197. The method of Claim 183, wherein the leukotriene synthesis inhibitor is selected from the group consisting of: 1-((4-chlorophenyl)methyl)-3-((1,1-dimethylethyl)thio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)-1H-Indole-2-propanoic acid otherwise known as MK-0591, (R)-(+)-alpha-cyclopentyl-4-(2-quinolinylmethoxy)-
10 Benzeneacetic acid otherwise known as BAY-x-1005, 3-(3-(1,1-dimethylethylthio-5-(quinoline-2-ylmethoxy)-1-(4-chloromethylphenyl)indole-2-yl)-2,2-dimethylpropionaldehyde oxime-0-2-acetic acid otherwise known as A-81834, optically pure enantiomers, salts, chemical derivatives, and analogues.
- 15 198. The method of Claim 183, wherein the leukotriene synthesis inhibitor is selected from the group consisting of: zileuton, atreleuton, 6-((3-fluoro-5-(tetrahydro-4-methoxy-2H-pyran-4yl)phenoxy)methyl)-1-methyl-2(1H)-quinolinone otherwise known as ZD-2138, 1-((4-
20 chlorophenyl)methyl)-3-((1,1 dimethylethyl)thio)-alpha,alpha-dimethyl-5-(2-quinolinylmethoxy)-1H-Indole-2-propanoic acid otherwise known as MK-886, 4-(3-(4-(2-Methyl-imidazol-1-yl)-phenylsulfanyl)-phenyl)-tetrahydro-pyran-4-carboxylic acid amide otherwise known as CJ-13610, their optically pure enantiomers, salts,
25 chemical derivatives, and analogues.
199. The method of Claim 183, wherein the leukotriene synthesis inhibitor is a FLAP inhibitor or antagonist.
- 30 200. The method of Claim 183, wherein the leukotriene synthesis inhibitor is a 5-LO inhibitor or antagonist.

201. The method of Claim 183, wherein the leukotriene synthesis inhibitor is a leukotriene inhibitor or antagonist, or an antibody to a leukotriene.
- 5 202. The method of Claim 183, wherein the leukotriene synthesis inhibitor is a leukotriene receptor inhibitor or antagonist.
203. The method of Claim 202, wherein the leukotriene receptor inhibitor or antagonist is an agent that inhibits or antagonizes a receptor selected
10 from the group consisting of: BLT1, BLT2, CysLTR1, and CysLTR2.
204. The method of Claim 183, wherein the leukotriene synthesis inhibitor is an inhibitor of a member of the leukotriene biosynthesis pathway.
- 15 205. The method of Claim 204, wherein the member of the leukotriene biosynthesis pathway is selected from the group consisting of: FLAP, 5-LO, LTC4S, LTA4H, and LTB4DH.

SUSCEPTIBILITY GENE FOR MYOCARDIAL INFARCTION,
STROKE AND PAOD; METHODS OF TREATMENT

ABSTRACT OF THE DISCLOSURE

5

Linkage of myocardial infarction (MI) and a locus on chromosome
13q12 is disclosed. In particular, the FLAP gene within this locus is shown by
genetic association analysis to be a susceptibility gene for MI and ACS, as
well as stroke and PAOD. Pathway targeting for treatment and diagnostic
10 applications in identifying those who are at risk of developing MI, ACS,
stroke or PAOD, in particular are described.

15

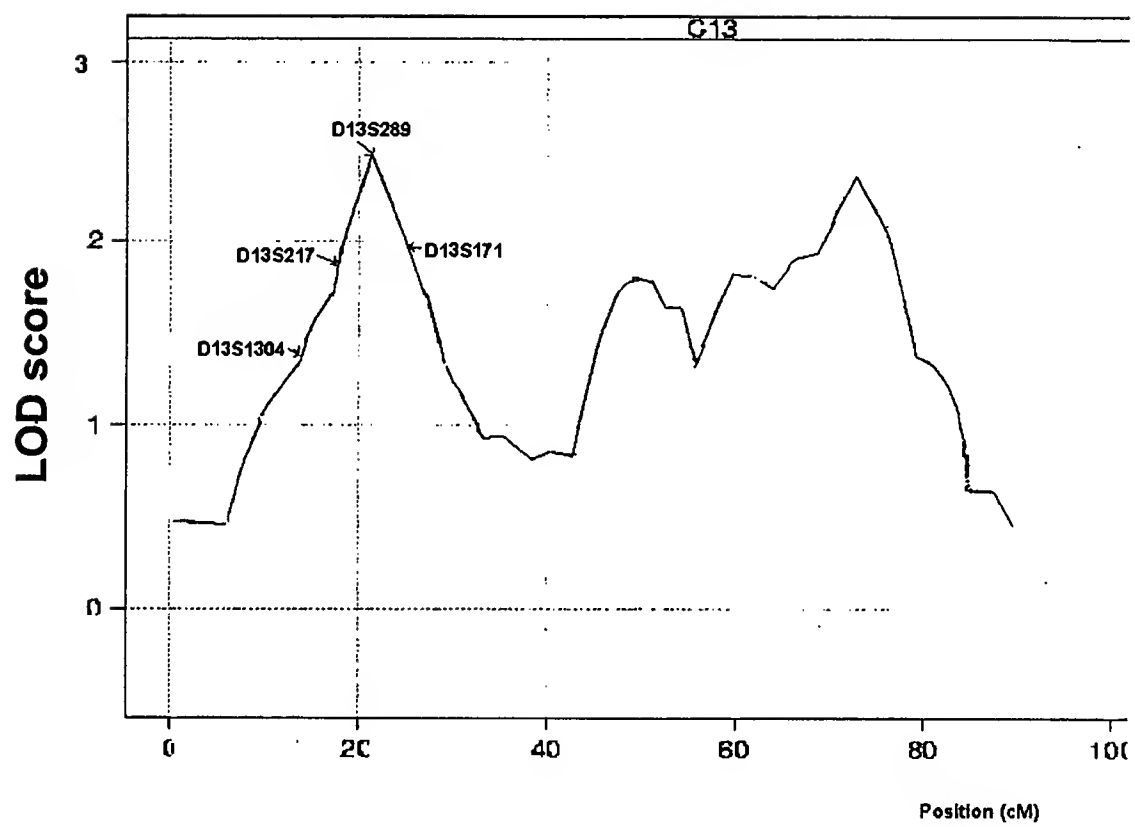


FIG. 1

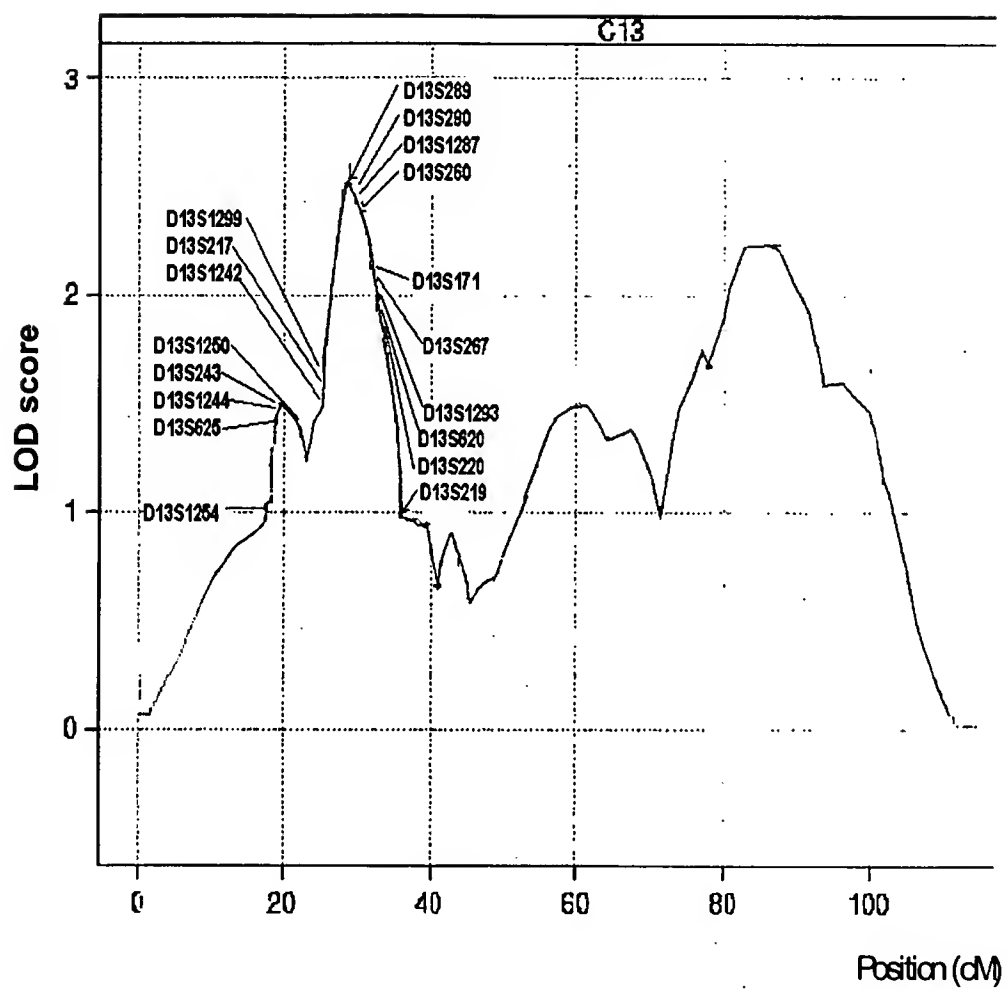


FIG.2

Location of haplotypes showing association
(p value $< 10^{-5}$) with the disease

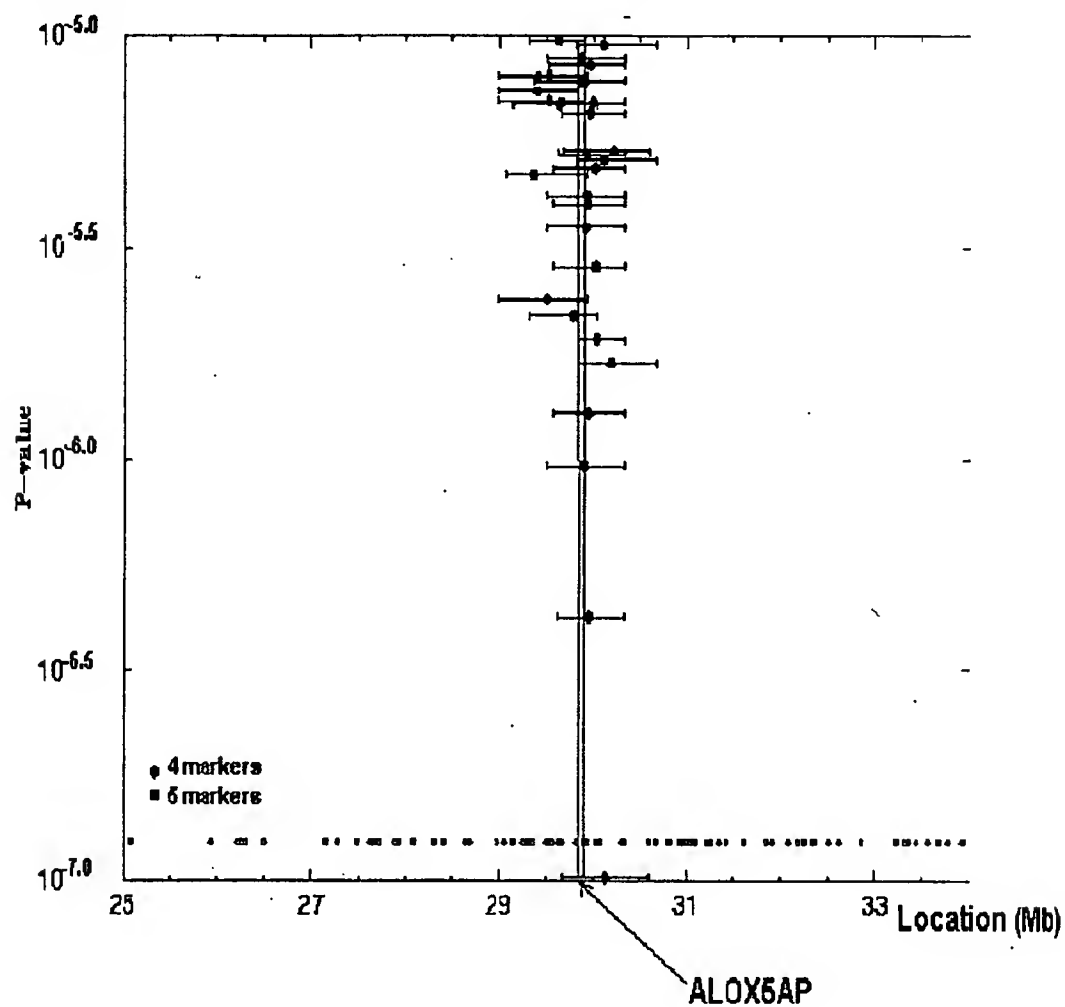


FIG. 3.1

Haplotypes showing association (p value $< 10^{-5}$) with the disease

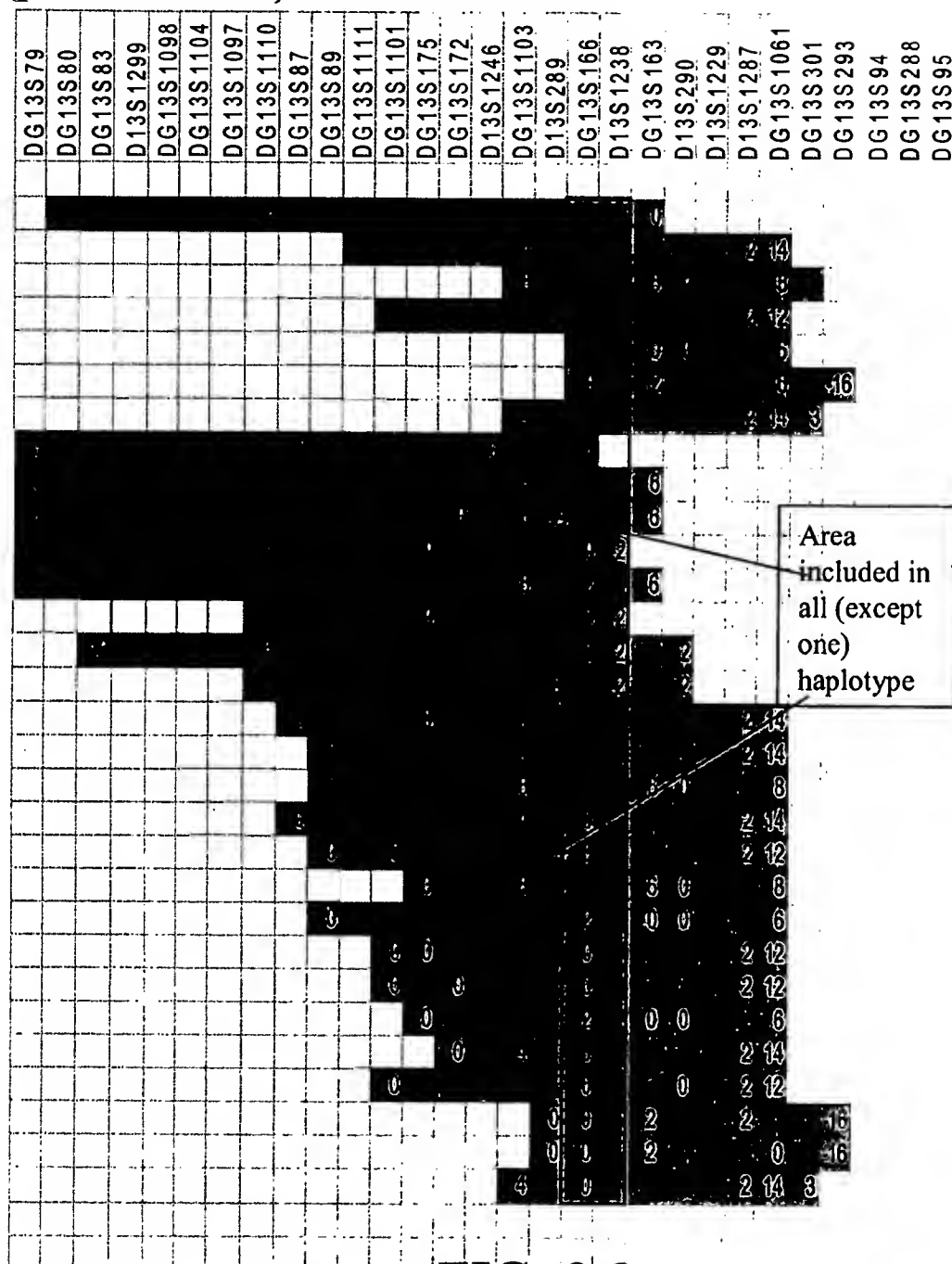


FIG. 3.2

Markers and genes around the FLAP gene

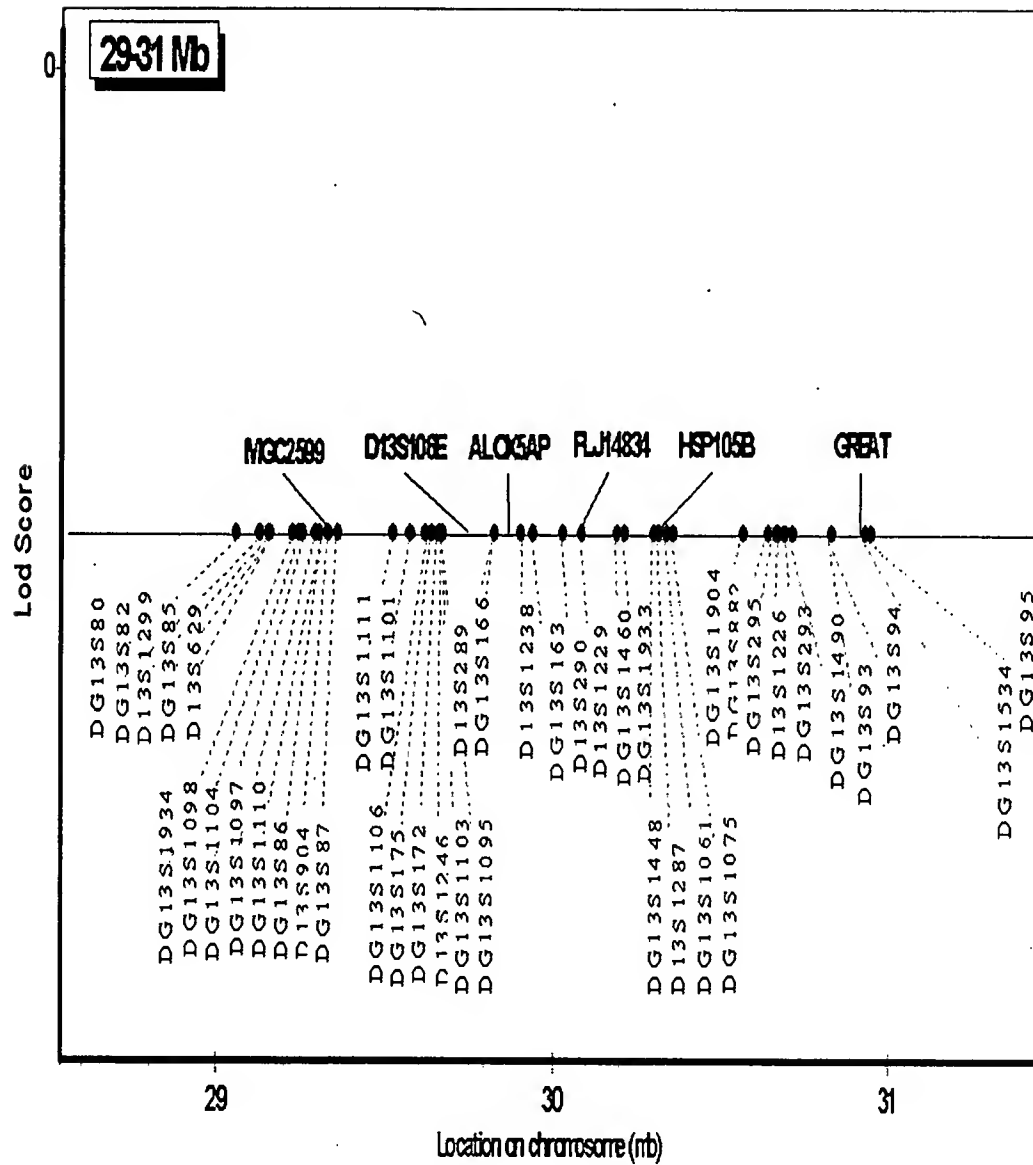
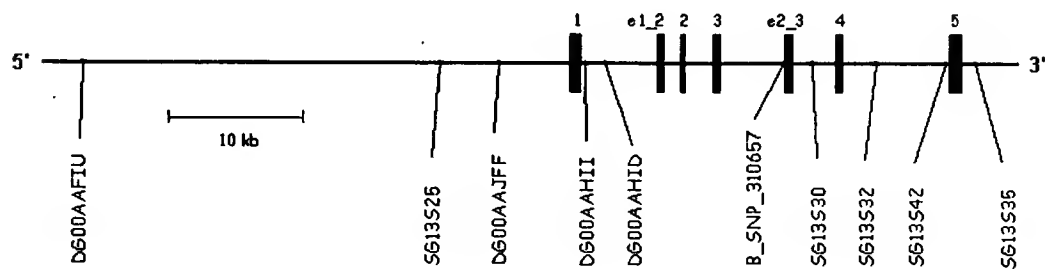


FIG. 4

FIG. 5 Relative location of key SNPs and exons of the ALOX5AP/FLAP gene (exons shown in vertical rectangles). Haplotype length varies between 33 to 68 kb.



ID CHROMOSOME 13: 28932001-29146000BP in NCBI build 34.

SQ Sequence 214000 BP

GACTAAGATG AATATGCATT CATTCACCAA AATCTCATAT TCCCAAAAAG CAGGAAAGGT	60
AGTACAGTGA GATGGATGAT GCCTTCACAT GACTCAGATG TCACGTGTTT CTCACCATTG	120
AGACCCCCAA GGCACCCCCT CCCAGCATTT ACCAGAATGT GTGTGTAAC TTTACAGTG	180
ATTTGTGTAA TTATTTGATT GTTTCTCTTG TATCCTGTAG CAATGAGGGT AGAGATTATA	240
TCCCACCTAC CACTGCAGCT CCAGGATCCA GCTTCACAAA CATTTGTTGA ATGAATGAAT	300
AAGAAAAGAG GACACCCCCA AAGAGGCTGC AAGGGAAAAA GCTACAAAGA CAGAAGCACC	360
AGGAAAAAGT AGGGTCATGT AAGTCAAAGC AGGAAAAAAG TTCCATGGTG GGGTGGTCAG	420
CAGTGTCTAA TGCCACGAAG GCACAAAGTA GGATAAAGGT TAAAAATCAG CCTTTGGTTT	480
TGGCAAATAT GAAGCTTATC GGTAGCCTTA GCGAGAACAA TTCCATCAGG GAGCAGAAGC	540
TAAGTGCAGT GGGTTGAGTC ATCAAGCAGG CATAAGGAAG TAGGGATACC CCATTATAAG	600
CTACTCTTTC AAGAAGCTCA AATCTGAAGG TTAGGAGAAT TAGGTGAGTA GCTAGAAGGA	660
AATGTGGAGT CGAGGGGGCTG TTTTCTCTCC CAAGGAGTAT AAAGGTGTAA CGTTGCATGA	720
AACCACTTCA GACAAAGGCC GATATCAATA GAGAAGTTAA AACGCACGCC TCAAGATTG	780
GGAAGGCTTG GGGTTGGGCT TAAAGAGGTA GGAGCATATT TCCTATCCTA GGACAGAGAA	840
TAAAGAAGAA AGGATAGGTT CCCATGGAGA TAAATTTCTA AGTGTTAAAG AAGAGGCTCA	900
GAAAATTCTA GCATGATAGG CTCACTTTTT TCTTTTCCA TGAAGGAGAT GGCAAAGTCA	960
ACTGACATGA GAAAGGTGAC AATACTGATG GGTTGAAGAG CGATGGACAT TTGAAATAAC	1020
TTCTTAGACC AGTAGAGGCT GGAGTTCATA AATCAGAACT GGCTACAGGT TATATATGTT	1080
TTTTTTTTTT TCTCCAACAG CATAAGATAA CAGAGCGAAG TCTGTAGAAA TGAAAGAAGA	1140
GTCAGATGAG GATAGCTGGA GCTAGTGCAA GGAGGGAAGC ACCACGGTGG GAGCCAGGTA	1200
CCCCCTGGAT TTATAATTCA TACTGAATTC CAACAACAGA AGGGCTCTAA GCAGGAGAGT	1260
GACAGATTTT AGAAGACTGA GACACATTTG GTAAAAAATA GTAGGAGGAA AACCTGATTC	1320
TGGAATTAGG GCAGCCAATA GACGGCAGTA TTTTCAGAAA GGAGGGAATG GTCAACAGTG	1380
ACTTTCTAGT CTGGAGCTCA GGAGGAAGAG GCAACTCTAC CTGATGGTAT TAAGATCATG	1440
GAGGTAGCTG AGATCACCTA GCTTGTGTGT GTCAAATGAG AAAAGAAGAA AGAATAGGAG	1500
AAGTTCCCCA GGAACACAGA CATTAAAGTG GGCTGTGGTG ACAACACAAG AAGAGAGGCT	1560
TGCAAAGGAG CCTGAGCAGC TGTGATGAGA GAGGTAGGAT GGTGGACTCG GAGAAGAGGC	1620
AGAAGATGTT CTAAAGGAA GGACACTGCT GCCAAGTAGT CAGCCAATTG GTGACAAAGA	1680
AAGACCCTGT TGCGAGAAAA AAAGTCAGTG AAGTAGTAGG AACGATGACA GATGACACTG	1740
GGTTGAAGAC TGAGGAGAGA GAAGTGTAAG AGTGGAAGCA GAGGGCAGAC CACTCTTCTG	1800
AGACACTGAA GAGGCATAGT TAGAAATAAA GGGGAGTCGC CAGAAAGGAA TTTGTGGCTA	1860
AGCAAGAGGT TTTCTTTAAG ACTGAAATAC ATAAGCATGA TTAAATGCT GCTGGGATGG	1920
AGTTCACAGA CCTGGAAGAC AGAAGACAAA GCGGATCATC AAGATAGTGG AATTTACTGA	1980
AATGAGAGAG GAAAATCCCA TCCACAGGAA ATGCAGACAT GAGGGAGGGG CCAGAAGGAC	2040
AGTGAAAACA TCAGCAACTG GTCCCCAAC TTCTGAGTGA ATGTGGAGAT ATAATCAGGT	2100
AAAGGACTGC ATCATCTCCC TGGTTAATGA TGGAGTCAGA GAAAAGAGTG TCTTATACAG	2160
AAGTTGTGAT ATACTTGGCC GGGCGCAGTG GCTCAGCCT GTAATCTAAG CACTTTGGGA	2220
GGCCAAGGCA GGCGGATCAC CTGAGGTCAG GAGTTCATGA CTGGCCTGGT CAACATGGCA	2280
AAATCCCACC TCTACTAAA ACAAAGCCT GTAATCCCAG CTACTAGGGA GGCTGAGGCA	2340
GGAGAATCGC TTGAACCCAG GAGGCAGAGG TTGAGTGAG CCAAGGTCGC ACCACTGTAC	2400
TCCAGCCTGG GCAACAGAGC TAGACTCAGT CTCAAAAAA AAAAAAAG ATGTATTTAT	2460

FIG. 6.1

TCTCACTGTA TAAATTTCTG TGTAAGAAAT ACTCTCTCAT ATAGAAGTAA ATTTATATAT 2520
AAAATTATAT AGAACCACTA TAAAATACTC AGGTTTATAA AATTTATATA TAAACTTGTT 2580
GACATATAAA ATTCCATGTA AATGACTATA AAGTACTCTT ATATGAAAAG TATATGAATT 2640
AAATTATATA TCAACTTACT TTTATATTAC AGTATTTTGT TTATACAGAA GTTTATATAG 2700
TGACAATAAA TATTTCTCAA GAACGATTTC ACATAATAGA AGTATAAATT ATCCATTTCC 2760
AATAGTGAAG AAGAAAAGCA GTTCCACACC AGTGACAGGG CTACGAATCT AAGAGGTACA 2820
AAGACTTCAT TCTTAGAGAC ACTGAGGTCA GGGCATGGCC AACACATCTG AAGCTGATAG 2880
AATTGGCGCT GGGTTGGTTG GAGACGGTAC GGTATTACTA TTACAATGGC AGACGCTTGG 2940
CCTTGATAAC TAGCCAATCA GGGGGAAAGA TTCTGGTTTC CTCTGTTATT ATCTGAACTA 3000
GTGTGTTCCC AAAGGGTTAA GATGGTTTAT GGAAGGCACA AGATCAGCAA ACCATAAAGG 3060
ATTAGCACTA AGAAGGAAGG AAGTAGACCA AGTGTTAATG GCGATGCCAT GTAAGAGCCA 3120
GGTCTGCGAT GTATGTTCTA CATGGTTTGG GGGGTAAAAA AAATGTCAGC CTCCAGAGCA 3180
CAGGGCTTTA AGCCTCAAGT ACTGTTAACA GTAGAGTTTA CTAGTCTACA GCAGGAATTA 3240
CAACCAGTAA TTCTAAGGCC AATTACTCAG GCAAGTTTTC CTAGAACAAG GAAGCTCTGC 3300
TTCGAGGTCA AATCGATTTC TGCAATTATA GAAGCATCTA GATGTTCTCT GTTCAAACAA 3360
TGGGGTAAAA TCCCCACACA TTTTATTTCT GACAGAGTGT TCCCTATATT GCCTGGCCAG 3420
GAGTGATAAC ATTGCTTGGC TATTATTAAT AAAACATTGC TGTGGCTGGG CGCAGTGGCT 3480
CACACCTGTA ATCCTGGCAC TTTGGGAGGC TGAGGCAGGA GGATCACTTA ACTCCAGGAG 3540
TTTGACAGCA GCCTGGGCAA CATAGCAAGA TCCCATCTCT CTAAAAAATT TAAAAATTAG 3600
CTGGGTGTGG TGGCAGACAC CTGTAGTCCC AGCTCCTCAG GAAGCTGAGG TGGGAGGATC 3660
ACTTGAGCCC AAGCAGGTTG AGGCTGCAGC GTGCTGTGAC TGTGCCACTG CACTCCAGCC 3720
TGCGCAACAC ACTGAGAGAG ACTCTGTCTC AAAAAAATAC ATCAAATAAA AATTTAAAGC 3780
CCATTTCTTT CTTTGGTAC ATTACAGCCA TGCACTTCAA AGGCTAGCAC AATTATTTTT 3840
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TGCTAATGAA GATGTGGTTT AAGGATTTTA TGCACCCAGT TCATTTATTA ACAACTTGTT 4020
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CTTCGTGGGC ATGGTGGCCA AAACATTTTA GCTGTGAAAA TAATTTCAAT TCATATTTTT 4200
TTGGAATCAA TATTTAAAGG TGATATATTC TCAATGAAA AGTGGACAAA TGATCAGTTA 4260
TAGGACATGA TTAAGAAACT AACCATGAGC CACGTGCAGT GGCTCATGCC TGTAATCCCA 4320
GCACTCTGGG AGGCCGCGGT GAGCGGATTG CTTGAGCCCA GGAGTTCAAG ACCAGGCTGG 4380
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TGTTGGAAGT AAATTTTAGA AGGTTTATAA TACCTAAAG TAATCACTTC TGTCTTATGA 4740
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ATAATGTGTA ACACTTTAGT GAACTAAAGC ATAAAGAACC ATGGTCTCCT AATGCAGCAA 5100

FIG. 6.2

ATTA AACAC ATGATAGCTA CAATTAATGA AGTACATAGT CCTGGCTGGG CACTATGGTA 5160
CGTCCTTTAC ATAGATTATC TCTTAAATTA TTAACCCCGT TTTAGAGATG AGAACATTGG 5220
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CAGGACTCCT AGTGAGCTGT CAAGGGGAAT GCTATAATTT TGGAGGTTCT AAATCTGAGG 5520
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TAGTCAATTT CCAGTGCTCC ATTCAAAGAA AAACCAAAAA TGTCCAGAAT ATAACCTTAT 7440
TTTAAACTT GTTAACCACT GATTTCACTT GTTAACCAAA TTTTTTTTTT TTTTTTTTGG 7500
AGAATGAATC TCACTCTGTC ACCAGGCTGG AGTGCACTGG CATGATCTTG GTTCACTGCA 7560
ACCTCCGCCT CTGGGTAAGT GGTTCAAGCA ATTCTCTGCT CTCAGTCTCC CGAGTAGCTG 7620
GGATTACAGG TGTGCACCCC CACACCCAGC TAATTTTTTT GTACTTTTAG TAGAGATGGG 7680
GTTTCACCAT GTTGGCCGGG CTAGTCTTAA ACTCCTGACC TCGTGATCCG CCCGCCTCGG 7740

FIG. 6.3

CCTCCCAAAG TGCTGGGATT GCAGGCATGA ACCACTGCGC CCAGCCTGTT AACCAAATTT 7800
CTAATCACAC AACTTTGAGG CCCAGTAAAT GCCTGCTGAA AAGAGGGTGC TGGTGGTGAG 7860
GCAACTGAGG GGCTAACATA CTGATAGCTG CTGAAATCTT CTACAGCTCT TTCTTGTTAG 7920
AACACTCCAT CACGGCTCCC AGGCCACAC CACATGAAGG AACTTCTAGC TCTCTTGCTT 7980
GCTCTTTACC CAAATGTAGT TAGCAAGTCC TGGGAACTAA ACAGCATTGA CACACTTGAA 8040
GAAGACAATT AGGCAAATCC CAACTGCTGT GCTCCTGCAG CTAAAGATGA AGACTCGTCC 8100
ATTGGGCAGT TGATTAATTG TACCTAGAAA ATTAATTTCA ATGGTCCCAT GACAACATAC 8160
GGGCAGTGAA GCTCTAGTGT TCCCCCTGGG TGGAACTTC CAGGATGTAT AGTCTCCCAT 8220
ACCAGCTCAT CCTCCCATTT TTCCAGATTG TGGTTCTTCT CTCTTACCTA GTGTGTAGTG 8280
GGCCAAATGG TGGTCCCCCA AAAAGATATG TCCATGTGTT AACCCCTGGAA ACTGTGGATG 8340
TAACCTTATT TGGAAAAATG GGGCCAGGTG CAGTGGTGTG CATGTGTAGT CCCAGAACTT 8400
TGAGAAAGCA AGGTGGGAGA ATCGTTGGAG CCCAGGAGTT CAAGAACAGC CCAGGCAACA 8460
TATTGAGACC CCCGTCTCTA TAAGCAATAA AAAATTAGCT AGGTGTGGTG GCATGCACCT 8520
GAAGTTCCAG CTACTTGAGA GGCTGAGGCA GAAGGACTGC TCAAGCCCAA GGAGTTCAAG 8580
GCTGCAGTGA GCTATGATCA TGTCACCCCA CTCCAGCCTG GGTGACAGAG TCAGACTCCC 8640
TGTCTCAGGA GAAAAGAAAA AAAGGTCTTT GTAAATGTAA TAAAGAATCT TGAGATAAGA 8700
TCATCCTGAT TTAGGATGGA CCTAAATCC AATGACATTT GTCCTTACAA AAGAAAGGTA 8760
GAGGGAAC TGAGACAGAC ACAGAGGGGA GGGCCTTGTG AAGCAGGAAG CATAGATGCA 8820
GTTACAAGTC AAGGAATGCC AAGGACTGTC TACAACCAGA AGCCAGGAGA GATGCATGGG 8880
ATGATTTCTC CCTCACAGCC TCCAGAACTT CTGGCCTCCA GGAAGTGAA GAATCAATTT 8940
CTGTTGTTTT AAGCCACCAA GTTTGTGTGT CATTTGTTAT GGCAATGGCA GTATTAGGAC 9000
TCTAATACAC AGTATAAAAA AATAAAAAA GGGCCAGGCG TGGTGGCTCA GACCTATAAC 9060
CCCAGCACTT TGGGAGGCTA AGGCGGGGAG ATCACTTGAG GTCAGGAGTT TGAGACCAAC 9120
CAGGCCAACA TGGTGAAACC CCATCTCTAT TAAAAATAAA AATTAGTTGG GCATGGTGGT 9180
GTGCATCTGT AATCCCAGTT ACTCAGGAGG CTGAGGCAGA AGAATCGCTT GAACCCAGGA 9240
AGTGGAAGTT GTAGTGAATG CCACTGCACT CCAGCCTGGG TGACAGAGCT AGACTCCTTC 9300
ATCCTAGGAC ACAGCCAAGT CTTACGTAGC AAAAAGAAGT TGTTAAAGGT CTGTAGTTCT 9360
GCATTAAGCA ACACAGGCAT GTACCTATGA ATTATATGAT TATAAAAGTG CTCGGACAGG 9420
CCCATTTCAA ACTTGGCCTC TTTCCACCAA CTGTGTACTG TTTCTCATT CATAACTAGA 9480
GATTATGTCT TTATATCCTG TCAAAAAAGT GAATTTTGT GGGCTAAGAC ATTATCCCTG 9540
TGTTAAATGC ACCAGTCTTA GTGTAAACAA GCCTAGTTCC TTTTTCATTT TGGCTGTCTA 9600
GTATGCATTT GTATATGCTA GGCAGTGTAC TAGGCACCTT AAATACATTA CCTTGTTTAA 9660
CCTCTACAGG ATTCTGGGAG GTAGGCATTA TCCCCATTTT ATAGATGAGA AACTGAGAA 9720
GACAATGTTT ATAAGTGCGT CACTTGTCTG AGATGACATA TTTACTAAGT AGCAGAACCA 9780
GGCCTCGAGC TACTCAGTCT GATTTCCAAA GCCCCTGCTC TTAATCACAT CAACTTCTTT 9840
CCTATATCAC CTTTCCCGA GTGCGCTCTC ATGGATAAAG AGCAGAAGTA TAAGTTACTA 9900
GGCAGCAGAA AACTGTAGAG GTGGGAAGAT TAGATAAAAA ATGTAAATAA GAAGGCTTTA 9960
AGACACCAAA ATCAAATGTA AATACTTTAT AACCTGAATC AGTGCTTGTG TTCATGAGGC 10020
TAGAGGTCGT GCATTTTATC TCTAGGTCTG GTGATGCCAA TCCTGATCTA CAGCCAGCAG 10080
CAACAGTTCC CTAGCCTGCC TAGAAGTTTG TAAATGCATG GGCTTTGGTA GGAGGAAGAC 10140
GAGAGAAAGC AGAACAGATT ATTACAAACC CAGTGCATTC CCCCTTGATG GGTCAACAGC 10200
GATTTCTTTG TAAGTGAAGG ACAGCACACT GGTTTTGATG ACTCACGAGA GAGTAGGAGG 10260
GAAAAAGAAG TCTGAGGCAT TGCCTGGAAG CTCGCTCTG CTTAACAAG TACACTAATG 10320
GCTCATGCCT GTTACTCCCA GCACTTTGGA AGGCCAAGAT GGGTGGATCA CTTGAGGCCA 10380

FIG. 6.4

GGAGTTTAAG CCCAGCCTGG TCAACATAGC GAGACCTTTT CTCTATTAAA AATAAAGAAG 10440
AAAGAAAGTA ATAATGATTC AAGTTCTCAT TCTCTACAAA ATTCACCTAT GACTTTCCAA 10500
ATGCTAGTGA AAACTTTTAG GTATTGCAAA ACTGCCTTAA TGCATAACGG GATTCTCATT 10560
TACTTAGTC TAAGATGACT TTTTCACTTT GAACCTCTGC ATCTTTATGA TCGCTTAGCT 10620
TTCTGACAAG CAATTCAGT AAGTGTTTAT CAATTTGCAT CCACACGCTG ACACATAGGG 10680
GTCTACTTAC ATATCCTTCA TGTAAATGAG CTTTTGTAAA TCATCTTTCT ACATGGTACA 10740
CTTCTGATTT TGTGTGCAGC TTTCTTGTTT AAGCACTGTA TTAATGCTC TGCTTCTAC 10800
ACCCTTAGGA ACAATGAGAA TAAAAGCGTA ATGTTGGTTA CTTCTTCATA TCAAAGGAAG 10860
TTCATCTCCT GGTTATTAAG AGCTATTATT AAATGGCCAT CTTTTGTGC CCCTGTGTTA 10920
AGCACTCTAC CAAGATACCA TTAATAGAT AAGGGCCACA CTCCATAGAG ATGATGGTTC 10980
TATATTCTGT ATTTTCTGGG GGAGTTCTAA TTTTCATGCAA TTCCTTCTTC TTAATAAAG 11040
GCAATTCTCT AAATATATTA CCTAATGTGC TTTCACTTTC ATATTCTTGT AAGATTTTTC 11100
ACATAAATCA ATTCTCAAAA AATAGTATCA TAGGCCTTTT AAAAATAGTC ATGTTCAAAA 11160
GTCAGGCTCA TGAATAAATG TGTGCATTCA TTACATATAT TTTCAATAAT TCAAATTTAA 11220
AAGAATAAGA GTAGCTAGAA GGTGGAAGAA AAATCTTATT CTGATTAGGA ATGCACAATC 11280
ACAAGAAAAT TTGTGATATA TATAGTCATT TTATTCTGTA TTGTTTTATT TTGATTTTGG 11340
TAAGACAAGA AACAATGTAG AAAGTTTGAC AACTTAAAAA AGTAATATGA GTGTGAGAAA 11400
GTCCTCTTCC AGGATTAGCA AAAAAATGGT TTTTTTTTTT TTTTTTCCG AGATGGAGTC 11460
TCGCTCTCTC GCCCAGGCTG GAGTGCACTG GCGCAATCTT GGCTCACTGC AACCTCCGCC 11520
TCCCGGGTTC AGGTGATTCT CTTGCCTCAG CCTCCCAAGT AGCTGGGACT ACAGGCATGT 11580
GCCACCATGC CCGGCTAATT TTTTTATTTT TTAGTAGAGA CGGGGTTTCA CCATGCTGGC 11640
CAGGCTGGTC TTGAACCTCT GACCTTGTA TCTGCCCGCC TTAGCCTCCC AAAGTGCTGG 11700
GATTACAGGC GTGAGCCACC GTACCCAGCC TAAATGGCCA AGTTTTATTA TGGACAATTA 11760
AGCTGTAGAA TAAAAATCTA CTTTTAATAG CTGGCATAGT GCCTAGTGGT TTTGAAGCCA 11820
CAAGCAGGTT TACAAAAAAC ATTTAAATCC ATCTGAATCT ACAGAAAACT AAGATTACCT 11880
AAGCAGAAAA TGAATAATAG TCAGGATTAA GGAAGATTAA CAAATGAAGA GTATATGTAT 11940
TTTAGAAGTA TTACTTTATA TTTTATAGT ATAATAATAA TATTTACGTT CCTACACTTA 12000
TAATGAGTTT CGTATATATA TAAAAAAT TTAATGGATT AGTATGTTTA TATTTGCTTT 12060
TAGTAAATTT GGTGTATGAT AAACCTCAGT GTCTACATTG TGAGACTACA CCTGAGGCAA 12120
TTTCTGTGTT GATATATACC TGAATAGCAG ATATTACTTG GGAGCAAATA AAATAGCTTC 12180
AGGCCTAATT TTGCAAGTTC ATGATGGGAG AGTAAGCATG ACTTCAAAGA ACTGACTTTG 12240
AGTTAAACT TGAAGAATGA ATGTGACAAC AGCAAGTATA AAACAATGCC AGGCAGAGGT 12300
GGGACTGTTC ATGGGTATCA GGGTAAGTGT GTTGATAAAT GCTCAAAGTA GGAAATACCT 12360
TTCTTCCCC ACACATGTCA GAAAATAACT GCAATAGAAT GCAACGACAT CTCAGAGATA 12420
AAGTGTTCAA CTTAGCTCTC AGAGACCGTT CAGTTACATT TTGTAATGAC ATTGGAATTG 12480
ATTGCATTTT GAAGGCAATT CTAAATGCAA AGTCTTCATT TTGTTGATAG AAGCTGGGTT 12540
ATTTATTATG AAATTTCAA AATTAAGTAA AATATCTAAT TAGGATTATA CCAGCAAAGG 12600
CAAATTTAGA ATTCAAGACT TCATGATCCA TGGTAAGATT ATTTAATGC AACTCTGCTA 12660
ATTAAGTAA ATTTCTTTA ACTCTCATAT CTGCCTTTTA CTTCTTAAGA CATTTTCTA 12720
GTATTTACC AGAGCAAGAT ATCAGAAGGG TAAATCTCTT ACCAATGAAC TTGCTAATT 12780
CTTAGTGAAT CCGTTGACCC TGGTGAAGG ATCAGGAACA AAGTGAATGA AATACATTTT 12840
AATACATTTT TGCTTTCTCT AATTCCAAAG ACCACTCTAA AGAATAAGTT ATTTGTGGGT 12900
ATTATCTGAA ACTTGGGATT AAAAGAGACC GTGATTACCC TTCAGGGATT TTGGCAAAAC 12960
TTAAGCCATT TCATCTGAAG AGCAAAGCAA GCCTCCCACT CTCTTGCTT ATTCTCACAA 13020

FIG. 6.5

TTATCTAGAT ATCTAGCAAC AAAACTCTTG AGTAGTTTGT TAACTACAGA TGCCAAGGGC 13080
TGACAGTTTC ACTTTCAGTT TTCAGAATAT CTTTGTTC AGTGGTGTA GCACACCATC 13140
AGAATCTCTA CTATTTAAAA TAATTAAGTT ATAATTGTAA CTTCCATTAG ATGTAGTACT 13200
TAAAGGAATC TAGAAGACAC AACTCATTA TTATAGGAAT TTGACTGCAA ATTCTTCTGG 13260
GGGGTCTGAA TTGCAAAGGA GGCATCTTTG TAAGTCAGAC TCAACTCATT ACTCTGTGAT 13320
GCAGGCTCCT CCAAATGGCA GCAGAAACGT ATTACTCTCT AGAAACACTA CAGTAGTGCT 13380
ACAATTTTCTAG GGTCTGTAG AGATAAGGAC AAATTGACAG AAACACATTC TTAGAAGGAC 13440
AGTATCATTT AAAATAAAAA TACTGTCATA ATTGTACACC AGGATAGCTT CTCCATAATA 13500
AATTCTTTAT GATTTTCTGA TTTTAGAAA TCAGAATTGA ACTTTTAAAT GTGAAAAAA 13560
TGAGAGAATT GTTCAAAAT AGGACCACAT TTCTGTGTAT AATTTTAAAA GTTTAAAAAT 13620
ATTTGATTAG TAGACTGATA AACTGAAACA TTTTGTATA GCTTTTCATT ACATACAAAC 13680
CATATAATTT GTAAAAAATT GGAAATTATT CAAAACCTCA CATAACTAAA GTGACCAAAT 13740
AAATACTGGA GAGGAAAGAA AAGGAGTCAA ATGAATCTAG CATTTTCTTT TTTTTTTTTT 13800
TTTTGGAGAA AGGGTCTCAC TGTGCCACCC AGGTGGGAGT GCAATGGCAC GATCATGGCT 13860
CACTGCAGCC TCAACTTTAT GGGCTTAGGT GATCCTCCCA CCTCGGCCTC CCAAGTAGCA 13920
GGGACTACAG GCATGCGCCA ACACGTCCAG CTAATTTTTT TGGTATTTTT TGCAGAGACG 13980
AGGTTTCACC AGGTTGCCGT GGCTGATCTG GAACTCCTGG TCTCAAGTGA TCTACCCAAC 14040
TCAGCCTCCC AAAGTGCTGG GATTACAGGC GTGAGCCACC GCACCCGGCC TAATCTAGCA 14100
TTTTCTAAAA GGAAGGACCC AGCAGTGAAC GGCAATATCA ATAATCATGT TCAAGACTAT 14160
CAGACATGCA AGCTGGGGAT GAATGGGTGG AAGGGGAAAA TGATGAATAA ATGATGAACA 14220
CAAGTATAGA CCCAGTGGAT TTGAGATGCC CAAGATGCCA GTGAGATATT CAAAGTTTAA 14280
CTCAAAGCC ACTTCCATA TGAAATCCTG ACAAACACTC CTACGTCCAA CTGGAATTAA 14340
TTTCTTTCT GGGCTCCAC AGCACTCTGT ATTTTCTAA TAGCATAACA CTATTTGT 14400
TGTAGATATT TCTCTGATAG CATTACTATC TTCTCTTT ATCACAAGT TTTGAAGTT 14460
TTTTGCCTCT TGCATCCACT GTTGCCCAAT CCCACTGCTG GAAGGCTCAT CTTATTAAGT 14520
TCTGTATTCC TAGTGCTAAC AACTGTCTA CCATAGATGA TGTTCATAA ATGGTTGCTA 14580
AATGAATTCT CTTGTGATA TAGCACTATG GCAACATAAT CGACGGTAAA AATTTCTTCT 14640
CAATGTTTAC TTTTAGCAGA ATGCATTCAT TTATCAACTT TCATTGAGAA TATGCTAATT 14700
TCCATGACCC TGCTAGGAAA TAGGAAAATA AAGATGAATG TAATAAGGTG CTCATTCTAC 14760
TGAAAGTCTT GACTAGTGGA GAATTATGGA TCCAACTTT CATGAAATGC CTTCACTGGT 14820
AAGAATTCTC ATATTTGGAA TAAAAATGT TATGGGTGT GCCAAGATAC CTACATACTT 14880
CATAATTTTG TAGAGGGCTG TCCTTACTGC AGAAATGTAT ACTACTATAG TCATATGTGG 14940
AAATCTTTT TATGATGCTA ACTGCATGCT AACCAGACTT TTTAATTTAA TACTTGCATT 15000
AAATAAACCA TGCTAGGAAT CCAGGAATCT AGCTTGGTTT ATTTTCCATA CAATGTACTC 15060
TTTGTAATAT GCATATACTA CATAAAAATT CTATTAATGG CCTCGTACTA AAGATGTGTC 15120
TGTTGGGGAA TCAGTTATTC TGTATAATT TATCTTAATT GATATATTAA AATCTACCAA 15180
AAATATAAAC TCCGAGTAAA AGTATCTGCA TGGTGTGCAT ATGTTTATTA TTTAAGTGT 15240
CAGCGTATAC ATTTTCATGC CATAAAGTTA TAAATGAAA AAATAGTAGC CTTTATATT 15300
AAGTTCATGC TTATGTAGTT AGTAAAAACA AGAAAGCAAT TAACATACAA ACCATGATGG 15360
TGGTTAAACT TGCTTCAGTT TGTGTTTTT AAAATTTGAA AGTGAGAAAT ACAGCTCGAA 15420
GTCAGCTCAT ATTTTCAGTA AGTACTGATG AGGATGTACT GGCCCTATTG ACTACGCTGA 15480
CCCCATTAAT ATATTTGTGA GTCTAAAGGT TCATATGACG CTGTTCTTCT ACTCTAGCAA 15540
CAGGCCATAC ATGTCTTACA TAGGGACTCT GTTCAATTCA TTAATACCTC CTGAAGTGCT 15600
CAACATCGTG GTTCATTTAT AGTAGATACT CAATACATAC TCCATTAAT GAATTCCTAAG 15660

FIG. 6.6

ATAAACTGTC TGTTACTGAC AGAAATTTTC ACTTAAGGGA GTCTCCGTGG CTGAAGGCAA 15720
TTTTGAAATC CTGTAAAAGA ACCCACTCCT CTCCCCAAGT AATGAAGTTT GTCAGTTTCA 15780
AGCCTGTAAT AAGGTACTGA CTTAAATTA ATTTTCTAAT AATACAGTAC TGCTATGTAT 15840
CTAATGTGGG GTTAGTCAAT GATAGGAAAA AAACATAAGA CAGAGTCACA TTTAAAAATG 15900
TGTGCTTAGG TGCATGGTGA CACCTGCCTG TAGTCCAGCT ATTCCAGGGG CTGAGGCAGG 15960
AAGATCCCTT GAGCTCACGA GTTTGAGGCT GCAGTAAGCC ACTGCACTCA GCCTGGGCAA 16020
CAGAGTGAGA CCCTGTCTCT AAAAAAATT CGTTTAAAGT GTGCTCAGGA CATAACAGGA 16080
GCCGCTGGTA ACATGCCATT TCCACTGTGA ATATGGTAAG GACAGAATCC CTGTCTCTAG 16140
GCCCTCTTCC ACTAGTCAAT CTCATCATCA CCATCAAGGC CAACATTGGT ATTCTCTCCT 16200
CTGAGACAAA GTCTTTGACA TTTTCTATAC TATACTATGT CTTCCCTCTCC CCAAATGCAT 16260
ATACAAATAA AATTTGAATG CTTCTTCTC CATTTAGTGT AATTTTTTTT ATAACATAGA 16320
CCCAATTTTC AAACCCCAACA ATGGTGGATT TTATTTGATG TATTGTAAAA AGCGCTGGAT 16380
TGAAGTCAAA TGGCTTGGGA GACCTAAATT CTA CTCTCTGC CTGTACCATG AAAGAGACAA 16440
ATCCCAAGGC TTTGCAGGGC TTCAGCTTCC TTGTTTGTAG AATAAAGAAT TATAAAATCA 16500
TCTCTTTTGG TCCTACTGGG CAATAAAAAAG CTATGATTCT AAGCCTGTTC CTTTTTCTCA 16560
CCTAAGAATA CAAATTTGAT ACAAAGAGGC CGCAGAATGT GTCAAACACT CCCTGTTGCC 16620
TGGAATTCTC TCTTCCTTTG GGTTCAAGGA TAAAGGTATG TTATTTCTTA AGTCTCCCTT 16680
TGCTTTCTTC TGCTTGCTC GTAAATATT TTCCATCTTG GCAGTCCTAC ATGTCTTCTC 16740
ACTCTACATG TTTTCCCTAG GTGATGTGAC CCAGCCTGTG GCTTCCACTG CCATCCACAC 16800
ACGTCGCTGC CTCTCTCCAC ATCAGCATCG CAACTATCTC CTGGAAGCTT TCCAAGTGCT 16860
GAACTACAGT AACCTCAACC GAACTGCTGT TCATTACCCC CACAGGCTTG CCCCTCCTCT 16920
GCATCTTTGT GAGAACCCTGA GAGTCATCCT AAACCTCTCC TTCCACCTCA CTCCCCACAT 16980
CAAATCGATT ACCAACTTGT GCTGATTTTA TCTTCAAATA CTCTCCAGAA TTGTGCTGT 17040
CATGGACTGA ATATTTGTGT TCCCCCAAAT TCATATGTCC TAATCCCTGA TGTGACTGTA 17100
TTTAGAGACG TGACCTCTAA GGAGTAATTA AGGTTCAAGT AGGTCAAAGG TGGAGCCCTG 17160
ATCTGATAGG ATCAGTGTCC TTATAAGAAG AACTAGAGC TGGGCACAGG GGCTCACACC 17220
TGTAATCCCA GTATTTTGGG AGGCTGAGGT GGGAAGATCA CTCAAGGAGA GGAGTCTGAG 17280
ACCAGCCTGG GCAACAGAGT GAGACTCCAT CTCTACAAGA AAATAAAATA GTCAGACACA 17340
GTGGTACACA CCTGTGGTCC CAGCTCCTCA GGAGGCTGAG GCAGGAGGAT GGCTTGAGCC 17400
CAGGAATTTG AGGCTGCAGC AAGCTATGAT CACACCTCTG CACTCCAGCC TGGGTGACAG 17460
CATGAGACCC AGTCTCTTTA AAAAAAAAAA AAAAAAAGGC CATATATAGC CCAGAAGAGC 17520
GTCCTCACCA AAACCCAATC CTGATAGCAC CTGGAGGACT TCCAGCCTCC AGAGCTGTGA 17580
GAAAATTTCT GTTGCTTGCA CCGCCAGTC TGTGGTATTT TGCTGTGGCA GCCCAAGCTG 17640
ACTCATCAGT GACCTTCTCT CTGTTACCGC AGAGTAGCTC ATCATCCTCT CTTCCCTAGA 17700
GTCCAGCCAC TCTCTACAT CTACCTACCT AGCAGTATCA CTGTGGGTTA GAGTCAGATC 17760
ACTGCGGATT AAGTCCTCAT TCTGCCACTG CCTGTGTAAT TCTGAGCAAG TTA CTTAATC 17820
TCTCTGTGTG TCAGTAACCT CCCTGTGAAA TGAGGCTAAT AATAGCAGGG TTGTTTCAAC 17880
AAGGCGATAC ATGCATAATG CTTACAACAC AGCTTGGCAC ATTATAAGCA TTCAACGAAA 17940
AGTGAGCTAC TATTATCTCA TCCGTTATCA GAATAAACCA CCTAAGCCAC AAGGCTGCCC 18000
ACATCATCCT CATGTTTTAA AACACTTCAG TGGGCTCCCC ACCATCAACA GGATAAAGTC 18060
CAAGCTTCCT TAGCATTTCT TAGAGGCTCC ATATGAATCC CCAAGTTCCA CTACAGGAAC 18120
ACAGGTGAAC TTTCCACTCC AACCTCAGGC TCCTTCGTGT CACTCCTCAT CCACATGGAG 18180
GTAAGCAGCA AGAGACTCCG TGCAGTTCCT GGTGGTTCCC TGACCCTCAG GCAGACTCTC 18240
CCCAGCCCTC TGCCTGCAAC GTCCTTGCCC TTTGCTTCCC TTGGCCAGCT CCCATTCAAT 18300

FIG. 6.7

CTCCTTGATT CTGCTTGGAA GTTCCCTCT CAGGAAGGCT TTATGAACCT TAGTGTAGGT 18360
TATGAACCCA TCTTTGCTCC TTTCATACCT TTTGCAAGCC TTTATTTATT ATGACACTTA 18420
ACCATTATCA TACTGAAGTG ACCTGTTGGT GTGTCTTTGT TCCCCACTAG ACAGAAAACCT 18480
CAAGATCAGA GACCAGTTCT TGTTCTTTT TTTTTTTTTT TTTTTTTTTT TTGTATCACA 18540
GTGTTTAGCA GCCTGCTATA TGGTAAATGT CAGTAAATGT TCCACAACT GAATGGAATT 18600
GAGCTCTGGA ATCTAGACCA TCTTTTCCAT ACCCATCACT CCTGTCTTAG TTGAAGTCCT 18660
TATTTCCCAT TTGAAGCAAT GCAAAGGATT TCCTAÂCTCT AATCTCTCTT TTCTTCACAC 18720
CATCCTTTAA ACAGCCGACA GAATGGTCAT CCTAAAGCAC ATATATCCTA TCTTACATAT 18780
CCTAGATTCTG GAACCTCTCT GGGCTTCTCA CCATATAAGA AGAAAGTCTA ACCTCCTTAG 18840
CAAGGTGCAT AGGTCTTCAA TGGGCTCCAC CTCACCTCTC TATATATACC TATACTCTTG 18900
CTACACTAAA CTTCTTTCTT ACTGTTGCTG GAACAAGTTC AACGCTTTC AACCTCCCTG 18960
ACTTTGCATA TGCAGTTCAT TCTGTCAGGA ATGCCCTTCT CTCTTATGCC TGGGATATTC 19020
TCATTCATTC CATATGACCT ATTCATAAG TCACTCCTTA ATGAAGCCTT TCTTAGATAT 19080
CCACTGGGGC AATCAGCTGC TTGCTCCTGT TTCCACAGCA CATTGTTTAC ACAGATAGCA 19140
CAGGACTTAC CACAAGTTAT TATAATTTTG TCTGTCTTGC CCATTGGAAT CCAAGGGCAA 19200
GGACGGAATC ATTCTCATCT TTGTATGTCC TGGGAACTAG AACTGTACCT GAGACATAAT 19260
AAACACTTGA TATGTTTGTA ATTTTAAAT AAGTTAATGA ACGGAATGGC TAGAAAAAGT 19320
GAGAAGAAAC TCTGGCTTAC TGTATATCAT ACTGTCATAC TAAAAATATA TACTGAAGAC 19380
AGAATCACAT TATATCATCA CTTTTCACGC TATAGGCCAT GATCCATTAT GAAAAAGAGG 19440
ATAGTAAAAA AATCACAGGG CACAATTTT GTTCTGTCA CACACATGTG TACCTGTATA 19500
TTGGACTGGA ATGTAAAACG CATGTTCCAT TGAGAACTG GTTTTAAAA GAGGCTTGGA 19560
AAACACTGCA TATGGTCATT TCTAGTTTA GTACAATTTA TTATTTTCGT AATAACCTCA 19620
GCTATAATAT AAGTCTACCA TGAAGCATTT TGGGGAGATT AAATGAGATG TGAAAAGTAA 19680
ATGTGTTAGA TAGACTGAAT TCATATCATA GCTTGCTCTG ATACTTTACA AAACATTTAA 19740
CCTTACCCAC AAGTTTTAGT TTCTCACTA AAGTCACCCT GAGGACAGTA ATGGGATCTT 19800
CCTCACAGAG TATTGTGAGG AATACATAAG AGAACGTACG TAAATGCCTG GCACTTAGTA 19860
TTTATTCAT AAATCTTAGC AATGATGATG ATAACAACAT GGTACCTGGC ACATAAGAGA 19920
GTAAAAAATT AGTTTCTTCA GTCAAATGTG CTTACATTGA TAGTTGATAC TAACTGGGGT 19980
TAAAAGGTCA TTGCTGGCAT CTCAGAAAGA TAGATTACAG TGAAATAAAA AATGACTACT 20040
GCTTAAATG AATGAAGACT TATTACAAA GTCATGTTCA TCTGGTACAA TAATGAAGTC 20100
GCTCAATTGG GAGAAAATGA CAAATAATAC AAGTGAATAT ACAATCTTAC TTAAGACGAA 20160
AGAAATAGGA CACCAGGCTA ACTATCAGTC TCCTAAACCA CAACTTTATT TCTGATACAA 20220
AGAGACAGTG AGACAATCAG GGCTTCCCTC AAATAAATTA CTTAATCTCT CTTCAATTCA 20280
GTTTTGCATC TGTAATATA AATACTACA ATTTACAGT ATTTCCATT AAAAAGTTCT 20340
AGTGCAACAT CAGAAACAAG AACTTAGTAG GTGTTCAAAA AGAAATATAA GTTCTGCTTT 20400
GTTAGCCAGC AAATAGTTGC CTGTTTCTAG CCCTCACTTC TTTTCTCCTA AATCCCTATA 20460
TTGCATTTAT TTAACCTAAA GTGCTGGATG TGGCACTACG AGAAAGAAAA AGATATTGG 20520
TAATCTTGTT AAAATCATT GACATCCCAG GCTATCTGGA ATCACCTTGG GCTCACAGTT 20580
AGACATCAGC TATGGCTTGT TTTATTTAAA AATTCATCCA CTGATGCATG ATAATGGAAT 20640
TCACAGGAGA GCAATTTACC AAAAAAAGA AATTTATTGA TTTATAATGT GAGATATTA 20700
TTTAGCCACA AATATTTATT GAGCATCTCC TACATGCCAG GGAATGGACT ATATATGGCA 20760
GGAAAAACAGA TACCAATCAT TTATATCAGG CATTTTTTTC TAATAGAAGG ATATTCGCAG 20820
GAGACAATGC ATAGCACCAT GCCTTGACG TAACAGACAT TTAATACTA TTAGTTGAAT 20880
AAAAATTGGAG ACTAGAATGA TACATAAAGA GGCAAGAAAG AGCAAAGATA AGCCTTTCTG 20940

FIG. 6.8

AGAATTTCTA TCATGTTTTG CTCAATAGCT TGTCTTTATC CACTGCTTGT ATTTTTCCAT 21000
GTAGCTAATC CTCATTGGTC GTTAGAATTG AGACACCCTT TCCTTGAAAT CAGGAGCTAT 21060
AGGAGGCCAT TCTTCCTACT GGGCATTTC TTTCTGGGAC AGGGTCTCAC TCTGTCACCT 21120
AGGCTGGAGT GCATCATAGC TCACTATAAC CTTGAAGTCC TGGGCTCAAG GAATCCTCTT 21180
GCCAAAGAGG TGGGATTACA GGCATGAGTC ACCATGCCAG CCTATTGGC ATTTCTACTG 21240
TAGACAAAGC AGACTTACAG CAGTAGGTCT ACCTGCCTAA TACAAAAGA AAAAAAGAA 21300
TTTTAACAAA CAAATGAGGG AATCAGATCC AGAAAGTGAT TCTTATAACT TAGATTACTT 21360
AGAGTAGATC TATAATCTGC TCTAGATCCA CTGCATACAG TGGGCCCTTC TTATCATATT 21420
CCATAAATAG CACTTTTCTC AGCCCAGCTT TTGATGATAG CTGAACAGAC TAACAGTTTG 21480
TCTAACAAAG GCTAGAGAAG GGGATAGCAA ATAATGGCCC ACAGGCTGAA TCCTGCCTGC 21540
TGCTCATTTT TGCAAAGTTT TATTAGAATA CGGTCATTTC CACTCATTTT CACACTGTCA 21600
ATGGCTGCTT TTGCGCTACA GCAGCAGAGC TGGGTGGTTG GGGCAGGGGT CACATGGCTA 21660
ACAAAGACTA AAATACTTAT CATCTGACCT TTTACAGAAA GTTTGCTGAT CCTTGGAGTG 21720
TACAAGTATT CTATATTGTT GATTAAGAAC AGAACCACAA GTATTAGAAG TTAGACCAGC 21780
AGGTGGTAAA GCTGATCATC TACTAATATA ATGGAATTG GGGTCCCAA TCAGGACTCT 21840
TGCTTTGATA GAAGGCCATC TTAACGAGGA GGGAGACACC TGCAGGCAAA GTCAGAATTT 21900
TCTGCAGGAA AAGTTTTGAG TCCATTTCCC CTTGTGAACA AGTGCTCAGC TATGCATTTC 21960
ATCTTTAGTA ACCATGCTTC TATACCTGGT TCTCCTGGC AAAGATTCTT TTCTTCAGTA 22020
AGTCTCAAGA CTTTCTGGGA AGGTAGGGAG ATATGGGGGT AAAAGTGTC CAGGACTTAC 22080
TGAAGGAAGT GTTTTATGAT TATCTGATAG AATCACTGTA TCATGGTAGA GAAGGCCAAAC 22140
AGAATATAAT CTGAAAATAG AGGTGAGGGT GAACAAATGG GCACTAAAAG TGAATCAGC 22200
ATCAGGAAGG TAGCAAAACA AGACATCAGT CAAAGATATG GGGTGATTCA GACCTAAGGA 22260
AGATTTAATG TGGGATGTTT CCGTGTGCCA GGAGCTGGAC ACTTAAGCAA GAGGAGATCC 22320
AGGAATGTTG CTAAAACCAT GGCCTCCATA CTTTATTGGA ATTAGCACAA CTTATCCTTG 22380
TTTCTTTCAT TTTGCAATCA AAATCTTTAA AAACACATTA TTTAAAAATA CATTATTTTA 22440
AAAGCTAGAA TGAAAATTAT GATATCATTT AGGTGGTTTA AAAACATCC ACCAGCCGGG 22500
CGTGGTGGCT CATGCCTGTA ATCCCAGCAC TTTGGGAGTC CGAGGCGGGC AGATCACGAG 22560
GTCAGGAGAT TGAGACCATC CTGGCTGACA CGGTGAAACC CCGTCTCCAC TAAAAATACA 22620
AAAAATTAAC CGGGCGTGGT GCGGGGTGCC TGTGGTCCCA GCTACTCGGG AGGCTGAGGC 22680
CGGAGAATGG CATGAACCCG GGAGGTGGAG GTTGCAGTGA GCTGAGATCG TGCCACTGCA 22740
CTCCAGCCTG GGTGACAGAG CAAGACTCCA TCTAAAAAAA AAAACAAAA ACCATCCACC 22800
AAAAATGGAA GAAGTGATGA AAAATTACAG TCCAAGAAGA AGGGCCATAG CTGTTTAAAT 22860
CAATTGGTAT ATTTGTTATC TAATATAACC CCACGTAACG ACAGGTATTT AACAAATGTT 22920
TCTGCTGAAT TTGACGATTG CATTTCCTT ACATCCCATG TGAATCCAT CAGCACCCCA 22980
CATCCAACCC ATCAGTACAT CCTGTCAGCA TTGGCTCCCA AATATAACCT AAATCTAACA 23040
CATATCCTAC TATCTCTGCT GCTACAACCT TAGTCTGAAA TCTCATAATC TCCCCTTGT 23100
ACTACTGTAG ATGACTCTGA ATGAGTCTTC TTGCTTCCAT TCCACACAGC ATCCATACTG 23160
ATCTATTTTT TTTTCAATT TTTGTAGAG ACGGGGTCTT GCCATGTTGC CCAGGCTGGT 23220
CTTGAACCTC TGGCTTCAAG GGATCCTCCC ACCTCAACCT CCCAAAGTGA TAGGATTTCA 23280
AGTATGAGCC ACTGTGCCTA ACCCTGACTG ATCTTTCTAA GCATAAATCT AATAATGCCC 23340
CTTCCTTGAT TAAACCCTTC AATGAATTCA CATTAGCAA ACAACCTGGC CAGGTGTGAT 23400
GGTTCATGCC TGTAATCTCA GCACTTTGGG AGACCAAGAT GGGAGGATCA CTTGAGGCCA 23460
GGAGCTCAAC ATCAGCTTAG ACAACATGGT GAACTACAT CTCTACAAAA AATACAAGAA 23520
TTAGCTGGGC ATGGTGGTGC ACCTATAGTC CCAGCTACTC GGGCGGCTGA GCTGGGAGGA 23580

FIG. 6.9

TCACCTGAGC CCTGGAGGTC AAGGCAGCAG TGAGCTGTGA TTATGCCACT ACACTTCAGC 23640
CTGGATGAAG TGAGACCTGG TCTCCAAAAA AAAAAAAAAA AAAAAAAGA AGCAGGGCAA 23700
GGTGGCTCAC ACCTGTAATC CCATCACTTT GGGAGGCCAA GGCAGGCCTC CTGGATCATG 23760
AGGTCAAGAG ATCGAGACCA TCCTGGCCAA CATGGTGAAA CCCCATCTCT ACTAAAAATA 23820
CAAAAATTAG CTGGGCATGG TGGCATGCAC CTGTAGTCTC AGGTACTTGG GAGGCTGAGG 23880
CAGGAGAATT GCTTGAACCC GGGAGGCGAA GGTTGCAGTG AGCCAAGATT GCCTGGTGAC 23940
AGAGCGAGCG AGACTCTGTC TCAAAAAAAAAA AAAAAAAG AAAGAAAGAA AGAAAGAAAG 24000
AAAGAAGAAA TCCTTAGTCC TGTCTTAAT ACTTGAGAGG CTGAGGGAGG AGGATCACTT 24060
GAACCTAGGA ATTTGAGGCT CCAGTGAGCT ATGACAGCAC CACGGTGCTC TGGTCTGGAG 24120
AGAGTGAGAC CTTGTCTCTA AAGAAGAGAA AAGAAAAGAA TGAATGAATG AACAAAAAGA 24180
AAGAAGGAAA GGAAAAGAAG AGAGAGAGAG AGAGAGGAAG AAAGGAAGGA AGGAAACAAA 24240
ATAAAATAAA ATAATAATA AATAAACCCA AATCCAACTT CTTTACCCTA ATCAACAAGG 24300
CTCAAATAAT CTCATGCCAA CTAAGTCTCT GAACAGCTCC TTCCATTCTA TTGCCAGATT 24360
ACTCCATCTT TCAGCCACAA GACCTTTTTA TCTTCTTTT ACCAGCCAAA CACAATCCTA 24420
CCTCAGAACA TGTGCACTTT TTCTTTTCTC TGACTTGAAT CTCCTCCACC CATTATATAA 24480
TCTTAGCTCA AAGAGGCTTT TCTTGACAAC TTAGCGAAAG TATTTATCCC AGTCATTCTC 24540
TGCTACATTA TTCCAATTTA TTTTCTCCAT AGTACATTTT AGCACATAAA GATTTCCTTA 24600
GTATGTGCTT GTTGCCCTTC CCCAACCTCC TAAATGTCA GCATTCCCTG AGGGCAGAGA 24660
CTGTTTCATT CCTGTATCAT CAGCACCTAA GACAGTTCCT GGAACATACC AAGTACTTAA 24720
TAAAAATTTG TTTATTGACT AGCTATGACA CATTTTACTT ATATAATTTT ATTTTCTCAG 24780
CAAAATGAAC ACTTTGAAAT GTAATTAATT ACTGATTTTT GCAGTATTTT CTAATTATTT 24840
AAATAAAATA TTTACTATTT TGGTCAACCA GAATTCCTTAC ATTGTTTTAG CACCCAGATA 24900
GCTTCTAAAA ATGCTTACAA TTAACACAAT TTTATCTAGC AATATGTATT TATCACTAGA 24960
CAGAATGCAC TGAACCTTC TTCATTAATA AAAAGCAATC CAGGCTGGGT GCAGTGGTTC 25020
ACGCCTGTAA TCCTAGCATA GTGGAAGGCC GAGGAGGGAG GATCACTTGA TACCAGGAAT 25080
TCGAGACCAG CCTGGCCAAC ATGGCAAAAC CCCATCTCTA TAAAAACAC AAAAATTAGC 25140
TGGGTATAAT AGCAGACATC TATAGTCCCA GCTACTCAGG AGGCTGAGAG GTGGGAGGAC 25200
TGCTTGACCC CAGGAGATTG AGGTTGCAGT GAGCCGTGAT TGTGTCACTG CACTCCAGCC 25260
TGGGCTACAG AATGATACCT CATCTAAAAA AAAAAAAAAA TTAGCCAGGC ATGGTGGCAT 25320
GCACCTGTAG TCCCAGCTAC TCAGGAGGCT AAGGTGGGAG GGTACCTGA GCCTGGAAGG 25380
TAGAGACTGC AGTGAGCCCT GGGTAGCCCG CGCCACTGCA CTCCAGCCCT GAGTGACAGA 25440
GACCCAGTTT CAAAAAACA CAAAAACAG AAAACAAAAC AAACAAACAA AAAAACCCAA 25500
TGCATTGCTG AAATGTTAAA TCCATTATAA AGAAAAGTAC AGGGGTGGGC ATGGTGGTTC 25560
ATGCTTGTA TCCCAGCACT TTGGGAGGCC AAGGTGGGCA GATCACTTAA GGTCAGGAAT 25620
TCAAGAACAG CCTGGCTAAC ACAGTGAAAA ATGCAAAATA CAAAATAAGC CGGGAGTGGT 25680
GGCGCATGCC TGTAATCCCA GCTACTCGGG AGGCTGAGGG GGGAGAATCG CTTGAACCTG 25740
GGAGGTGGAG GTTGCAGTCA GCCAAGATCG AACTCCAGCC TGGGTAACAG AGACTCCATC 25800
TCAAAAAAAAAA AAAGTAAAAA GTATATAGTT GATTCTGCAG GGACTTAAAA AAGTATAAAT 25860
ATCTTTTTTA ACATCACAAA GCTCTGATAT CTGCAGGTTT ATGACTAACT ACTAGCTCAC 25920
TCCCATGAAT ACACGTATGT AAACAGGCTC TATACAATCT ACAATCCCAG ACTAAGGGGA 25980
AAAAACTGTC CTGTCACTGT GGTCTCCAAC CCTTGGCCCA TTTCTTTCCT CTTGACCACA 26040
AAACTTCTCA GGAGTTGCTT GTTTCCTCTT GATCCACTTA TCTTAGCCC ACTCCAATCT 26100
GGCATCGGTT CTCAGTACTC TCCACTAAAA CTGCTTTTAT GAAGGCCATC AATGACGTTT 26160
ATGCTGCCAA ATCCAGCAGA CACCTCCTGT TTTCTAATTT TTTTATTGT TATTTTTTAA 26220

FIG. 6.10

GAGACTGGGT CTTGCTCTGT CACCCAGGCT GGAATGCAGT GATGCCATCA TAGCTCACTG 26280
CAGCCTTAAC CTCCTGAGT TCAAGAGATC CTTCTACCTC AGCTGGGACT ACAGGCATGC 26340
ACAGCTATGC CTGGCTAATT ACTCAATCTT TAACATAGCT GATAATTCCC TCCTTGAAAC 26400
ACTCTCAACT TTTAAGAAAC CCTGTTATTT TCCTCCTACA TTTTATAGCCA GTTCTTCTAT 26460
CAGCTTCTCC TTATCTGACC TCTAAATGTT AAGAACATTA ACAAAGACTG AACCTAGTTT 26520
TTTTCTCCCC TTAGTGTACT GCTCCTGGGC GATGTCAATC AGTCCATTG CTTTAGATAC 26580
TATCTGTTGA AACACTGAAA TCACTGGTTT TTTTGTGTTT TTTTTTTTTT TTTTTTTTTT 26640
TTGAGATGGA GTTTCGCTCT GTTGCCCAGG CTGGAGTGCA GTGGTGCAAT CTCGGCTCAC 26700
TGCAAGTTCC ACCTCCTGGG CTCAAGCAAT TTTCTGCCT CAGTCTCCCG AGTACTGGGA 26760
TTACAGGTGT GTGCCACCAT ACCCAGCTAA TTTTCTATT TTAGTAGAGA TGGGGTTTCA 26820
CCATGTGTCC AGGCTGGTCT TAAACTCCTG ACCTCAGGTG ATCTGCCAC CTTGGCCTCC 26880
CAAAGTTGG GAAAAGATAT CCCAATCTT TTCCTATGAT TTCTTAATTG ATCTACTTGA 26940
CATATCCACT TGGACTTTTA ATAGGCATCT CAACTTAAT GTGTTCAAAA TAAACCTCGT 27000
GACTTTCCT CCCAACCTG TCCCTACCTC CCTCAATAAC TAATATTATC ATTCTTATAT 27060
TCATATATTG AATAAATGTT TGTCCCCCA AGTATTTGTT GCTATAAATT TATGAAGAAT 27120
TCTTTTCTCA CTAGTTATTA TAATTAAAT GTAATATTTA TTTTCTTAA AAACCTTACT 27180
TTGTAGGATT ATTATTTTTT AACACGGGAC CAACAATAAA TAACTTCTCT ACTTGATTAA 27240
AACTAGGGCT TCCTCTGTG CTCCCTCAGG ACTATTTCTT TGTA AAAACA ATAGGCTAAA 27300
TCAGTACTGG TGTC AAAGAA ATCATAATCT CACAACCTTA TAAATACAGC ATGTGGCAAG 27360
GGATTTTCCC ATCTTATATA GTAATAAAAT TTTCAGCTGT GCCATGGCTA AAAGTTTACC 27420
ATCAAAGTTG GAATTTTAAA TTAGAGGTAG TCATCTTTCT TTCTTTTAA AGAAATGGAG 27480
TCTCACTATG TTGCCAGGC TGGAGTGAG TGGCTATTTG CAGGCATGAC CACAGCACGC 27540
TACAGCATCC TGGCCTCAAG CAATTCTCCT GCCTCAGCTT GCCAAGTAGC TGGGACTACA 27600
GGTCCCTGCC ACCACACCCA GCAGAAATAT TTAGCTTTCT GAATTTCTCA AGTGTGTGTA 27660
TGAATGAGAC TAGTGGGGTC CTTAACCAAG ATTCACAGGA TTTTATAGTA TTTATTAAT 27720
AACTTGGATT TGTATCTACC AGCATGTTCT TTGAGGTACA GGTATGTCTT TTATATCTCC 27780
TAATATAGTT CATTACAATG CTAAATACTA AGATGTGATG CTCACACACT ACAGAATAGC 27840
CAAGCAAATG AACTACTTAT TCTCATAGGG CTATTATAAT TAACAAATTC TTGTATCACC 27900
CCATCATTAT CAACAACAAC ATGATAGGAT TTCCTTTTAT CTTGAAGAGT CTGGAAAAAG 27960
GGTAACAGAG AGATATTTCT GAGGAACAAA CTGGTAATGA GGGAGCTACT GTGTCCATTA 28020
CAATACTCCT TCTAGAAGCT CAATACATAA TGAATAATCT CTGGAAAAAA GCAAGTGTGA 28080
GAATGGAAGG CTCTTCTTCA AACTATGCAA AATGAATCAA TCAGCAGTGA ACAAATTTAT 28140
GAGCCAAACA AATTCCTACA AAAATTACCA TCATATGCTG TCATGCATGT CTGCCAGTCT 28200
ATTTATCATA TTATTTAAGA AACAAACATT TATTGAAGAT TTATCATGTG CTCAGCACTG 28260
CCAAAGAGGA AATAAAGAGC ATAATATCTA TTCTTAGAAA ATAACATTAA CACAAATAGA 28320
AAACAAGAAA CCATAATGTT AAAAATATTA CATAGTAACA CAGAAAGACA ATGTATAATT 28380
ATACATACGC ACTAAAGCAA AGATAACATA ATTTATAAAT TATGAGGTAC AGAATAGTTA 28440
GATTCTGAAA ATTAAATAA TCAGGAAAAA CTTTCATGAAG ATGAGATCTG GGCTGGATCC 28500
CAAAGGATAG GCAGGTGGAT CATGTAGAAC AGGGGAAAGG AGTTCCTGAT CGGGGATACA 28560
ATATATGTAA AAACCTGGAG ACAGGACTGA GCGTGAATG TTAATGGGAC AGTAAAGAAA 28620
TCTTCTCTG CAGCGGGGGA AAAACAGAA TAATGGGAAA CTGCATGGTT AAAAGGTTTG 28680
ATGTTAAGAT AGTGCTTGG CACAAAAGAT CTAAAGTTG AGTCAAAAGA GTACAATGAA 28740
AGCATTAGAA ATAGAAGATA AAACACAATT AGGCCGGGTG CAGCGGCTCA TGCCTGTAAT 28800
CCCAGCACTT TGGGAGGCCA AGGTGGGTAG ATCACTTGAG GTCAAGAGTT TGAGACCAGC 28860

FIG. 6.11

CTGGCCAACA TGGTGAAACC CCGTCTCTAC TAAAAATACA GAAATTAGCC GTGAATGATG 28920
GCTCGTGCCT GTAGTCCCAG CTATTTGGGA GGCTGAGGCA GGAGACTCGC TTGAATCTGG 28980
GAGGCGGAGG TTGCAGTGAG CCGACATCGC GCCACTGCAC TCCAGCCTGG GTGACAGAGC 29040
AAGCCTCTGT TAAAAAAAAA ACGGTAAAAA TAAATAACAT TTAATTTGT TTTCTGATGA 29100
TATATATGGC CTCTAATTGT AAAGCTGAAT GCCTAGTTTA CCACTTTTTT TTTTTTTTTG 29160
AGACGGAGTC TTGCTCTTGT TGCCCAGGCT GGAGGGCAAT GGCACGATCT TGGCTCACCA 29220
CAACCTCTGT CTCCCAGGTT TAAGCGATT C TCCAGCCTCA GCCTCCCGAG TAGCTGGGAT 29280
TACAGGCATG TGCCATCATG CTCAGCTAAT TTTGTATTTT TAGTAGAGAT GGGGTTTCTC 29340
CATGTTGGTC AGGCTGGTCT CAAACTCCCA ACCTCAGGTG ATCCACCCGC CTCAGCCTCC 29400
CAAAGGGCTG GGATTACAGG CGTGAACCAC CGCGCCCGGC CTATCATTCT TATTTTATGC 29460
ATTAGGAAAC TAAGGCTCAA CAAGATTAAG GCTGTCTAGG GTCACAAAGA TTGTAAGTGG 29520
AGGGGCTAGA ATTCAAAATG AGACCTGCTT GACTCCTAAG CCTGTACCAT TTCTACTATA 29580
TTTAGAGTGA AGTAGATGGG TTGAAGAAAT ATTTAGGAGG TGAAATTTCA AAAGTGATCA 29640
GTCAGAAGAG AAGACATATA TGGAAACCTA AATTTTCACA CAGTAAAGTG TCAATAATAA 29700
AGGCATAATG CCAAAATGAC AGAGGCTGTG CATGGTGGCT CATGCCTGTA ATCCCAGCAC 29760
TCTGGGAGGC TGAGGCAGGA AGATCACTTG AGCCAGGAG TTTGACACCA ACCTGGCCAA 29820
CACAGCGAAA CCCCATCTCT ACTAAAAATA CAAAAATTA GCTGGTAATG GTGGTACACA 29880
CCTGTAATCC CAGCTACTCA GGAGGCTGAG GCATTAGAGT CACTTGAACC TGGGAGGCAG 29940
AGGTTGCCAT GAGCCAAGAT TGTGCCACTG CACTCTAGCC TGGGCAACAG AGTGAGACTC 30000
TGCTCAAAA AAAAAAAAAAG GAAGACTCGA GGGCTAGAAC CCTGAAATTG GGAATGAACA 30060
GGACTGGCTG AAAATGTTTC TTGCACCTGA TAAAAATCTT GAAGAAGAAT GCTTTAAATA 30120
GATAAGAAAG GAGAGAGAGA GGTGGGCAGT GAGAGGAGAC CACCCTAAGT AATCAGAGAT 30180
TACTTACGTT GGTTACTCAG GCTGGTCTCT GAATCTGATT ATAAATGAAA TAGAGATTAC 30240
TTAAACAAA GGGCTGTAAG GTAGCACTGT CCAGCAGCAC TTTCTATGAT GGAAATCTTC 30300
TATATCTGCA CTGTCCAATA AGGTGTAGCT GCTAGCACAT GTGGCCACTG AGTACTTAGA 30360
ATATAGCTAC GACAACCGAG AGGCTGAATT TTAATTTTAA TTTAATGAAT TCAAACAAAT 30420
TTATTTTAA TACAGCACTT TAAATTTTAT TTTTAAATTT TAATCTATTA TTTATTTAGA 30480
GACTGGGTTA TGAGACTGGC TAATTTTTGT ATTTTGGTA GAGACGGCGT TTCACCATGT 30540
TGCCCAAGTT AGTCTCAAAC TCCCGGGCTC AAGTGATCCA CCTGCCTTGG CCTCCCCGCA 30600
AAGTGCTGAG AATACAGGTG TGAGTCACCA CGCCCGGCCT AAATTTAAAT TTAAATAGCC 30660
ACGTGCGGGT AGTGGCTACC ATACTGCACA TGCAACTGTA AGATGTAGAA GTCAGATGTG 30720
AGCAAAGAAA TGACAAGCCG TTCAATGCTG TTAGAGAAAT AAATTCAAGG TTCCAATGAT 30780
CTGAACCTGT GTCCCTCAA ATTCGTATGT TGAAATCTTA ATCCTCAATG CAACAGTATT 30840
AAGAATTTGG GGCTTTAGGA GGTAATTTGG TTTTGAGGGT GGAGCCCTCA TGAATAGGAT 30900
GAGCACCTGA GTAGCCTCT TTGACCCTC CACCATGTGA GGACACACCA CGAAGGCACC 30960
ATGTTGGAAG CAGAGAGTGA GCACTCCCAA GACACTGAAT CTGCCACATC TTGATTTTGG 31020
GCTTCTCAGC CTACAGAACT GTGAGCAATA AATATCTGCT GTTTATAAAT TATCCAGTGT 31080
AAAGTATTTT GTTATAGCAG CCTGAATAGA CTAAGACAAA GGTGGACTAA GGCAGGATAA 31140
CAGGTTAGAA AAGGAGGCAG GGCCTTTTTT TTTTTTTTTT TTTTTTTGAG ACAAAGCCTC 31200
ACTCTACCC AGGCTGGAGT GCAATGGCAT GATCTTGGCT CACTGCAACC TCCACCTCCA 31260
GGGTTCAAGC AATTCTCTG TCTCAGCCTC CCAAGTAGCT GGGATTACAG GTGTGCACCA 31320
TCACACCCAG CTAATCTTTT GTATTTTGTAG TAGAGACGGG GTTTCATCTAT GTTGCCAGG 31380
CTAGTCTTGA ACTCTTGACC TTAATGATC CACCCGCTC GGCTCCCAA AGTGCTGGGA 31440
TTACAGGTGT GAACCATCGC GCCTGGCCGA GGCACAGTGT TTTTACAGAG AAGCCTGTTT 31500

FIG. 6.12

AAGGTTTAAT CATATAAAAT GTATGATATC CAGTAAGTTT TGATATAAAA AAGAAACACC 31560
TGGCGATTTT ATATAATATA TTGTGCTAAG GAATTTTAAAG CACTCTACAT TCTGCTCTCT 31620
AAGCTCTGTA AAGAGCACCA GGGATTTTTT TTTTTTTTTT CTTTTTGAAC AGGGTCTTGC 31680
TCTGTCAGCC AGGCTGGAGT GCAGTGGCAC AATCTTGGCT CACTGCAACC TCTGCCTCTC 31740
GGGCTCAGCG ATTCTCCAC CTCAGCCTCC TGAGTGGTTG GGACCACAGG CGCATGCCAC 31800
TACATCTGGC TAATTTTTTG TAGAGATGGG GTTTTGCCAT GTTGCCAGG CTGGTCTTTA 31860
ACTCCTGGGC TCAAGCGATC CTCCCACCTT GGCCTACCAC GCATGCCTGG CCACAACAGG 31920
GATTTTTAAA TGTAAGACTA CCTAGTCAAC TCTTATTCTA TATTAACAAT ATAGACAAGA 31980
AATAACCTCT AAGTAATCTC TATTTCAATT ATAATCAGAT TCAGAGGTTT TCTTATGCTT 32040
TACAATATTG TCCTACTGTG GGTAGCGCAA TAACTAAGGT AATCTGAAAG ACCAGTTATA 32100
TTATATACTA TAGTTAAATG CATTTCAACT GCATGGGAGA AAGCAACTGT GTTCTTTCCCT 32160
CTCAATTTTA ACAGAAGGAA AATTGTCAAA ATTAGCTTAT TTAGAATGTC CTATCAGAGA 32220
ATTATTTTGA TTAATAATATA TTTTAAATCA ATAAATATT TCTCTTGGT CAATACTTGT 32280
CAATATAGAA TAATATCTAG CCACAAAATT AAAAAAAAAA CATTTTCCCC TATATTACAT 32340
TCATGGATCT TCTTGAATTT CTGTTATCTA GGTGCTTTTA AAAGTCATAT TTCTGATAAT 32400
ATGAAATCAC AGCTCCTTTT CTTTGGCATA TTTAGTTACT GTATTAAGAA AATGTACAAC 32460
ACATAATTTA GAATGGGTAA TTATTATATT CTCTTTATTC TTATATTGAA AATGACATGA 32520
AAATTACCAG TCTTCCCAGG TAATATAATT TAAGTTAAAG AACATCTACA TACTACAACC 32580
AATACCCATT CCCCTATGTT ATGTTTGGAA AAACATAGAA GTATCTTTAG TAGTACTCTT 32640
AGAAATTATC CCAGGTTTCT CATATTGGTA TTTTATTTC AGGTTTAAGT TACAGTATTT 32700
TGGGCACCCC AAGTTTAATA AACTATTCCC TGCAGAAACC TGACAAGTGA AGTTGTGGCT 32760
GGGAATATGT TAGTCTTCAG ATAAATGAA TTGTTTAAAG ATTTGCTAAA GATCTCAAAG 32820
CATCTTTCTT AAATCTAAAG AAAGTCAGGA ACAAAGCCAC AACCAGGACC ATAGCATCAG 32880
AAGATGGAAG GTTGCTTTGT CTTCAAACCT AAAAAACATT TTCCATTTTA AAATAATTTT 32940
ACTATTTACC TGTGATACTG TTGAAAATTA TGAAAAACA GATAATTTAA AATTAGTGC 33000
TTTTTTTAA AAAAAAAAAA AAAGCGAATC CCTGGGACAC TTCATATAGT GCAAAACAAC 33060
AATCAAGAA TTCAAGCATT GAAAGAAATA ATCTCTTATC CCCCAGTCTC TGAAAGGGAT 33120
TGCCTTTACT ACTGTTCCCA TCTTTATGTC CATATGTACC TAAGGCTTAT CTCCCCTTA 33180
CAAGTGAGAA ACTATTCAGT ATGGCTTAGT CATTTTAAAT GCAAGAGAAT AGGTAAAAAT 33240
GCCAAGCACC AGCCAGAGTT TTTTCTTTC AGATAGATGT GACTCTTACA GGAGCAGCAG 33300
GGATTTCCCA CTTTGGGCGG AAAGCAGCAT TTAGGTATTC CCCCTCCAGT GCAGTTACAG 33360
ACCACCCCCC CGTAGAAGCT GCTCCTGTCC TCTGTGGCAT GTCAGCCTCT GATTATCTTT 33420
TAATAAACAA TATGGCATAT TAAGTCTCTT TTATGCCCTT CTTTGTATTC CCAGGTACCA 33480
CCTCCATGTC AGGATAACAA GAATTTGGTA ATGTTTGTG AATAAATTTA GCAGAAAGTTG 33540
AAAGAAAAAT CCTGTTTCTA CAGAAAGATA CCACTGGCTT TTGGGGAGCC CGAGTTCATG 33600
ATGAAACTAA AGAAAGCCAC AAAAGTTCAC CTCAATGCCA AGACATTTCT TGATTTTTGA 33660
AAACCCAGTT GTCGAACCAC CCATCTATAG AAAGTTGAAA GACTAAAAAC TATCTTACTC 33720
TAAACATTTT CTAGGAAGTT GATTCTACAA CACATTTTGG TTTTCCAATT TGGCTTCTAA 33780
TAATTATTTT AAAGTTTCTG TGGCCTAAAT TTTGTTTAC ATTGATCCTT TGAATGGACT 33840
ACTGTTTCCA CATTTTAGAA CATTTAAAAA GATATCTACA ACCCGAGTCT AATCATAAAA 33900
AAAATCAGAC AGATCCAAAA TGTGGAACAT TCCACTAAAA AAGGAGTGGG GAGAGGTCTT 33960
TATCTTCCA AAAATATCAA TGCCATAAAA GACAAAGACG GCTATGGAAA TGTTACAGAT 34020
TGAAGGAGAC TAAAGTTAAA TGCAAGAAAG GAAAAATGG CATATAGGAC AGTATTGAAT 34080
TGACTGACAA AACTGGATTA CAATAGTAGA GTATCAATGT TAACTTGCT GAAGTTGCTA 34140

FIG. 6.13

ACTGTATTTT TAGGAATTA TTCACCTAAG AATTTAGGCA CACAGATATG ATGTATGTAA 34200
GTTACCCCTTA AATGGCTTAG AAAAAAATGT GTGTATATTC ATTTACATAC GTATCTACAC 34260
ACACGTGTAT TAGCGGAAGA GAGCAAGGCA CACATGTGCA TAAGTGATAA AGCAAATGAG 34320
ATGAAATCTT TATTTTAAA TTTAATTTTG TAAGTTTCAG CTTTTTAAAA TTTTAGATTCT 34380
CGGGGATACA CGTGCAGTTA TTACTTGGGT ATATTGTGTG AAGCTGAGGT TTGGACCTCT 34440
AATGTTCTCTG TTGCCACAAC AGTGAACACA GTACCCAGCA CGCAGTTTTT CAGCCCTTGC 34500
CCCCCCTC CCGCTCTCCC TCCTTGCTTT TGGAGTTCCT AGTGTCTACT GTTCCCATCT 34560
TTATGTCCAT GTGTACCCAA GACTTATCTC CCACTTACAA GTGAGAGCAT GCAGTATTTA 34620
GTTTTCTTGT TCTGCGTTAG TTCCGTTAGG ATAATTGCCT CCAGTTACAT TCATGTCAC 34680
GCAAAGGATT TGATTTTCACT CTTTTTAATG GCTGTGTAGT ATTCCATGTT GTATAGGTAA 34740
CACATTTTCT TTATCCACTC ATCAATTAAT GGGCACTTAC ATTGATTTCA TGTGTTTGCT 34800
ATTGTGAACG GTGCTGCAAT GAACATCTGA GCGCAGGTGT CTTTCTGGCA GAATGATTTA 34860
TTTTCTGTG GGTATATACC CAGTAATGGG ATTGCTAGCT CAGATAAGTA TTTCTATTTT 34920
TAGTTGCTCT CCACAGGGGT AGAACTAATT TGCATTCCCA CCAACGGCGT GTAAGTGTTT 34980
CCTTTTCTCC ACGGCCTCGC CAACATACGT TCTTTTCTGA TTTTAAATAG TAGCCATTTT 35040
GAACTGGTAA GAGATGGTGT CTCATTGTAG TTTGGCTTTG CATCCAAATG AGACAAAATC 35100
TTAATGACAG GTGAATCTAG GTAAAAGGCA TACAGACGTT CTTTGTGTTG TTTTAAATC 35160
TTACATTTGA AGTTATTTT AAATGAAAAA TAAAGCAAG CAAAAAAGG TCATTCTTCA 35220
TCTAGTAAAC TCTTCAAAGA TTACCACCCC CTTCAACAGT TTTTCTGGT TCTAGTGAGT 35280
CTTCTCCCAT TTGTTTAGAT CTTTGTGTGA ATGTAGTCTC AGATAAAAAA TTGTATTTT 35340
ATTTCTTTTA CATATTTCAA ACAATCTAAA TTCTTTTAA ATGAAACTCA TTAATAATAC 35400
TGCATTTGTT TCTAAATAAA ATGGTAGAGG TAATTGTCAC CTTTCCAAAC AGAAGCAATA 35460
GGAGCAACCC AGATGTTCTA GCCACGATCC AAGTCAACCA CATTCAATCT AAGAAGTAAT 35520
TGAAGGCTGT AACGACTTCT GTAAGGCCTA CAAAAATGAG TTCAGACACA AGCTCTGCTC 35580
AGTAAAAATC TAGTGGCAGA TGATATATAC AATGATCTGA GAAAAAGGCA GAATCAACAA 35640
AGGTTGTATT TTTATCTATT GCTGCGTAGC ATATTTCTT AACTTTAGTA GCTTGAACA 35700
ATAAACATTT ATTATTTTCA AAAGTTTCTG TGGTCAGAAA TCCAGGAGCA GCTTAAGTGG 35760
GTGGATCTGG CTCAGCTGTA GACAAGATGT CGGCTGGGAC GGCCATCCTT TGAGGGCTCT 35820
GAGGGCTTTG AGGGCTGCAC GATCCAATTG CAAGGTGGCT CACTCACATA CTAGGCAAGT 35880
TACTGCTGGG TGCTGGGAGG AGACCTTAGT TTCTTATCAC ATGGACCTCT CCACAGGGCT 35940
GCTGGAATGT CCTCATGACC TTCCCCATAG TGAGTATTCC AAGACAGGAA AGTGGAAGCC 36000
ACAATGTCTT TCATGACCTA GCCTCAAAG TGACATACTG TCATTTACAC AATATTCTAC 36060
TGGCTGTACA AGTTAATCCT ATTTAGTCTG GGAGGGGACT GCATAAGGGC ATGAGTAACA 36120
AGAGGCAAGA ATCCTTGGGG GCCATCTTGG AAGCTGGCTA CACAGAAGAG AAAACACCAG 36180
GGGAGTGCGA AGAAGGTGCA ATTAACTCA ATTCCTTGGT ATGCCAATGG TAAGAAATAT 36240
TAGGTGATCT CTGGGGTGTA ACCTTTTAA TTTAGTTCTT CACTGAATAA TCTGGCCAGT 36300
AATTGTAATA CAAAATACGG CACTCTGACA ATATTCTCTC CCTTTATAAT CAATTACACA 36360
CCAGAATATA TATAAGAAA GACTTACAAA GTCACAAGTA ATTGTTTGGT ATTATTTTAA 36420
TAATCACATA CTAGGGCCCT ACAATTAGCA TTCACAAACA TCACTCCATG TTGGCCAGAT 36480
AAGTCTGTCT TTATAGTGGT TTACCATACG CGCCTTAGCA TGAAGTTACA TGTGGTTTCC 36540
TTAGCCATCA GATGCTCCAA ATGCAAAAAA TGTCTACCA CAGTCACAGA ATCATGGAAT 36600
CCTAAAGTTA CCTGGGGTTT CTGAAAATCT CATGGGAACA ACTCACGAGA ATTAAGGCTT 36660
AAGAAAGTGA TTTATCAAAG AACAAAACCA GCAAGACTTG AGTTTAGAAC TCGCAGCAGA 36720
GTTGTGACTA GAACCTGTTG AAATAGGCAA TGAGAAACC CAGACTAAGG CACATTCTCT 36780

FIG. 6.14

ACAACTTTAC TATGCAAGTA TGCTTAGATA CTCCTTAGCA AACAGCAGGC CTTGAGTAAA 36840
TTCTTTCAGA ACTGAATACA CAAAGGATAC AGAACGGAAT AACTAACAA TAGTGCATGA 36900
TGTGCTCATT TCTGTAATAG AAATGAATTA ATTCTGATCC ATCTATAATT TATTATTGCT 36960
CCATGATTAA CGGAAGGCAT AGGAAAGATG ACTGGAATAG TGTAAGTAGT ACAAACAAGT 37020
ATTACACTTG ACTGAACCTC ATTACACTGC AATTGCATAT TATATAGTAT GTAGGTGAAC 37080
AAATACTGGG TTAGTCAGTG GACCTACATT TGAATACTGG TTCTGCTCCT AGACAGCTGT 37140
ATGATTTGAA TGACTTCTTT ATACTTTTAT AGTTTTCTCTG TTCTTCTCTG TAAACAAAAG 37200
GCTTAGAAGA TATTATGGGT TAGATTATGC CCCTTACAAA AGATGCTGAA GTCCTAAACT 37260
ACAATACCTG TGAATGTGAC TTTATTTGGA AATAGGGTCT TTGCAAGTGA TAAAGAAGAG 37320
GTCATGGAGT GACCTAATCC AATACGACCA GTGTCCTTAT AAAAAAAGG AAATTTGGAT 37380
ACAGATACAC ACAAACAAGG AGAATATCAA ATGAACATGA AGGCAGAGAC CGGGGCGGTA 37440
CATCTACAAG CCAAGGGACA CCAAAGATTT TCAGCAAATC ACCAGAAGTT AGGAAGAGTC 37500
ATGGGACAGG TTCTCACAGT CCTCAGAAGA AACCCACCAT GTCAATACAT CATTTTGGAC 37560
TTCTAGTCTT CAGAACCGTA AGAAAATAAA TTTTGTGTG TCAAGCTACC CAATTTGTGG 37620
TACTTTGTTA CAGCAGTCCT AGCAAATAA TACAAATGAG CTCTTAACAC TGGTCTAAAA 37680
TAGGATAATC CTATGAAATG CTACAAATGT TTGGGAAGAT TTCTCATACT CAACTGTTTA 37740
CAGTATACCA CAAGCCTGTC AGTTGAAGAT ACAAACAGAC CCTCTATAAT CCTCTATACT 37800
TATATGCAAG GAACAGCACA CTTTTCTGC AAAAGGTCAG ATAGTAAACA TTTTAGGCTT 37860
TGTGGGCCAA ACAAGGTTTC TGTTACATTT TTTTTTATA ACTCCTTAA AATGTAAAAA 37920
TCACCCTCAT CCCAACGGAC TACAGGAACA GACCTCAGGT CACATTTGAC TCATAGCCTG 37980
ACCCCTGGTG TGTAGGGTTA ACAAGCCTCC TTTCCCTGGG CTCCTTTTC TTTACAGCATT 38040
CCAAGCCAAA GGAACTATC TTTTCAAAT CATTTTCTCT CCTAGGTGGG ACATCTTACA 38100
CCAGCCCAGG CATGCTTCCG ATAGCCTTAG AGTAGCTGTC CCTTCCTCAG AATTACTGTC 38160
TAATTGGCTA GAAGTTAGCA ACTTTTTACA TTTTCTTC AATTCCTTC CATTAGAAG 38220
AAGGCATGCA CCGGCAAATT ACTTGTGACT ATCAATGACA TACTCTCAGA AGCACCAGTA 38280
CCCCTGTGTT GTTTCTAAAC CCATTCTAAT AGACACATAC CCAAGGTTA TGCTGTTTGT 38340
CATCTACAA AATGACTTAC ATCTAGAGAT TAAATAATT AATGTACTT TCATAACTAC 38400
CAGGTACAGT AGATCTGATA ATGGCAGAGC TAAGCACATA TACAGAAAGT AGGGCAAGGG 38460
CCAGAGACTC ATTTTAAAGC AATGTTACAA GATCGTCACT GTTGCTTTTC ATTTTCTAA 38520
ATGTGGCCAC TGCTGTTTTC TACTAAAGG AAATGTTTGA TGTAAGTGA ATAACAGTAC 38580
CTGGCATAAA ATAAGTGCTC AATAAATGTT AAGGCCTTCT CTCCTCTTC AACTGGCCTC 38640
CTCATTTTTC ACAAAGTGAA ATAGAAAAAC AACATGGAAG ATAATCCTGT TGCTTAGGAA 38700
AAATACTAA AGCTTGCTAG ACAAATACA CCTGAAAATA TAGGAAGTGA GCTATAGCTG 38760
GCCTATATGC ATGTATGTTG GAACAGGACA AGATAGTGTA GGGTGGGGTG AAGAGGACAG 38820
AGAAATGGAA GGAAAGGGC TACAGCCTTG GTGGCAAAAT AAAGGATAAG ACGACTCTT 38880
TAAATGGTC TATTTCAAAT GCTGGGTTGT GAACTTAAT TTGATTACTT CATGAGAAAC 38940
AGCATCTATA ATCCATCCCT GATTTTCTA CAACAAAAAT TTATTATTTA TTTTATGTTT 39000
GTGTGTAGAT CTTTATATA TATACATGTA CACACGTATA TGTATATATT ATATATGCAT 39060
ATGCATATAT ATGTGTATAT ACATATATAA TATATTGTGT GTGTATGTGT GTGTATATAT 39120
AATTTTTTTA AAGGAATGGG GTCTCACTAT GTTGCCAGG CTGGACTTGA ACTCCTGGGC 39180
TCAAGCAATC CTCCACCTCA GCCTCCAAG TAGCAACCAA CAGTTTGTAG TTTGAAAAAA 39240
TAACAAATAT TAAACACCCA TGTGTAAGGG TTGGTACTGG GCCCTGTGTT AGTTTGCATG 39300
GGCTGTCGTA ACGTAACACT ACAGGCCGGG CACAACGGCT CACGCCTGTA ATCCCAGTAC 39360
TTTATGAGGC CAAGGTGGG GATCACCTG AGGTACAGGAG TTTGAGACCA GTCTGACCAA 39420

FIG. 6.15

CATGGAGAAA CCCCGTCTCT ACTAAAAATA CAAAATTAGC CATGTGTGGT GGCTCATGCC 39480
TGTAATCCCA GCTACTTGGG AGACTGAGGC AGGAGAATCG CTTGAACCTG GGAGGCGGAG 39540
GTTGTGATGA GCTGAGATCA GGCCATTGTA CTCCAGCCTG GGCAACAAGA GCAAAACTCT 39600
GTCTCAAAAA CAAAAAACA AAAACAAAAA AACCTTGATA AACTACAGA CTGGGTAGCT 39660
GGACCAACAG AAATTTATTT TCTCACAGTT CTGGAGGCTG GAAATCTAAG ATAAAGTTGT 39720
TGGCTGGTTT GGTTTCTGAG GCCTCTCTCC TTAAGTTGCA GATGGCTGCT TTCTTGAAAT 39780
GTCCTCACAT AGCTGTCCCT CTGTCTGTTT CTGGTGTCTC CCCACGTATC CAAATTCCT 39840
CTTCTTATAA AGATACTAGT CATATTGGAT TAGGGTCCAC CATAAGACC TCATTTAAAC 39900
TTAATCACCT TTTTACGGCC CTGTGTCCAA ATACAGTCAC ATTCCGAGTT CCAGGGGATT 39960
AGGGCTTCAA CCTATGAATT GGGGGTGGGG CACAATTCAG CCCGTAACAG GCCTAGACCT 40020
TAATTTGTCA AACTACAGT TAGATTTATA GTATAGTAAC TGCATCTGTG CTCATCTAAA 40080
TGTCATACCC AAATGAAATA ATATAGCATG ATGATCTGAA TTTATTAAAG GCAATTTTTC 40140
CTATAGAAAC CCAAATCTAT AAATTATATA CAACTGTGG TAAGTTACTC GATACCTTGC 40200
CAGGACTCAT CTATGGTGGT AGATAGACCA CAAAGAGTAC CACTGAAAGA TCCCTTTCCT 40260
AATCACAGTT TCCTCACTGG CTTGCCACAA AACCTAAAAT TCTTCTATTC TTTCAATGGC 40320
AATTTATTTT CCCTGAAAAT GTAAATAATC TCTGGCAGAG CAATCTATTA AGTGATCATC 40380
AGCCACTAAC ACCTTAGGGT AGAACAGCTC AGATCACAGT CTAAAATAA ATTCCATCAG 40440
TATGAAATTT TCTTTATTAC TGCTCCGCTA CTGGAATGTT AGATCACTGT CTGCTTTAAT 40500
AATAATTCTG GTGTAGGTCA TTCAAATTTT GTTTAAGATA ATAAGACAAA TAGCAGGTAT 40560
AAAAACATTC CGTCATCTAA TAAAGCAACC CGAGAACAGT AAGAAGAACG TGATGAAATT 40620
AACATTTTGT AGTACCTGCT AGGAATCAAG TATTCTGCTA GATATTTTAG AAATCATCTC 40680
AATTCATCC TAAAAATTAT TCTGTATAAT AGTATAGGTT GAGTATTCCT AATCCAAAAA 40740
TCTGAAGCTT TTTTTTTCCT GAGACGGAGT TTTGCTCTTG TTGACCAGGC TGGAGTGCAA 40800
TGGCGCAATC CTGACTCACT GCAACCTCCG CCTCCTGGGT TCAAGTGATT AGGGATACTC 40860
AACTGGCTAA ATATAATGCA AATATTTCAA AATCTGAAAA AACCCAAATC TGAAACACTT 40920
CTGGTCCCAA ACATTTTCAGG CAAGGGACAC TCAAGTTGTA TTAATCCCAT TTTACAGAAG 40980
AAGAAACAGG CTCAGATAAA TGAACATCTC AGAGCTTGTT GATAGCAAAG GAGAGATTGA 41040
AACTGTCAGG CCTCTGATCC CAAGCCAAGC CATCACTTCC CCTGTGACTT GCATGTATAC 41100
ATCCAGATGG CCTGAAGTAA CTGAAGATCC ACAAAGAAG TAAAAATAAC CTTAACTAAT 41160
GACATTCTAC CACTGTGATT TGTTTCTGCC CCACCCTCAC TGATCAATGT ACTTTGTAAT 41220
CTCCGCCACC CTTAAGAAGG TTCTTTATAA TTTCCCCCAC CCTAAGAAG GTTCTTTGTA 41280
ATTCTCCCA CCCTTGAGAA TGTAATTTGT GAGATCCACC GCTGCCCGCA AAACATTGCT 41340
CTTAAGTTCA CCACCTATCC CAAAACCTAT AAGAAGTAAT GATAATCCAC CACCCTTGC 41400
TGAATCTCTT TTCTGACTCA GCCCGCCTGC ACCCAGGTGA AATAAATAGC CATGTTGCTC 41460
ACACAAAGCC TGTTTGGTGT CTCTTCACAT GGACACGCAT GAAAGAAACC CTACCTGGTT 41520
CTGTGTCTTA CCTGTTGGGG GCCTGTGGTC AACTACTAG TACGGAGTTT TAGTGCTCTC 41580
ACTTTAAAAA TGAGGGTTGT GGCCGGGCGC GGTGGCTCAC GCCTGTAATC CCAGCACTTT 41640
GGGAGGCCGA GGCGGGCGGA TCACGAGGTC AAGAGATCGA GACCATCCCG GCTAAAACGG 41700
TGAAACCCCG TCTCTACTAA AAATACAAAA AATTAGCCG GGCGTAGTGG CGGGCGCCTG 41760
TAGTCCAGC TACTTGGGAG GCTGAGGCAG GAGAATGGCG TGAACCCGGG AGGCGGAGCT 41820
TGCAGTGAGC CGAGATCCCG CCACTGCACT CCAGCCTGGG CGACAGAGCG AGACTCCGTC 41880
TCAAAAAAAA AAAAAA AAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA 41940
AACTACCTAC TTTTATAGC ATTGTAGTGA AGTTGAAATG AATTAATCCA CATATATTAT 42000
AGTGTGGTAG AATGCAGCAG AACTGATGAT GTATGACTTC TAAGACTAGT CCTTAAGAGA 42060

FIG. 6.16

CCTGCAGTTT TTGCTTTTGC CCTCTTGGAA CACTCCTGTT GCCATGTAA GAAAACTCT 42120
GGGGAGACTA TGAAGGAAGA GAGCATACTC GGGGCAGGGG GGTGAACAGG ACGTGCACAT 42180
GTACGAGCGT ACAAGCCAGG TGACACCAGT ACCACAGCCT CAGACATGTC ACCGGGGATA 42240
CCAGCACCAC AGCCTCAGAC ATGTCACCGG GGACACCAGC ACCACAGCCT CAGACATGTC 42300
ACCGGGGACA CCAGCACCAC GGCCTCAGAC ATGTCACCCA GGGACACCAG CACCAGCACC 42360
ACAGCCTCAG ACATGTCATC GGGGACACCA GCCCCATGGT CTCAGACATG TCCCTGAGGC 42420
CCACTTAGAC CCTTCAACCC CAGCCCAGCT GCTAACTGAC TACAGCCACA TGAACAGAAC 42480
CAGGTGAGAC CAGAGGAAAC TTCCAGTCAC CTACCAGATC ATGACAAATA ATAAACGATG 42540
TTTTTTAAAC CACAAAGATT TGGAGCAGCA TTTGTTACAC AAAATTAGAC AACTATTACA 42600
GTTGCACTAA AAACATGTTT ATTTACAATA CTAAATTAGA AGTGTAAAGAA TGGGAGAAAA 42660
ACTTCATACT TTAAGTCA TTTTTCCTC CAAAACTTC CAACTTTGAA AAACGATT 42720
TTATAATGCA TAAAAATTAA AATAACCTTA GAATTTATAT GAGTAGCATA GCCAGCTGGC 42780
TTTATTATCT GTTGTACTCA ACACTTCAAT AATCACTGAT GTTTTAGAAC TCTTCAGATT 42840
TAGAACTCTT GCCCTTGCTT TAGTCTGGT TAAGCTAAAT AATTGTTCTT CCTCAAGAAC 42900
AAATGACCTT ACCTCGTTTT GTTTTCCTG TCTGAGAGAA ACACATTAGC AGTCTCCCAT 42960
CTGTTTTTC CTTTTCTGT CACCCAGGAC AGAGGGCAGT GGTGTGATCA CAGCTCTGCA 43020
GCACGACTTC CCCAGGTTCA GGTGATCCTC CCACCTCAGC CTCCAAGGA GCTGGGACCA 43080
CAGGCACATG CCACCACGTC CAGCTTAATT TTGTATTTT TTGGTAGAGA TCAGGTTTTG 43140
CCTTATTGCC CCAAGCTGAT CTTGAATTCC TGGGCTGAAG CAATCTGCCT GCCCTGGCCT 43200
CTCCAAGTGT TAGGATTACA GGTATAAGCC ACCGTGCAGC CTTATATTTT GTTTTAAATT 43260
TTCCTCTGTA TTTTCTCTC TGGCAAATTG TTAGGGAGT TTCTTTAGTT TATCAGACTA 43320
AATTTCAAGG CTTTCCTTCC AATTTTGACA TGTAACAGT CCCTCATTC TGCTTATCTA 43380
GTGATTATTC CCAAATCTGT GTTTACAGTC TAGCTGTCTC TCCTGAGATT AAGACTTGTT 43440
TCTCTAACTA CCTGACGGCA GAATCTCCTC TTGGAAGTAT CAAGGAGGCA GTTCAAACT 43500
GAACTGGGCA TTGGCTCCAC TCCTTCTCCT TCTCTTACT ATTAATACCC TTTCTCTCCT 43560
TCTATATGAC CACACTAAGT CTTATTTAGG CATCGTTTCT TCTGGGAGAC CTTGTAGAA 43620
TCTCTGAGGT TATGTAAACA TGCTAAGGT TTCTTGACAT TCTCAGATTG GGTTAGGTGA 43680
ACTTTTAGCA ACTTATCTT TTAATAAAAA GTCATCCCTC AGTATCTGTG GGGAATTGGT 43740
TCTAGGACTC CTAAGGATA TCAAAATCTG CATGAGCAGC CCAGGTGAGA CCAGCAGAAG 43800
CACTTTACAG TCACCTACAG GATCATGACA AATAATAAAT CATGTTTAAAG CCACAAAGTC 43860
CTTTACATAA AATGGTATAG TATTTGCATA TAACCTACAC ATCTTCCTGT ATCCTTTAAA 43920
TCATCTCTAG TTTATAATAC CTCATACGAT GAAATACTA CGTAAATAGT TGTTATACTG 43980
TATTGTTTAG GGAATAATGA CAAGGAAAAA AGTCCACGCG TGTTCAAGAT AGATGCTTTT 44040
TTTTCTCGTC TAATATTATG GATCCACAGT TGGTTGAATC CACAGATGTG GAATCCATGG 44100
ATACCAAGGA ACGACTGTAT GCATTTTGAC AATTATACTT CTCATCTTAC CATGCATTCA 44160
ACAAACAGAA CATGTAAAGC GGTGATAATG CTGTGATGAA AAATAAAGCA GGGGAAGAGG 44220
CTGCATCCAT CTAGTGGAAC CGATGCCCTT TTCAATCTGC ACAAAGAGAA AAAGCTGCTC 44280
TCCAAGTTGG GGGGTGGGTG GGTCAAGTAT GTAAATTGGT CAGGAAGGGA TCTGTAGGCA 44340
CTTACAGATT TGACGCTAAT GAGATGGGAA GCCACAGGAA GGTTGTGAAG AAAAGACAAG 44400
ACATGATCTG ATTCATGTTT TGATCTGATA CACTGGTTGC TAGATGGAGA ATAAGCTGCA 44460
TGGCGGTGAG AGGAAGCAGA AACAAATAGGA GGGTAATGCT ATAATCCAGT GGTCCATAAT 44520
CCAATATCCC CCAAGGAAC AGTTCGGCAA TGTCTGGTGA CATTCTGGC TGTCACAACT 44580
GTTGGGGCGG AGTGCTACTT GCATCTAGCA GGTAGAAGCT AGGGATGCTA CTAACATCC 44640
TACAATGCAC AAGACAGCCC TTCCCCAAC ATTGCTGGCC CAAAACGTTG ATAGTACCAA 44700

FIG. 6.17

GGCTGAGAAA CTCTGTTATA ATCTGTCTA GAATGTAGCT TGGATTGAGA TGGCAGTGGT 44760
AAGAGCTGGA GAAGTGCTTA GCTTCCCAAT GTTTTTTTGT TTGTTTGT TTGAGACGGA 44820
GTCTCGCTCT GTCGCCCGGG CTGGAGTGCA GTGGCGTGAT CTCGGCTCAC TGCAAGCTCT 44880
GCCTCCTGGG TTCACGCCAT TCTCCACCT CAGCCTCCCG AGTAGCTGGG ACTACGGGCG 44940
CGTGCCACCA CACCCAGCTA ATTTTTTTGT ATTTTATAGTA CAGACAGGGT TTCACCATGT 45000
TAGCCAGGAT GGTCTCCATC TCCTGATCCC GTGATCCACC CACCTCGGCC TCCCAAAGTG 45060
CTGGGATTGC AGGCGTGAGC CACCGCGCCC GGCCTGAATG TTTTAAAGT ACTGGTGACC 45120
ATATTGCTG AGGGATTAAA TGTAAGGTAT GAGGGGAAAA TAGGAATCAG ACACCAGGGT 45180
TACTGCCTG AGCAATGAGA AGAACGACGT TCCTCATACG GAGATGAGGA AGAATGTGGA 45240
ATAGCAGGTA AATAGCATGT GCTTGCTTTG TTTGGGGCTG TGCAGAAGAG ACTGATGGGA 45300
CCAACGTGCT CAGTTCTGGA TATATTAAAC TTGGAATGCC TATTTGGCAC CAAGTGAATG 45360
TATCAGGTAG GCAGATGGAT AAATGAGTCT GAAGTTCAGG GGAGAGGCTG GGGTGGCAAT 45420
ATGAACTTGG GAGTCTCCAC ATCTGAATAG TATTTAAAGC TATACAACAG GATAAGGTGA 45480
TTTAGGAACT AAACACAAAT TGAGACGAGA TCCGAGCCCA GAGGCACTCC GATGTTTAAA 45540
AAAGAGGAGG AACCATCAAA AGATACTAAG GAGAAGCCAA GAAGTAGGAG AACTGAGAGT 45600
CTGAGAGAAT CATTATACTC ATTTGATCGA CTGCAACAAA TGCTGCTTAG AGGTCAAGCA 45660
AAATGAGGAC TAAGCAAGGA CCACCAGGTC TGGCAACATG GAGGCCAATG CCGACGTGGA 45720
AATGAGAGTT TTGGTGGGAA GACAGGAATA AAAGTCTCAC AGGTCTGAAT TCAAGAGAGA 45780
GAACAGCAGA AGAAGGGTAG AGGTGGTAGC CATAAACAAT GATACATTCT CTTGAGGCCT 45840
TTTCTTGCAA AGCTCAGTGA AGAAACATGG TTCCAGAGAG GGATTTTTTT TTCTCTCATT 45900
TTACATATGC AACATATAA AAAAGCTGAA AGAATTGTTT GACAACCACC CTTATTCTTA 45960
CCACAGATTC AACATTTAAT GCCATATGTT TTCCCTGTAT GTACTGTGTA TTGTTTGAGG 46020
ATAACTTCCC CTCTAAATAT ACCTCGGATG TATCTCTTAA AATAAGTCCA TTCTCCTACA 46080
TAGCCATAGT AACCATGAAC ACACCTAGGA AAATTAAAAA TATATTCTCA AATATATTAT 46140
ATAGCTGGGT ATATTACAAT TTCCCCAATA TGTGATTGTC AAACCAGGAT CAAGTCAAAG 46200
TCCATGCACA GCATTTGGTT GTCATGTGTC TTTGGTCTCT ATTAATAATG ATGACTGTTT 46260
GAAAAGACCT GTCCTATAGA ATAAATTTGA CTGATTATGT CATGCCATTG AACTTGTTTT 46320
TCTATTCTAG AAGGATAGTT TTTAGGGTA GTGAATACAT TTATTACTCT TGGCACAATA 46380
GTCTAACATT TCCCAATTC CTTATATCTC TGCCCTTTCA TTTTCAGAAA ATCAATTATT 46440
CCAAGATTG TTTTTCATTT ATCATCACTT ATTAGCTCTG AAGACTCAAC TGAGCAACTT 46500
TCAGGGTTTA TATACCCTAT ATTCAGAAAA AACTACTAC CATCTCTCAT TTACCCTAAG 46560
AATTCATAGG AGAGCATGTC TTAAAGCTGA TCAATAACCA AACCAAACAT TTTATTGATC 46620
ATATTACATT TGGAAAGCAA AATGAATTTT CTAATAATTT TCCCTGATT AGCAAAATAG 46680
TGCCCTCGAA CACTTGAGGG TGAAAGTTGT TGTCAAATAT GCCTACATGA CTGGAATTA 46740
TGACATCCAA ATGAGTTCAC TGGGTCTGAT AATAATATGC TCTACATGCT TATGTCTATG 46800
TAATAAACAG CTTACATCTG GATGAGAAAA TTGATTATAC AAATATTTGG GCTTCTACAA 46860
CTGGTCACTC ATCTGTAAGT ACTTAAAGCA ACTTAAATG CAACTGACC TAACAATGCT 46920
TATGGTTAGA ATTCCAAAGA ATGTTTAGGC ATTGTCAGGT TATGTTAAAA CATCTTCTGC 46980
CACAATCTTC AAGTGATTGA TCTTTCTGT TGTGTTGAAT AGCTATAGAA GACAAATGAA 47040
TTCTGCACTC CTGAATTCAA TGAACATTTT AAGTTTCTC ACTTACTG TAAGATTACG 47100
TAGCATATTT TAAGAAATAA ATTATAATCA TTTTATTTCA CTTATTGAAC TTCTTTTAAG 47160
CTTTGGCATT AGAATTTTAA TCAAAGCACT GCCACTTGCT TACAGTGATG GTTTTATAGG 47220
TCTTTGGGCC TATGGACTAT TTCAATGACC TTCACTAGCC ATCTAGTCCA CCTTATCCTA 47280
ATTATTACCA CTGCAAAAGA AACCTCACT TGAATAAATC AGTAGATGGG CATGAGGCAC 47340

FIG. 6.18

CTCCCAGGAG ACTATAATTA TTAAC TCATA CTAAATCAA AATTGTAGCT ATTATCACTC 47400
ATATGGTTTG GCTCTGTGTC TCCACCCAAA TCTCATCTTG AATTGTAATC CCCACGTGTC 47460
AAAGGAGAAG CCTGGTGCGA AAGGACTGGA TCATGGGGGC GGCCTTCCCC CTGCTGTTC 47520
TTGTGAAAGA GTTCTCCGAT GGTTTAAACG CATGGGACTT CCTCCTACTT GCTCGCTCTC 47580
TTCTGCCACC ATGTAAGATG TGCCTTGCTT CCCCTTTGCC TTCTGCCATG ATTTTAAGTT 47640
TCCTGAGGCC TCCCCAGCCA TGCAGAAATG TGAGTCAATT AAACCTCTTT TCTTTGTAAA 47700
TTACCCAGTC TCAGGTAGTT CTTTACAGCA GTGTGAAAAT AGACTAATAC AATCACCTTA 47760
TGGTAAGTCT GTCTATAAAT CACCTGAAC TACACAGACT ATCTAGAAGA ACATGTAACC 47820
AGAGTAGTTC TTGATCATGC TATATAAATT ACTGATACAG AAATAGAGCT AGACAGGAAG 47880
GGGCTGGTAG TAGAGAATCA TCCTCTGGAC ATATTCTCAC AGCCTAATCT CTAGCTAGCA 47940
AATTTTATAA TATATATAAA AATACAATTA TTTCACAAAA TTACCATGAA ACGATTTTAT 48000
TGGGATATTA GACATTACTG AATTACTTGT TCTGTGAGGT ATACAGTGAA ATTAACATGT 48060
TATAAAATTG TGGTAGCCGG CCCCCAAGAT GGCCTCCAAT GAATCCTTCA CCTCTTGGTA 48120
TTCATACCTT TGTGTAGGTA GGTCTGTGTA ACCCATAGAA TACAGCACAG TGACAGTAGG 48180
TCACTTCCGA GGTTAGGTTG TGAAAGACAC TGTGGTTTCT GCCTCTCTCT CAGATCACGT 48240
GCTCTGGGGG AAAAGCCAGG TGTCATTTTG TGAAGACACT CAAGCAGCCT TTAGATGACT 48300
GCAACCACAT AAGAGGCTCC GAACTGGAGC CACTCAGCTA AACCACTCCC AGATTCCTGA 48360
CCATGTATCA TTTCATACAC AATGTATGAA ATGACAAATG TCTGTTGTTT TAAGCTGTTT 48420
GGGGAATAAT TTGTTACATA AAAAAATATA ACTAATACAA TAATACATAC TGATTTAACT 48480
GAAGTTGTAA CTTCATAACT TATTTAGGTA CTAAAAATCA CAGCAACCCG ATGCAAAGTA 48540
CTAAAAAATA AATCCATTAA TACCTATTGA GTACTGTTGA GGGCATGAGG AAAGCTCTTT 48600
CATACTCCAC ATAAACTTTC CTTACCGTAA TATTCATGGC TGACCTCTAC TCTTAACTCC 48660
TTTCTAGGAT AGGAGGGGCT AACTGATCTG ACAGCAAGTT TGGGAGAAAA AATTCTGAGG 48720
CTCGGCCAAC TTCCTCTCTT CTTTCCATTT GGGATTGCGT TGAAGTGAAGA GGGTCATTTG 48780
TTTTGGCCTG CTCTCTTACA CAGTAAATGT AGTGGGACAA GCTCTATTCT TGTGATAGA 48840
AAAACTCGAA TTTTAAATCT GCCTAGTTCT TTGCAGCTCG TTGTTGCTCC AAATCTCAGC 48900
TACCTTTTGA AACAACCTTT TACAGTAAAC TTAATTTCAA TCTTCATGTG ATTAACTGG 48960
ATCCAAACAC AGGCAGATAA AAAAGGTGGG GCATTACTTA TCAACCTCTA AACTAAGTTT 49020
AATTTTGTGC CCTCATGGAG TTTATAGTAT ATTTGAGGTT TAACTAAAA CACCTGGTTT 49080
TAAACAGAAA CTATAAAAAA CACGATTAAT AGGTGAGGCC GGGCGCGGCG GCTCACGCCT 49140
GTAATCCCAG CACTTGGGGA GGCCAAGGCG GGTGGATCAC GAGGTCAGGA GATCAAGACC 49200
ATCCTGGCTA ACACGGGTGT AAACCCCGTC TCTACTAAAA ATACAAAAAA TTAGCCCGGC 49260
GTAGTGGTGG GAGCCTGTAG TCCCAGCTAC TCAGGACGCT GAGGCAGGAG AATGGCGTGA 49320
ACCCGGAAGG CGGAGCTTGC AGTGAGCCAT TGCGCCACTG CACTCCAGCC TGGGTGACAG 49380
AGCCAGACTC CGTCTCAAAA AAACAAACAA ACAAAAAACA AATAGGTGAA AGGCCGTGAT 49440
CATTGGTAAG CGTAAGAAAA TCTGAGGGAG AAAAAATAT AGATGCCAG GCCCCATGCC 49500
AAACTCATGG AATCATGCAT GAAACCCAAG CAGCTGCAGT TTTAACAAGT TCCCAATATA 49560
TAGTTGACCC CTGAACAATG CAGGTTTGAA CTGCCTGGGT CCACTTATAA AATGGATTG 49620
ATTTTTTCA ATAAAAGTTA CACCGAGTGT GCCTGCCTCT CCTCCCTCCC TCCCTACATG 49680
CTCCTGCTCT TAAGCCTCTG CCATGAGGCT TAAGACAGCA AGAACAACCC GTCCTGTTTA 49740
TTTCAATAGT TTTGGGGGGT GCAGGTGGTT TTTGGTTACA TGGATAAGTT CTTTAGTGGT 49800
GATTCTGAG ATTTTAGTGC AACTGTCACC TGAGCAGTGT AACTGTATC CAACATGTAG 49860
TCTTTAACC CCCATCCAAC CTTCTTCCCC AACCCGAATC CCCAAAGTCC ACTGTATGAT 49920
TCTTATGCCT CTGTGTTTTT ATAGCTTAGC TCCCACCTTT AAGTGAGAAC ATACCATTTT 49980

FIG. 6.19

TGGTTTCCCA TTCCTGAGCT ACTTCACTTA GAATACTGGC CTCCAGCTCC ATCCAAATTG 50040
CTGCAAAAGA TATTATTTCTG TTCTTTGTGTA TGGATGAATA GTATTCCACG ATGTACATAA 50100
ACATTTTCTT TATCCACTCA GCTCCTCTTC AGTCTACTCA ATGTGAAGGT GACAAGGACG 50160
AAGATCTTTA TGATGATCCA TTTCCACTTA ATGATTAGTA AATATACTTA CTTTTCCTTA 50220
TGATTTTCTT AGTAACTTTT TTTCTCTAAC TTACTTTATT GTAAGAATAC AGTATATAAC 50280
ACATATGACA TACAAAATAC GTTAGTCAAC AATATATGCT ATCAGTAAAC TTCCAGTCAT 50340
CAGTGGGCTA TTAGCAGCTA CGTTTTTTTG GCAGTCAAAA GCATGGGGAA GGAGAGGGTG 50400
GTCCCTAACC CCTGTGTTGC TCAAGGGTCA ATTGTAATAA TACCCATTTA AGAATCCATG 50460
GTATATATGG TAAGTGCAAC AACTCTAGAA GAGAGTGCTA GGAGTTGGAA AAGGAAAGAG 50520
AAAAAGCAAT TTAAAGCAAT CTGTAAAGGA CATGCAGGGT TTAGATGAGG TGGAAGGGTG 50580
AGGGAAAACC AACATCTGCT GTGAGGGCAT ATTAAGTCC AGACATTGTT CTATGTCTTA 50640
CCTCATTTAA GAGAATTTCA TTTACACAT GGAAAACTG AAGCCCAGAG AGGTAAATA 50700
ATTTGCCTGA GGCCAAAATT AGTTAAATAA CAGAAGTGGG ATTAGTAGAT GTTTTCATT 50760
TATCAGTGAA ACTGAGCCTC AGGGAGGTTA AATATTTTGT ATGAAGTAAC AAAACTGAGA 50820
TTAATATATG GCCAAGTTTA AATGAGATCT GTAAATCTAA TGCCTACACT AAAACAAAAA 50880
AAAAAAGTG GGAAGAAAAG GTCTATATTG CTTAGCAAAA CAGAGGTAGG GAAGCAAAAA 50940
TAACTTACA AAATCAGATT AGACCACCAA AAAACAGTCC CCATTTTAACTTATGTGGTG 51000
AGAACCATAT ATTAAGACC ACCAGTGGCT TAAAAATCTT TTTAAAAAT GAATCTGTTT 51060
TCATTATCA TTAGTTTTTA TCTAATGAAT AATGTATCTT AACTGATACA TTTACTAAAC 51120
AATTACCAGC TCCAATTAGC ACTCAGTTAC AATTCAATCA TTAAGTAC CCTCAATTTA 51180
GCTGTCAACC TAGTCAAAAC AGTTAAGTGA TTTTACGGTC ATCCTCAGTT GCAGAAGTAT 51240
AATGTTTATG GCTGGAGTCA TTTTATTTT AACTAACATT TTTAAAAAG ATTGCTTTGT 51300
AACAATGTGT TATGAGTCCT TTGTGGTAAA TACTGCTTTT TTTTGAGAC GCAGTCTCGC 51360
TTTATTGCCC AGGCTGGAGT GCAGTGGTGC GATCTTGGAT CTGAGGCTCC TGCCTCAGCC 51420
TCCTGAGTAG CTGGGACTAC AGGCATGCGC CAACGTGCCC AGCTAATTTT TTGTTTTTTT 51480
AGTAGAGATG GGGTTTCACC ATGCTGGCCA GGCTGGTCTC GAACTCCTGA CCTCGTGATC 51540
TGCCACCTC GGCTTCCAA AGTGCTGGGA TTACAGCTAT TTTAAGGACT TTTTAAAAAG 51600
TGAAGCTAAA CATTTATTCA TCCCTATTCC TCATCTATAG GGACTTGTGC TCTATTTTTC 51660
TTTGAAGACT GAAGTAAAAA TTCACCTTTG TGAGGGTCTT CCTATAATTA AAATTAATCA 51720
TTTTTCTCT CATAGCTTCT ACAAACATT GCCTGTACAA CTCTATTTAG CACTTATTTT 51780
ATCCCGCCTT GTATGAAAAC TATTTGTTA CAAACGTTT TACTTCTCT TAGGAATAAG 51840
GACTATGCAT TATCACTGT TGTATTCTCC CTGCATTAT GGCAGTCCTT TGCACATTAA 51900
ATACAAGCTT TTTGGCTCTG TGCATCTCTT CATCTGGCTG TTCATCTGTA CCCTTTAAAA 51960
CATCCTTTAT TAAAAAACA GTAAATGTAA AAAAAAAAAA AAGCCATTGA TGAAAAAGTT 52020
AATAGCTTTC TCAATAAGAA AAGAGTATCA ATTATGCATA CGTCTGAAC AACAAACATG 52080
AATGAAATAG GCTATTTAAT ACATTCTGTT TAAAAGTAG GTTTGGTCAG CCATGTAAAT 52140
TGAAATTTGG GAGCCACCAA GATAACTCAT CAACAAATAT GCACTATGTA CTAGGCACTA 52200
TATAGATGAT GGTGAACCAA ACAGATGTAA TCCTTGCTCT TACAGATCTC ACAACCTACT 52260
ATGGGGCCAA AAATATATGT GTATGTGTGT GTGTTATACA TATATACACA CACATACATG 52320
TATATATACA TATACACATA CACATATATA CATACGCACA CATACACATA TATACACACA 52380
CATACATATG CTATGAGGAA AACAAACAGG TGGTGAGAAA GAATTAGAGT AGGGGTAGAG 52440
GACAGAGGGC TCCTCAAATA GGGTGGACAG CTTGACACAA GACACTCGAG CTAAGACTCC 52500
AAGGATGAGA AGACAGTTAT GTAAAGAAAA GGGGACTAGC ATTGTCAGCA GGTAGCTAAG 52560
GCCTTAAAGC AGACAGTCAT GTGCTGCAAT GCCAGCTTCA AGCGAATACA GTTACTAAAG 52620

FIG. 6.20

CATATCTAAC CTTCTATGTG AATGTAGTTA CTAAGCATA TCCTCCAAC TTCCATTTTT 52680
CTTTTGCTAT TGTTTCTACC ACTTCTCCTT TTCTGTTGAC AATTATTTTA AATTTCCTGG 52740
CTAAATTA AAA TGATGGCATG AACTCTGGGG AAAGTAAGAC TACCTATGTC CAAATAATCC 52800
TAAATTCCTT CTAGTCCTTA TGA CTGATCA ATTCACCCTG AAGTGACAAC TATGTCCCAA 52860
TTAGGAAAGA GTGTTTCTTT ATCTGCACTT AATTTTTTGA TTTGGAGGCT TCCTGATTGC 52920
TAATCAACAT GTTGTTGAT TACTTCAACA AGTACTTATA GAACGTTATT TTGCTACTGG 52980
AAAAACGTTT TGCTGCTTTC TGAACCTTAG GTTGCTCTAG AGTCTAGGAA GAGTGACTGT 53040
ACCTAAAGCA GTTCCTAATT ACTGGACATT CTCAGATCTG CTAGAGCTAC ATGTCCAATT 53100
ACGAGAATAT ACTGGAAAAA GCCCTGGATT AGAAATGAGA GGATGTAGGT TTAGTAGCCA 53160
GGTCAGCCAC CTTGTTAATG CAAATTTGAG TAAATTGTTA CTTCTTTTAG GCCTTGTTTT 53220
TGCTGTTTTG TTTTCTGAC AGTATGGTCT CTGTGGTCCA GGCTGGAGTG CAGAGGCACA 53280
ATATCAGGTC CCTGCAGTCT CTACCTCCCA GGATCAAGCC ATTTTCATGC CTCATCCTCC 53340
TGAGTAGCTG GGATTACAGG CATGTGCCAC CACACCCTCG AACTCCTGAC CTCAAGTGAT 53400
CTGCTTGCCT CAGCCTCCCA AAGTGCTGGG ATTAGAGGTG TGAGCCACTG TGCCTAGCCT 53460
TACACATTGT TTTCTTACTG GTAAAGTGGG AATATCTAGA AGTTGCATGC TACATAAATT 53520
CAACCATATA TTATTGGCAA AAAATTTTAA AGAAAAACAT CAGCTTAAGA GTACTAATTG 53580
AGTACATGCC TTGGAATGAG CATGAGCTGG AAAGAACAAA CCTGTTGTTA CATCACTCAT 53640
TGCTGTTTTT ATATGCTGCT CATTGTAAAT CTGTCTCAGT GGCATGATTT TAGTGTTTAA 53700
AGATTTATTT GTTTGTTTGT TTAGGACAAA GTCTCTACAC ATAATCTACT TGCTTCATAT 53760
ATACATACTT ATGCATATTA TGTATGTACA TACATGCTCT CAGGGCTCAC ATGAAAAAAC 53820
AGCCATTGAG GTGATGTGAT TTATCTCATA TGCTTACTTT AGAGTCAACA GGGTGTGAC 53880
TCCACTATAC AATACTGGCA TGGAGAACAC ATAAGTCAAA GTAGACAGGA CCCAGCCGTA 53940
CCATTGGCTA GGGCACAAAT ATATTCACAT ATGTGGAGAA TGATGTACGT AGAAAGGTCT 54000
TCATTGCACA ATGCTCTTTA ATAAAGATCT GGAAAAAAA AACACCTAAA TGTTCAAAG 54060
GATAGGGTAG ATGAAATAAT GGTACATTAT AAAATGGAAG ATTATGCAGC CATAAAAATA 54120
AGGAAATACC TTAAATAATA ACAGAACAAC TTTTAAGGTA AGTGAACAAA TAAGGTACAT 54180
AATCACTATG CATAGTATGT ACCATTTACA TAGAAAAAGG GAAGAAAAAT AAAATATATA 54240
TAGTAATTTA TTTGTTCTTA CATGTGTAAA ATTTTCTGA AAAATATACC AGAACTGGT 54300
AGCACTGGTT GCTTCCTAGG CAGAAAATGA CTGAGTATCC TTTTGTACCT TTTGAATTTT 54360
GAACCACTG AATGAATGTG TTACCTATGA ACAAATGAC AAGTTTAGAT CAGCAAGACA 54420
GCAGTTTGAG ATGAAATGGG ATTACACCCT TAGTAGGAAA AACTTTTTAA AGCAGGTGGT 54480
ACTTCTAAGA GCAAATACCT GCACATGGAA TGTGAAACT ATAAGGAACT CTCCTTAAGA 54540
GATCCATCTA TTCCAACTT CTCATTTTAT AGATCTGTAA ACTGAGACCT TAAAAATTCA 54600
GTGACTTGCA TAAGGTCACA CAGCAGAAGA GATGGGATTA GATGCTAGAT ATTCCAATAT 54660
CAAGTTTGA CTATTA AAAA TTCAGTGACT TGTGTAAGGT CACACAGCAG AAGAGATGGG 54720
ATTAGATGTC AGATATTCCA GTATCAACTT TAGACTATTA TCACACCATC TTCTCATTTT 54780
CTGGGGGCAA AACAGAACCA AGTAAGTTTG GGCTACATTA CGAGTTGTCA TGTTTTTGTT 54840
TTTGTTTTTT TGAGATGGAG TCTTGCTCTG TCGCTCAGGC TGGAGTGCAG TGGTGTAAATC 54900
TCAGCTCATT GCAATCTCTG ACCCCCGGGG TTCAAGCAAT TCTCCCTGCC TTAGCCTCCC 54960
GAGTAGCTGG GTTACAGGC GCCTCCACCC GCGCCCGGTT AATTTTTGTA TTTTTTTTTT 55020
TTTTTTITAG TAGAGACGGG GTTTCACCAT CTTGGCCAGG CTGGTCTTGA ACTCCTGACC 55080
TCGTGATCCA CCCACCTCAG CCTCCCAAAG TGCTGGGATT ACAGGTGTGA GCCACCACGC 55140
CCGGCCGAGT TGTCATGTTT TATCTAAATT TTAGAGTCTA ATGTATAAAT TAACCTTAAG 55200
CCCTGAAACT ACTAATTCT TGTGTTGATC ACTATACGGC TACACTTAAA AATATGCTGT 55260

FIG. 6.21

GCATACCTCT ATCATTGCAT GTATACAATA TGATAGATGC ATGATATGAC AGACACACAA 55320
TATGATACAC GTATTTTTTT CTATCCTAAC ACATCTGAAT TTA CTGAAAT AACTAAAATG 55380
TCTTAAGTTA CTTTTTTAAA TATACACATG CATAGCACAA GCGTGTTGCC AAAAAATATGA 55440
ATACAGGTTT ACAATTCCTT AACTAAAACC CAAGGGTTGG ATGTGTTTTA GAAATAAGAA 55500
TTTCATACAA TTTTAAAGTG TTACAGGGTA TATAAACCAT TATATAACAC ATACCAGGGG 55560
CCAAGGGCAG CACCCCATAA TCAAACATAT TAATATAGTT TCAGCAAAAC ACATGGGATA 55620
AAGACTATAT ACAGCTTCTC AATAGTTCAG GTCATATTTT GCTACCAAAT GAATTTTGTT 55680
GCCAAGCTTA AGAAGTTTTT GGTTCACC GCTTCTGAA TGTTAGATTG AGATGTGGGA 55740
TTACAGACTG TACTCATAGA GTGCTTCTAG AAAGCAGTCA GTCACCTCAA CTCTCATTTT 55800
TTTTTTATGA GACTAAAAAA GAAATCATAG CAAGTAGCTT TTATATCCCA GGTTTGGGCC 55860
AAAGACTTGT ATTGTGGTTA AGGAATCTAA CTTAGTAGAA GGTGCACGAG CTGACATCGT 55920
GAGTGGCTAA AATGAGAGAA AAAAGAGAA AATCCTAATC ATACAGAAGC ACTGAACCTAC 55980
TGCAGCTGTT CGTTAGTTAT TAATTTAATA AAAGCTTCTC CCCTTTAAAT CATGTGAGTT 56040
TATAACTGGA AATAGGTCAA TAAAATTTCT GTCCACACT GCTGACAAGC GATGGACGCA 56100
ATTAGCTTTA ATCCCACTGG AAGGTACTGC ACTCTCTCTG GGACCAGGAT ATGTAGAAAA 56160
AAGCATTTCA AATATATAGG AATAACCAGA AATGTATACA GTATTCTCAA CTTGGGACCG 56220
TTACTCTATA ATATAACGA AAGGGGTTTT CTAGTCAATC TCTGCTGATC TCCTGTACCA 56280
AAGTTCTTCC CTTTATAAGT CTGTACTAC CTTTACAAG AGGAAAAAGC TCTAGAGCGA 56340
AAACACAGAA CACACTAAAA TCCCTTCCTT TCTCTTTACA ACTCAAGCCC CGCCTCCATT 56400
TTGTTTCTGT TACTAATTTT TCTTCTGAAA AAATACCAAA TTTACACTGA AAGACTAAAA 56460
TTCAACTTTG CAGACAACGT TTTAAAAAAT ACAATTCAGT TTGGTGATGT TGTTTTCAG 56520
TCTTACAATT TTAGCTACAT TTTAACTGAA CCAATTGTTT TGTTCAATTT ATGAGTTAAT 56580
ACTCAGCAAG TTTGTTTTTT ACAAATAGTG TATTCCATTC TAAAAATGGA AGTAGCAGTG 56640
GTGAACAAGA AAACAACCCT CTGAGTTTTG TCTATTTTCTGAGGAGTAC TACTTTCTCC 56700
AATTTTAATC ACAATTCATA AAAAGAAAAA ACCTAACTAG CTAGATCTTA AATATACAAA 56760
TACATTAACA ATCTAGTAAA GCAACAGAAA AAGGTAAACA AACTAACCAG CCTATTTTTG 56820
TCTGGAGAAA CCCCACAAA CTGCTGGATT CCTTGGCCAT TTGCATTCTAG AAGTACCAAA 56880
AACTAAATC CTTTTTACTA AATAATTTCT TCTACACGAG ACTTGTTTCC TCCACACCAC 56940
CCTATCCAAA TTGTCAGCAT TATTCCAGAA TATAATCATT TAGTTTGAGA CCACTAAAAA 57000
ACCCCGCAGT CAAAATACC AATTGTGTT TTTCTGTAAGAAATGGTCA GAACTACAA 57060
ATTGTTATCC TAGGACACAG AACCAATCGA CAAAAGGAC TTCTGGAATA TGCTGCCCCC 57120
AAGATTTAGA ATGCACAGGC AGAAATAGCA TACGCGGTCA CGATGTCCCT TAAGCCACAT 57180
GACCTTCTTA CGAAAGCAAA GGCTTAACT TATCAAATGA GAACTCCCCC TTTCTCTGAA 57240
GTAAAACAA GGCAGGGCAG CTGGAATTAG AGCAGCAGGG ACAGATCGGC TGTTGACTAG 57300
TCAGAACGGG TCGTGGAATG CAAAGTCCCT GCGCTTCGC TGCTCCCCTT ACCGTGAGAA 57360
GATCTGGGAG GGAGGAAAGG AGGAGAAACA CCCCAGAATC CTGGTAGAAA AGCCCTGGC 57420
CTCGAAGATG GGCTCTAGGG AGACAGGGAG GGGCAGCTCC GTGTGTGATG ACCCTTTGTG 57480
AACATGCACT CTGTGGCAGC TTCAGTCCA CCGAGGCTTT GGGAGAGCGG ACTACGGATG 57540
CCCGGCGCGG CCCAGCTGTG AAGGCCGCGC CGGCGGAGAG GGTCCATGGC ACCCCGCGC 57600
GCTTCGGAAG CCCTCCCTC TCCACCTCC GCGGGTCACC CCAGGAACCA GCGGCTCCG 57660
ACCACGCTCG CGCGGACCAC GGAACAGCGA CGCGCAAGCA GGTCTCTTTC GTCAGCGTAA 57720
TCCCTCCGCA GAAAGCCGCG CACTAGTTTT AATCACGCCC CACCCCTGG CCGCTGGCGC 57780
CACCTCCGCC ACTCGGGCGC TTTCCAGCAG CTTCCAGAAA CGTCGCTCC CCAAACCCAG 57840
CCACTCACAC ATGGCGGGCT CAGCAGCCAC CGGCCCGCC CCTCCTCGTC GCCGAGTCG 57900

FIG. 6.22

CAACTGCGTC TCGGGCCACA GGGCGGACAG CCAAGCCTCT GCGGAGGGCG ACCGGAAGTG 57960
CTCAGCTCTT CACCTTCCCC GCCACGCCAC CGTCCTTTCA GGCCCAGCGT GCAGCAGGAA 58020
GGAGGACTCT TTTGCCGCGG ACTCAAGCCG GAAGCCGCCT TCCTAGTGGA GACGCGAGTG 58080
GGGGAGGAGC AGTCCGAGGG GAACGTGGGT TGAACGTTGC AACTAGGGTG GAGATCAAGC 58140
TGGAACAGGA GTTCCGATCG ACCCGGTACC AAGAAGGGGA GTGCCGCGG CAGGTAAGGG 58200
AGAAGAGGGA GGGGTTTCTT TCCGCTCTCG AAATTGGGAA AAGAGACAGA GCTGGGATGA 58260
CCTATGGGGT AGTCGGCGCG CTGAAAGGAT GGGCTGGGCT GGGACGGGGT TCAAGTGGGA 58320
AAGGTTGATG ATTAAGGTAT AGAGTTGGAC TTACAGATCC GTTGGGGCG AGAGAGGTGA 58380
ACGCTGAAGA GAAACCAGAG TTTGTTTTCG TTTTCCAAGG AGCGTGGAGA TGGGCAGGGT 58440
TAACGGACCC TCGCCTCCTT TCGGCTTCTT AGTTTGGGTG TTGAACTCA CCTCCTTTGG 58500
TCCTGTTCTG CTCTGATTCA AGACAGTTGG GTTTGGTACC TGACAGGGCT GGGTGCAGAA 58560
AGCTGACCCT GTTCTCGGC TTCCAGGTCG GTTGTGGCCT CGCTTTTGAC AGTTCACGTG 58620
CCGAGCCTAC TCGCTCTCG AGGGCGAGCT CAAATGGGTG GGTTTAAGGC CCCCTCTTCG 58680
AACAGCTGTT TCCCTGGGTT TCTCCATTTT GCACACAGGA GTGTGAATTA AGTTTAATTG 58740
AATACTTTT GCGATTCCCA GGGCCACCTT GACACGTTCA TTGTGCTATC TAACTGGGTT 58800
CATGCTGGGC TAATAATTCA CATTAAAGGCT TCTGGAGTAT AAGTGGTTCA CAGAAGTATG 58860
AAAAGGGGAT GTTAGAAGAA AGATGCTGGG GGTGAAGTAG AGTTGAGGAA GACAGAACTG 58920
GAAAGCTAGG TTGGTTTAC AGTACAATGA GCTTTAGGTC ATAATACTAC CTTTAGGTTA 58980
TATTGGGCTG TTTGGACGGA GTTTGCTGTA ATCAGGCTAG AGTAAATAGA GAATTTTAAA 59040
CTAAGCATTG ACAGGCTCAG ACTTGTAGAG GCATCATTTT GACAGTGATA TGGAAGGGAA 59100
AGAGGTAGAG ATTTGAGACC TTTCCAAAGA ACTGTCCACA GAATTTGGTG ACTTACTGTG 59160
CGAAGAGGGA AATAAAGAAT AGGGAACAAC TCAAGACTTT CTAGTCTGTG TGTTTGAAG 59220
GATGGAGACG CCCACATTTA AGTGAGATAT GGGAAGGAGG AGCAGATTGT TTTTGAAGGG 59280
AGGAAGAGCA GTTACTTAGG GTCAAATTA GTTGTAATTA CCCCCCGGG ATTTTGTATG 59340
TAAGTCAAAG TGAATTGTAT TTGGAAGAAG AACTGGGGAG CCCACCTCTG GTATTTTTTT 59400
TATGTCCCTC ATATGGACAA ATAAACCTCT GGTATTAAT GAATTTTCTT TTGGGGGATT 59460
CTATATATTC GGGATTTCAG CCACCAACCT ATCTGGTTTT TCCCGCTGAA ATGTTGGGTG 59520
ATGGAATCAG GAGAGCAGAT TTGGAGACTC TTTATATTTT ATAATTGAGA GAGACAAAGA 59580
GAAAACCGTT TGATTTGAAA AAGTTTTCTA GGTTCCCTCA GGTAGATGGA AATTTTCATC 59640
AAAAACAGTT TATTCAAGGT ACATAGCCTA CTAGTTTCCC ATTTGAGAGT ACCGCAGAAT 59700
GATACGACGT GTAGTGCTTC TCTACGCAGA ATGAAGTATA AAATTAGCAC CAAATAGTAA 59760
CTTTAATTTG TCAGGTGCTA AACTTTTTAC ATGCTTTATC TCATTTAATT CTTAGAAGAA 59820
ACTAATTTTA CAAGTAAGTG TCTGGACCAA CATCTGCAGG TACAAAGCCT GAAAAGCGTA 59880
AGTTTGACTC CTACATAGTT CTCTTTTGTA AGTAGATTAT AAATAGAACC AGCCAAAGGT 59940
AATAAGTTGT CTGTGCCTAA AAAGAAAGAA AAAAGTTAGC ATCAGTAGTT CTCACCAGAA 60000
GGGGTGATTT TGCTTACCAG GGGACATTTG GCAAGTCAGG AAATTTTGG CTGTTGGATC 60060
TAGAGGGTAA AGGTCAAGTGA CGCTGCTAAA CATCGTCAGT GCATAGAACA GCCTTCACAA 60120
ACAATTATTT GGTCAAAGAT ATTTGTAGTG CTGCAGTTGA GAAATTTCTG TCTTATGGTT 60180
ATTTCTTCAG GAATAGGAAA TTAAGATTGG CCGATACTTT CTTTAAAAAG CAGTTTTATT 60240
TTTGAAATTA TTCCTTGGCT TGAAAGGTTT GTGAAGTTTA TATAGCCGAA CCAGAATAGC 60300
GTAATTAGAT TTTAAAGTGA ATTTGTAGCC ATCGATTCCC AGGAGATGGG TGTCATAGAA 60360
TCATGGATTC TTGGATTTGG GAAAGACTTA TGCCTAGAAT TATTTTACAA CATTTCTGCT 60420
AAGTGGTAAT TCTCCTCTGC CCTAAAGGTC TCCTGTATTT GATTTTCTTA TCATTGTGAA 60480
CCCACAATTA AATGCTCTT AATTATTTT TGCTTACACT GAGCTCCGGT CTCTTGTAAT 60540

FIG. 6.23

TTTACTCTG TTAATGTGG TTCTGCACCA TAGGACTGCA CTCAAAACAA GCTTGCCACA 60600
TATGTAATTT GTACTAGGAC AGTGTTTATA TTTTGTTCAGATAACAAAA TAAGTTAAAT 60660
GTGGTGTAAG TTAGATCATT TACAAATAAT AATTTGTTAG CAGCTTTTAA TAAGTAGTAT 60720
TTTTCCCAAC TGGTGAAGTA TTAATGTTGG TAGTTGAAAA CAATAGGAAT GTATGGAATA 60780
TATGGTTCAC TGGTTCTTTT GTTCCTGTCA AATAGTGGCA CAATGGATCT GGGGTTTTTC 60840
TCAGTATAAT GCTGGCATAT TTGTTTCAAA TTGTACATAG ACTCTAAAAA GTTAGGCTTT 60900
CAAATCTGG TCAATATAGT TTGCTTTAAA TAGTAGCTGC CTCTACTACA AGTTTTATTT 60960
AATTTGTTGA CAAATGAGTC TGCTATGAAA ACCGGTCTCTG TTGCCAGTCA CTACCCTCTG 61020
TTCACAAATT TGCTGGGTTT ATAAATATAG GTATCATTTT CACTTCAAGA TTATAATTTT 61080
AGAATATGTT TATTCTAGGA CATATAGCCC TCAAAATCTG CTTACTATAT ACGTCTTATA 61140
AAATAGCATG GTTCTTTTTT ATAGTAAATA GAATTTTTAT TTAATTGTCT ATTGACTTTT 61200
TTTTTCAGG GTTCATTGAA AAAATCCTTA GTGATATTGA CATGTCTCAA GTGACATAAA 61260
TTAGCCAATG ACTCGGAATG ATGGATTCTC CGAAGATTGG AAATGGTTTG CCAGTGATTG 61320
GACCAGGGAC TGATATAGGG ATATCTTCAC TCCACATGGT GGGGTATTTG GGAAAAAGTTA 61380
GTGAACTTAT TTTTGCCTG AGTGCAAGT TTTTTTTTTT TCTCTATTTT TGAGACTTAA 61440
ATTCAATTTT GATGTTACCA GTTAACCTCT AAAAAATTGT GTCTTCCACG GAAATCTTAC 61500
AGTAATGGCG AAAGATTGTT TTAATGTGTT TACCTTCTG TGTTTTATTG ATACATGAAA 61560
GTGGAAATAA AACATAGACC TTATGATTGA CTGTTCTTTG AAAATATGGT ACATAAATTC 61620
TCCCGGGTAA TTGATGTTAC TTTTTCCTT GCAAATAAAA TTGATACTAT TCTTAACACA 61680
TAAAATTTAA TATTTAAAC TATAACATAA TTCTTTTGG AATAATAGCT GTATTTAAAG 61740
GCTTATATGC ATTTCTTTT TTTGCCATGT TAAAATACC TTGTCAGGAT ACTTGTAATT 61800
GAAATTATA ATTTTCTG GTTACCTTTC CATTTAACTT TTAATATTTT GATATATTCT 61860
AGGAATGTCT ATATTTTAA TTGCTTTATT TCTCTTTTAG AATTTTGATT CAGCTAAAGT 61920
TCCATCAGAT GAGTATTGCC CTGCTTGTAG AGAGAAGGGA AAGTTAAAAG CCTTAAAGAC 61980
TTACCGAATT AGTTTCAAG AATCTATCTT TTTGTGTGAG GATCTGCAGG TAAAGTATTA 62040
ATCTTATATA GTATATATA GATTTTCTT TTTCTTTTG CTTTTTATT AATTGTTTAA 62100
AAAGTTTACT CATTTTTTGT TTTTAGACT AGATTTTAA TATGTAATCT CAGTTTGTA 62160
GTCTGTCTGG TATACAATGT TATTTTCCA CCTACCTTTA CTGGTTGCG TAAAGATGTT 62220
CGTTTTTATT GCCATTTGAT TTGCGAGAGG AGAAAATACA TTTCAAGGTT TTTTCTTTT 62280
TTTTTAACCT TTTGGAGGTC CTGTTAGCT ATTAGCATAT AGTAGTACT CTCTCATCTC 62340
TTTGGTTTAT CTTTGCAACT GATGGGAAAA GTTATGAATT TCTAATGTAC CTGGAAGAGT 62400
ATTTTGAAAA TTGGTTAGTC CAAAACCAAGT ATATATACTC TGAACATAAG AGAGTATAGA 62460
ATCTTGTAAG TTCTAAAAGA TCCTTTTAGA AGCTCTAAAT CGCTTTTAGA ATTATAGTAA 62520
TTTGTAACGA CTGGTACGGC TTTTATATAG CAGCTCATTA AATTCTGTAA TACTCCACAT 62580
TTTATTGTAT TTGACAGTTT ATGAGACTGT CTCATACACT TTTAATTCTC AGAATTTTGC 62640
AAGATTTGTA TTCCTATTTT ATGAATAAGA AAATAAATTG ATTTAGAGG GTTTGGGAAC 62700
ATAAGATCCT GATACAGTGG CAGAGCTGTG GTTGAATAC AGACTTCTAA TTTCAGATCT 62760
GTTTATTCCA GCAAAAAATT AGCAGTTCAT CAGAATTACC TGGAGTGCTT TTAATAAATT 62820
TCTGAGTATC ACCCCCAGAT GCTGATTCAA TAGAGTTGGC CCAGAATTCT GTGGTTTTGT 62880
AACATTTGAG GATGAGTCTG ATCATCATCA GCCAGGTTTG GAAAATACTA GACTAAATCA 62940
CATGGTTGTT AATAGATACT TATGCTGGGT ATAATTTGAA GTAAAGTAAT CCCAGGCGTG 63000
TCTACAAATA TAAATTTCTT TATGTTTATA TTCAGTAATT TTTTTATGA GTGTCACTGT 63060
TTGGCACTGT TGCAGATACA ATGTTAGGAT ACAATAATAA AACAAAAATT TCTTGCCCTT 63120
AAGGAAGTTA TGTCATAGAG TGGGAAAGAC AGTGAACAAG TATGTGTTTT TCTGTCAGGT 63180

FIG. 6.24

GATAAAAGT GCTGTGGAGA AAAATAAGGC AGTAGGGACT GGAATGCCAA AGTAGGGGGA 63240
GTTTGCAATT TTAATAGGA TGGTGAGGGG AACGCTTCAA TGAAAAGTGC AATTCGAGCA 63300
AAAGCCTGAA AGAGGTGAAG AGCAGTGAGC TTTCTAGGCA GGGGAAGCAA GTTCCAGGAA 63360
GGCCCTGAGA GAATGGAGGC TGCCTGTCAT GTTTGTGCTA CTGCAATGAA AGCAGCAGAG 63420
CGATAGAAGG TGGATCAGAA AAATAATGGG GGAGCTGGAC CAAGTAGGGT CTTATAAGCC 63480
ATTGTAAGCT TTCTGGCTTT TACTATGGGT GAAACCAGGA ACCATGGCAG AGATGTTGGC 63540
AGAGGAGTGA CATAAGTTGA CTTCACTGTT AAAAGCATTCT CTGTGGCTGC ACTGTTGAAA 63600
ATATATGTAA TGGGCAAGAC CTGAAGCAGG GAGATTAGTT ATAGTATAAT ATGAATTATA 63660
TTTGGTCCTT GTCTATGGTT TCCGTTACAG AGCTAAAAGT CTTGGAATTT CCTGAATGAT 63720
AAGAGTGTCC TGTATTTCAG AATGAGCCTG TTTGCTAACA CCGGGGTTCA TACTATTGTG 63780
GTGACTTAGG ATGGAGCCGT AGATAGCCTC AGATGGGGCA AGTAGCTGGA AAGACCACAT 63840
GATTAGAGAA TTAACGGGTT AGAACTTTTA GCCCCACGTA CAGGCCTCCA GGAAAGGAGT 63900
GGAGGGGCTG GAGATCAAGC TGTATAAAAA TATCAAGATT TGGATTTAAT GAGTGGGTTG 63960
CTGGGGGCTG GTGCCGTGTA GGAGGTGGTA TGCTTAGAGG AAGTGAAGC TTCATACCTC 64020
TTCTGTCCCA TACCTTGCCC TACTCATTTT TCCATCTATA CCCTTTATAA TATCCTTTAG 64080
GATAAACCAA TAAACATAAG TAAGTGTGTT TTTGAGTTCT GCGAGCTGTC CTTGCAAAC 64140
AGTTATGCCC AAGAAGGGGG AGTGGGAACC TTTGTAGCCA GTCAGTCAGA TGTAAGTGGT 64200
GCCTGGATGT GGGATTGGCA TCTGAAGTGG AGGGAGTCAT GGGACTGAGC CCTCAACCTG 64260
TAGGATCTGA CATGGTCTCT AGGTAGATAA CATCCAAATG GAATTGGATT ATAGGATACC 64320
CATTTGGTGT CCTCTGGAGA ATTGCTTGGT GTGGGGAAAA AGCCCCCACA CATCTGGTCA 64380
CAAAAGTGTG CTGGGAGGAT AGAATATGTG AAAATTGTCA TAATCAAAAT GGAGTCACTT 64440
GTGTTAAAAA AGAAAAAAA ATCTGACTG GCCAGGCACA GTGGCTGACA ACTGTAATCC 64500
CAACACTTTG GGAGGCTGAG GCAGGAGGAT TGCTTGATCC CAGGAATTGG AGACCAGCCC 64560
ATGCAACATA GTGTGGCCTT GTCTCTACAA AAAAAAAT TTAATTAGC TGGGCATGGT 64620
GGTGTGAGTC TGTAAGCCCA GCTACCCGGG AGGGGGACTA CGGGTGCACG GCACCATGCC 64680
CAGGAGGTCC AGGCTGCAGT GAGCTGTGAT TGTGCCACTG CATTCCAGTC AGGATGACAG 64740
AGTGTGAGAC CCTGTCTCTA TTAAGAGAAA AAAAAAGAC AAATAGATCC AGGAAAGGCT 64800
ATGAAGAGAG AGCTTCATG CATAAATACC AAAATATCTC AAAAGACTCT GCAAAAACCA 64860
CACCTTGCA CAAAGGCCAT CATGAAATAC TTCTGAAATA CACAGAAAAT ACATCATGAA 64920
ATAAATACAC AGAAAATACT TCTGCAAGGA CATCTGCCCA GCAACTGCCT GGTCCATCTG 64980
TGGACGGGTG TCATCCTTGT TATTGATCCT TGTAAGCAAG GGTAATTATC TCAAAACAAG 65040
TATGTGATCC TCCTATTTT CCTTTAAAAA CCTTTTGTCT TCCCTTACCT CCCTGAACAC 65100
ACACAGTTTA CTATGGCATG TGTATTCCCA TTGGAATACT TTATTCCTGA ATAAATGTCA 65160
CTTTCTTTT AGAAGCTTCT CTTTCTTTT TATTAGATT GATAAGTAGA AAGGAAAAA 65220
AGCTTTTTT CCTTTGGACT AGTTGAAGGC AGTTGCAGTA TTCTGGGGGA GAGGGTGGTG 65280
GCAGAGGTGT TGAGGCATGG TTGGAGTTTA TTTATACTTT GAAGGTAAAG CCAACAGGAT 65340
TTGCTGAAAG ATTGGGATAT GGGGTTGGAA AGAGGAATCA AGGATAGTTC CAAGATTTT 65400
GGCTTGAAAA ATTAGAAGAA TGAATCGTG AATTACTGAG CTGGGAAGAC TTGGAAGAGC 65460
AAGGTTTTGG GGAGAAGATC AGGACTGTAA GAATAGAGAA GTCCTTGTC CCAGGAGTTA 65520
GGTTTTGGC TATTAAAGTT AGATGTACTA CATAGATTTT TAGTTGGTTT TTTGTTTTT 65580
GTTTTTTTTT TTTTTTTTTT TGAGACGGAG TCTCGCTCTG TCACGAGGCT GGAGTGACAGT 65640
GGTGCGATCT CGGCTCACC CAACCTCCGA CTCCCTGGTT CAAGGGATTCT TCCTGCCTCA 65700
GCCTCCTCAG TAGGTGAGAT TACAGGCATG TGCCACCCAG CCCAGCTAAT TTTTGTATTT 65760
TTAGTAGAGA CGGGGTTTCA CTATGGCCAG GATGGGCTTG ATTCCTGAC CTCAGGTGAT 65820

FIG. 6.25

CCACCCACCT CGGCCTCCCA AAATGCTGGG GTTACAGGTG TGAGCCACCA CGCCCAGCCC 65880
GGAGTTTTGG TTTTGAAGC ATTCTTTTC AAGTGATAAA GCAAAAAATA TATAATCAAG 65940
AATTTTAAGT ATATACTTTG GAAATGTAA AAAGGAACAT GAGTAATTTA TTATTATTTT 66000
TTTAATTTCT AGTCAGCAAT GAGAGCCCAG TGTACTTTAT GAAGTAGATT GGTTCACACC 66060
AGGAGTGAGC AGACATTTTG TATGATGCAC AAACAAGGAA TGATTTTTTT GTTTTTTAAA 66120
TGGTTAGGAA AATATCAAAA TAAAAATGC CAGAAAAAAT CAAAAGAAGG GCCAGGTGCA 66180
GTGTTTCACA CCTGTAATCC CAGCACTTTG GGAGGCCAAG GTGGGTGGAT TCTCTTGAGG 66240
TCAGGAGTTC GAGACCAGCC TGGCCAACAT GGTGAAAACC TGTCTCTACT AAAAATACAA 66300
AATAGCCGGG TGTGGTGGCA TATGCCTGTA ATCCCAGCTA CTTGGGAGGC TGAGGCAGGA 66360
GAGTCGCTTG AAGCCAGTGG CAGAAGTTGC AGTGAGCCAA GATTTGAGCC ACTGCACTCC 66420
AGCCTGGGCG ACAGAGGAGA CTCTATCTCA AAATAAATAA ATAAATAAAT AAATAAATAA 66480
ATAAATCAAA AGAAGAATAC CCTTTCATAA TATGTGAAAA TTAAATGAAA TTCAAATTTT 66540
AGTGTTCATA AATAAAGTTT TACCGGAACA TAGCCATGCT CAATCATTTA TGTATTGTTT 66600
ATGGCTTCTT TTGCATACAA CAACAGAGTT GGGTAGTTGT GACAGACTAT GTAGCTCATA 66660
AAATCTAAAT ATTTATTATC TAGCCCTTTA TCAGTAAACT TTGCTGATCC CTGTATAAGT 66720
CCTCTGAATC AAATTATTTT CAAAGAGTTC CGTTATAAAA TTTGAGTTTT ACTCTGCTGT 66780
AAATTGCAAA GAACCATTTG GAAAACCTCT TTTAGTCAGG TATTACATT AAAATGTTCC 66840
TTGATTGTGA AACACTAATA TTCAAGACTG GTCCAAAATT ATACCAAATT GAAACTCTCA 66900
AGTGTTTTTA AACAGTAGGA AGTTTTAACT TTTTTTTTTT CGTGGAGTAG TCTATCATT 66960
AGCGTTTACT TTGGAACATT TAATTAGTCT TTTTAAAAA CCCATGAAAT TTATAATAAA 67020
AATTTTAAAT CATTAATGTT GAGTAATCAA AGAAAACTTT TTTTGTTC TCCATTTGTA 67080
AAATGAGTAC ATTATTATTA TAATTGTCT TTGGCCATAC CTTGTTGATA ATTACTTATA 67140
CAAGTATAAG AAGACATGGT ATGTTTTCTT TTTTCTATT TCACAAGAAT AAGTACAGGA 67200
ATTTACTTAA GCTGCTCCAA AACTCAGTGA AAGAGACAGG ATTAGGTTTT TTTTACGATT 67260
GGATTTTAAA TGATACTAGA TGGTTGCGCT GGGCTAAAAT ACTAATGCTT TGTGTATATT 67320
TTTATGACTT TTTGAAGAC AGCTTAAAAA CTTTATTCTA GTTATAAAAA TGATACATGT 67380
TCACTGTAAA TAGAAACAAG TCAGGTATAC AGAGATACAA ATATTTAGAA CATGTGGAAA 67440
GAGGCAACAA AATTTTATAA AAAGAAAAAA GATAAAAATC TGAAATCATT AATTTATAAG 67500
GGAAAAATCA GGGCAAGGAC AAATTATATT ACAGATTGGC CTATGGTGGG AGCACAGATT 67560
ATATAGAGAA AAGTCAGTGA AGACACTTGC GAAGAGTGTG GGTGGAAATC ACTAAGTTTT 67620
GCAGTCCCGG GGCCTCTTAT GGTTTATTAC TGTTTTGTTT TTTTTTTTTT TTTAATATGC 67680
ATTCCTTTGG AACCAAGGGT TTATTATGTT TTGAATAAAG TAGAGGTGTA AGTAGGATGC 67740
ATATACCATG ATCTTGACTA CTTGAGATTC ACAAAGGGTT TTCGTCTCAG GATTTTTTTT 67800
TCTCTTAAAA AAATTGTAT TAATTTTAA ATTGTAAAAA AATTCATCAA CTTAACCATT 67860
TTTATGTATA GAGTTCAGGA GTATTAGGTA TATCACTTG TGCAGCAGAT CTCTAGAACT 67920
TTTTTCATCT TGCAAACTG AAACCTGTGA CCCATTAAAC AACCACTTCC CATTTTCTCT 67980
TCCCCAGCT TCTGGCAACC ATTCTAGTTT CTGTTTCTTT TCTTTTTTTT TCTTTTGAGA 68040
TGGAGTCTCT GTCGCCCAGG CTGGAGTGTA GTGGCATGAT CTCGGCTCGC TGCAACTTCT 68100
GCCTGCGGGT TCAAGCAGTT CTCCTCCCTC AGCCTCCTGA GTAGCTGGGA CTACAGGGGT 68160
GCACCACCAT GCCTGGCTAA TTTTTTTTTT TTTTTTTTTT TTTGATTTT TAGTAGAGAC 68220
GGGGGTTTCA CCATGTTGGC CAGGCTGGTC TCGAACTCCT GACCTCAGGT GTTCTGCCTG 68280
CCTCAGCCTC CCAAAGTGCT GGGATTACAG GCTTGAGCCA CTGTACCCGG CCTCTAGTTT 68340
ATGTTTCTAT GAATCAGACT CAGTACCTCA TATAACGGA ATCATACAGT ATTTGCCCTT 68400
TTTGTGACTG GCTTATTTC CTTGGCATAA TGGCCTCAAG ATTCATCCAT GTTGTAGCAT 68460

FIG. 6.26

GGATGAATAT ACAGTTAGGA GTTCCTTTTC TTTTAAAGT CTTAATCTCC AGTTTATTTT 68520
TGTTTATTTA TTTATTTTAT TATACTTTAA GTTCTGGGAT ACATGTGCAG AACGTGCAGG 68580
CTTGTTACAT AGGTATACAC GTGCCATGGT GGTTTGTTC ACCTGTCAGC CTGTCATCTA 68640
CGTTAGGTAT TTCTCCTAAT GCTATCCCTC CCCTAGCCCC CTACCCGCCG ACAGGCCCGG 68700
GTGTGTGATG TTCCCCTCTC TGTGTCCGTG TGTTCCTATT GTTCAGCTCC CACTTACGAG 68760
TGAGAACATG CGGTGTTTGG TTTTCTGTTT CTGTGTTAGT TTGCTGAGAA TGATGGTTTC 68820
CAGCTTCATC CATGTCTCTG CAAAGGACAT GAGGAGTTTC TTACTTTTAA GGTTGAGTAA 68880
TATTCCACAT TATGTGTATG CCACATTTTC TTTATCCATT CACCTATCTG CAGATGTTTG 68940
AGTTGCTTTC ACTTTTGGG AATTGTGAAT AATGCTGCAG TGAATGTGGG TGTGCAGGTA 69000
CCTTTTCAAG ATTCTGCTTT TGAGTTTTTT TTGGATACGT ACCTTTTAT GATGCTTTAA 69060
ATACATATAT GCTATTTTAA AAGGATTCTC AGTTTCTGA CATATGATAG GACTTAGGAA 69120
GTAATCTCAA AGCATCATGT TGACAGGTTG TTAGTTGATG GTGACTGCAG CTAGTTGGAA 69180
AGTCAGAAGA ATCTAGAAGT TGTCATTTA TACTAAAGAA TTTCATAGTA AGTGCAGTAT 69240
TATGAGTGTA ATGTTCAATT GGTAGAAGAG GCTATCTGAG GGGATTTAGT GCATTTCACT 69300
TATCTGTTGG TGTGAAACGA ATCACCTTGA AACTTAGTCG CTCAAAAATT TTAATGGTGG 69360
CTGGGCATGG TGGCTCACAT CTGGAACCTC AGCACTTTGG GAGGCCGAGG CAGGCAGATT 69420
GCTTGAAACCC AGGAGTTTGA GAGCAGCCTG GGCAACGTGG TGAAACCTTG TCTCTACAGA 69480
AAATACCGTG GCAGGCGCCT TTAGCACCAG CTACTTGGGA GGCTAAGGTT GTAGGATCTC 69540
TTGATCCCAG GAGGCAGAGG TTGCAGTGAG CTGGGATCGT GCCACTATAC TCCAGCCTGG 69600
ATAACAGAGC CAGACCCTGT CTCAAAAAAA AATTTTAATG GCTCCATTTA TTATTTCACA 69660
TGATTATGTG AGTTGACTAG GGAATTCTTA CACATCACAC CATGTCAGCT GGGACAGCTG 69720
AAATGTCCAC ATGGCTGGCA GTTGGTACTA GCTGCTAGCT GGAAGTTGAG TTCAAATAGT 69780
CAGCCAGGGG TCTCAGTTAT TTTCCATGAG GTTCTCTCCA TGAGGCCAGC TGGGCTCTTC 69840
ACAGTGTGAT AGCTGGGACT AAGAAGGAGT GTTCCAGAAG AAGGGCTTGT CCTCTTGAGC 69900
CAGTGCTTAT CAGGCCTCTA TGTATATCAT GTGTGCTAAT GTTCCATCAA AGCTAGTCAC 69960
AGGGCCAAGC CAACTCTGTA CAGTGTAGGG ACTGGCTGCA GGAGGGCATG AATTACCAGG 70020
AGGTGTAGTT CTCTAGTTCA TAGGGAGGGC CATCAAGATA GTAGTCTACC ATACTTGTGT 70080
AAAAGAAGGC ATTAATTAAC TATTATTATT ATTATTATTA TTATTTTAGA GACAGGGTCT 70140
TGCTCTGTTG CCCAGGCTGG AGCAGTAGAG TGGGGCAATC ATAGCTCATT GCAGCCTCCA 70200
ACTCTGGGC TTAAGCAATC CTCCCATCTC AGCCTCCCAA GTAGCTGGGA ATACGGGAGT 70260
GTACTGCCAT GCCCACCTGA AAAAGAAGGC ATATTTTAAA AGCAGACCTT TAGTGTAGAG 70320
GGTTCTTGAA TTTGTTATTT AAAATATTCT GGTAGTTTTT AAACCTAGGA AAGACCCACT 70380
GATTCTTTTA GTGATATGTT TACATTGTTG TTATTTGGCA TAAATTGTGT TAATGCACAG 70440
TAAGATTTC AAGATCATT AAAATTCAGC CACTTGGACT CTAAACCCAA TAAAGATGTA 70500
AAACAGCAGT GCTATGAGAT GCATATTGAG TTTCAAATA TAGGAAACAC AGAAATTACT 70560
CTGTGCACTT TTAATTTGAA AATACTTTTA AAATGTGTAG TATAATGTAG TGTCTGTCCC 70620
AAAAGAGTAA CATTCAATTAT AGTGTCTCTT TACGTTGTTG AAAATTTTAA ATTCACTTAA 70680
CATTAGATTT TTATTAAGC AAAAATATGT TTTCTTATT AGCTTACCCT TTTGTAATC 70740
AGATTAAACC CTTGATTGTT CAAATTAACC TGAAAAAAT TATTCTTTG GAGGCCAAAC 70800
TTTTGATTAA GTAGTTGTTT GTCTCTAATT TTTCAAATT TATGTGTATA AATATAACCT 70860
GTCATCAAAT CAATGCTAAC ATTCTATACA TGTTTTTCAT GATATGAAAA CTATAAAACA 70920
TGAAGTTATT TGAATTTGTG TAGTTTTTAT CATTTTATTT TTACTTTCCA GTGCATCTAT 70980
CCTTTGGGCT CTAAATCACT TAATAACCTA ATTTCTCTG ATTTGGAAGA ATGTCACACT 71040
CCACATAAGC CTCAGAAAAG GAAGAGCTTA GAAAGCAGCT ATAAGGATTC ACTTCTTTTA 71100

FIG. 6.27

GCAAATTCCA AAAAGACTAG AAATTATATT GCTATTGACG GTGGAAAAGT TTTGAACAGC 71160
AAACATAATG GAGAAGTATA TGACGAAACC TCGTCAAAC TACCTGATAG TAGTGGTCAA 71220
CAGAATCCAA TTAGGACAGC TGATTCCTTG GAGCGGAATG AGATTTTGA AGCTGATACT 71280
GTTGACATGG CTAATAACAA AGATCCTGCT ACAGTTGATG TCTCTGGAAC TGGCAGACCT 71340
TCCCCTCAAA ATGAAGGATG TACATCTAAA CTGGAAATGC CACTGGAGAG CAAATGTACA 71400
TCATTTCCCC AGGCTTTATG TGTCCAGTGG AAAAATGCTT ATGCTCTCTG TTGGTTAGAC 71460
TGTATCCTGT CAGCTTTGGT GCACTCGGAA GAGTTAAAGA ACACCGTGAC TGGACTGTGC 71520
TCGAAGGAGG AATCTATATT CTGGCGGTTG CTTACAAAAT ATAATCAAGC AAATACACTT 71580
CTATATACCA GTCAATTGAG TGGTGTTAAA GGTTGGTACT AATATTTTAT TTTTATTTAC 71640
TTATTTATTC ATCTGGAGTC AGGGTCTCAT TCTGTCACCC AGGCTGGAGT GCAGTGGCAT 71700
GATCATGTCT CTTGACAGCC TTGACTTCCC TGGCTCAGGT GGGCCTCCCA CCTCAGTCTC 71760
CCAAGTAGCT GGAACACAG TCGTGCACCA CCATAGCCAG CTAAGATAGT GAGATGGTGG 71820
CCCCACTGTC TTGCCAGGC TGGACTCGAT TTCTGGGTG CAAGCACCTT TCCCGCCTCA 71880
GCCTCCCAAA GTGCTGGGAT TACAGGCATG AGTCACCATT CCAGCCTACT TGTCTTTAAT 71940
TCTTAAAAAT ATTAATGTTG AGTTTGTCT CCCAGCATGT GGGAAAGATG TCATCCATTG 72000
CTTCTGTTT CTGGAGGCCT GGGAGCAAGG AGCCCAGGAA CAGTATCACG AAGCTTGAGA 72060
TAATACCAGT TACATTATCC TGACTGCCCA AAAGGCAGTT TTTTGTGTTT TTTTATTTAT 72120
ACTTTAAGTT CTGGGGTACA TGTGCAGAAC GTGCAGTTTT GTTACATAGG TATACGTGTG 72180
CCATGGTGGT TTGTTGCACC CATCAACCCG TCACCTATAT TAGGTATTTT TCCTAATGCT 72240
GTCCTTCCCC AACCCCTCCA TTCCCCATCA GGCCCCAGTG TGTGATGTTT CCCTCCCTGT 72300
GTCCATGTGT TCTCATTGTT CAACTGTCAC TTATGAGTGA GAATATATGG TGTGTTGTTT 72360
TTTGTTCTTG TGTTAGTTTG CTGAGAATGA TGGTTTCCAG CTTTATCCAT GTCCCTGCAA 72420
AGGACATGAA CTCATCCTTT TTTATGGCTG CATAGTATTC TATGGTGTAT ATGTGCCACA 72480
TTTTCTTTAT CCAGTCTATC ATTGATGGGC ATTTGGGTTG GTTCCAAGTC TTTGCTATTG 72540
TGATTTTTTT TTTTTTTTTT TTTTTTTAA GACAGAGCCT CACTCTGTTG CCCAGGCTGG 72600
AGTGCGATGG CATGATCTCA GCTCACTGCA ACCTCCGCCT CTCAGGTTCA AGCAATTCTT 72660
CTGCCTCAGC CTCCCAAGTA GCTGGGACTA CAGGCGCCCA CCACCAGGCC CAGCTAATTT 72720
TTGTATTTTT AGTAGAGACA GGGTTTCACC ATGTTGGTCA GGCTGGTCTT GAACTCCAGA 72780
CCTCATGATC TGCCTGCCTT GGCCTCCCAA AGTGCTGAAA TTACAGGTGT GAGCCACCAT 72840
ACCTGGCCTA GGCAGTCTTT TTCAAACTC TAAGACTGTG CTTGTGTCTC AGGGTGTGAG 72900
GATAATAGTG GTTAGTTTTA AGTGTTTAAA CTAAGTAAAA GCAGAATGAA GAAGTGAGTA 72960
AAAATCACCC ATAATCACAC AACCTCCTAA GATCTCTTGG CACAATAAGG GATATGTTTT 73020
TCATTTTATT CTCTGTAAAA TAGGATACTT ATGAACCCAC CTCCCAACAC AGGAAGAATT 73080
AAAACATTCC CAATAACTTA CATTTACCTA TGCCTTTCCT CCCATCCCAT TCTCTACCTC 73140
CCCCCATATA GTAATCATT TCTGAAATGT GTTTCATCAT TCCATCTTTT CTTAGTTTTT 73200
CTTACATGTG TTTATCTAAA CAGTATACAG TAGTCTCCCC TTATTGTAGT TGTAATTTTC 73260
TTGGTTTCAT TTAACCCGAG GTCTGAAAGT AGATGAGTAT AGTACAGTAA TATATTTTGA 73320
GAGAGAGGGA GACCACATTC ACATAACTTT CATTACAGCA TATTGTTATA ATTGTTGTAT 73380
TTTATTATTA GTTTTAATCT TACTATGCCT AATTATAAAA CTTGATCATA GGTATGTAGT 73440
TATAGGAAAA AGCATAATAT ATAAATGTT TAGTTACTAT CCAAGGTTTT AGGCATCCAC 73500
TGGGGTCTTG GAAGGTATCC CTCTCAGATA ATGGGGGATG GATGGTACTG AACCTGTAT 73560
ATACAATGTT TTTCCCTATA CATACTAAT TATGATCAAG TTTAATTAAG AGTAAATTAA 73620
ATGTGGGCCA GGTGCAGTGG CTCACATCTG TAATCCCAGC ACTTTAGGAA GCTGAAGCGG 73680
GCAGATCTCA TGAGGTCAAG AGTTCGAGAC CAGCCTGGCC AACATGGTGA AACCCCATCT 73740

FIG. 6.28

CTACTAAAA ATACAAAAT.TGGCTGGCTA TGGTGGCACA CGCCTGTAGT CACAGCTACT 73800
CTGGGAGGTT GAGGCAGGAG AATTGCTTGA ACCCAGGAGG TGAAGTTGA ACAATCACTT 73860
GAACCTGGGA TCACGCCACT GCACTCCAAC CTGCCGGGT GATAGAATGA GACTCTGTCT 73920
CAAAAAAAAA AAAAAAAAAA AAAAAGTAAA GTAAATGTGG CTCAACATGT TGCTGTCAGT 73980
TGGAACATTT GTTCTGATC GTGTCTTCCA CCCACAAATT GAATGCTTTT TCCATCTTAA 74040
CACTTATCAG GCACTGTGGC CATAACTTGA GCAGTTGAGA TGCAACAGCA AAATTAGCAC 74100
AAATTTCTTT TTCTTTCTTC GCAGTTTCAT GGATAAGAGA TTTGTTCTTA GATCTCAGCA 74160
ACCTCAGCAT ATGATTTTTT TCTTAAAGTT GAGAACTTTG ACCTTTTTAC TTAGAGAAGC 74220
ATTTTACAGC TTCTCTTGG CATATCTGAA TTGCCAGCAT TACTATGCTC GTGCTTTGGG 74280
GCCATTATTA AGTCAAATAA GGGTTGCTTG AACACAAGCA CTGCAATACC ATGGCAATAG 74340
ATCGCATCAC CAAGATGGCT GCTAAGTGAA CCACAGGCAG GAGTGTAGAC AGCATGGACA 74400
CATTAGACGA AGGGAAGATT CACGTTGCCA GTGGAACACA GCAGGACAGC AAGAGAGTTC 74460
ATGATGCTAC TCAGAATGGC ATGAAATTTA AAGCTTATAA ATTGTTTCTG GAATTTTCCG 74520
CTTAATATTT TCAGACCACG GTTGAGTTCA GGTAAGTAA ACCATAGGAA GCAAAACACG 74580
GATGAAGAGG GACCACTTCG TATTGCCTAA TTAGTTTGT TTTGATCTTC TGGGACCTTT 74640
TTTTCTTGT GTAAAAATTT ATGGGGCTGT TTATAGTTGT GGCTCATTGA TTTTTCATTG 74700
CTACATAATA CTTCCATTTT GTAAATATAA CAGAATATTC ATCTACCTGT CAGTGGACAG 74760
TGGGGTTTTT TTGCCATTAT AAATGCTGCT GCTGTGACCA TTTGGGGGGC AAGTCTCCTG 74820
GGGCACAGTA TGAGTTTCCC TTCTGTATAA CAAAGGAATG GAAAATTATA GACTTTCGTG 74880
TCCAAATTTA CAAGATAATG ACAATTGTTT TCCAAAGTGG TTGTACCAAG CAATTCTCCC 74940
ATTAATAGTG TATATAAGAG GTCTTCTGA TCCATATATT CTTCTTGGTT TATTTTACCA 75000
CTTTTGAGAT TTTTGCTATT TGAGTGGTAT AAAATGGTCT GTGATCTTGA TTTGCCGTTT 75060
CCACATTTTG AAGAGGTTGT CGGCTCTATG TGTATATATT GCTCATATTT GTTCCCTCTT 75120
CTGTGAAATG CCTTTTGTAT CTTATCCCTA TTTGTTCTGT TCTGTTGATT GTCACGTTTT 75180
AATTGATTG TATGAGTTT TCCCTGTAT CATTGTTGCT AGAGTTACAT CAGATGTGTT 75240
GCTGAATCTG CTCCCAGTTT GCAGCTTGTG TTTTACTTT TAAAAACTG TCTTGATTTA 75300
TAGGGAAGTC TTTATCTTTT CATTGGAGC TAGTAATGTT TGTGGCTTTT TAAAGAAAT 75360
ATTACTATTC CCAAGGTCAG AAAATCATTC ACCTATATTT TAACTGAAAA GTTATAAAGT 75420
TTTGCTTTTG ACATTGAAAT TTCTCATTCA GTTGAATTC ATATTGATGT GTGGTATGAG 75480
GTAAGGATCC ATTTTTTCC CATTTCATA GCCAGTTTTT GTAGCTCCAC TTTATTTTCT 75540
CACTTGATCT GCCATGCCAC CTCTAGCATG TATCAACATA TCATGTATGT GTGCAGCTGT 75600
TCCTTAATC TCAATTTTAT TCTCTTGGTT ACTTTGTCTA ACCCAGCACT CATACTTTTT 75660
AAATTATTAT GGCTACCTTG TAGGGCAAGA ATCCTCACTT TTATTCAACT TCTTTTGAAG 75720
TGTCTTGATG CATATTTTTT CTGATCTTAC TTGGCCATAT ATATTTTGGG GACAGATGTG 75780
ACATCATACC AAGCTTTCTT TGCTTGACAT TGATAGATATT TTCTTATTCA TTAATGTGCT 75840
AAAAATTTTG AGTTTGGTCA TACAGTCTTT TATATGGATC TTATACATCG TTTCCCTCTT 75900
GTTAACCATT CAGGCTGTTA CTAGTTTTTG CTGTTGTGAA TTAACACCAG GACAAATATC 75960
CATATATCTT TTGAATTAAT TACTGACTAG TTTCTAGGA AAGATATTAG AATATGAATA 76020
TTAAAGGTCT TGCTGAATAC AGTTTTCAGA ATGGTTGTAC CAATATATAA TTCCATTTTC 76080
ATTATGTAGA AAAAATACCT CAGTGTTTTT TAACCACTT TGGTTAGAAC ATTCAAGACG 76140
TTATGGTTTT GTTAGGTAAG AAATATTTTG TTTCAGTGTA GGTTTTCTTT GAGACTGAAC 76200
TTTTTTGTGT GTGTCAGTCA TTTACAGTTT TTGCAATTT TAAAAATTCA GTTCTCACA 76260
AGCATTTTGC CTTTGACTTT TCTTCTATTT CTGCTTTCTC TAATTACAGA AACCCCACTG 76320
TTAAGTAGGT GACAGTTCAG TTGTTTGCTG CAGAAGAGCA GCAGTTCAAT ATTGGAATTA 76380

FIG. 6.29

ACTTTAATTT TATGTTTTTA ATCTGTTACT AATTTTTTAC AGAATAATTG TAGTTTTTAT 76440
AATCTGGTTA ATTATATGTT TGAGCTGCAT TACTTTGCAA TGTAAGTTTT TTTTTTGGC 76500
ATGGTCAAAT AACAAAAATT CTGGTTAATG CTTATTTTCAT ATTACAGGAG AATCCAGATA 76560
TTTCATTAGG GAAACATATA AGCAGAGTGT GATCAGGCTG TATGAATTAT TTATAAGAGA 76620
TGTGAGTGAA AAGATCTATT TGTAGCTTAA GAGTAAGTAG AGTCAGATGC ATGTAGAGTC 76680
TTTTATTCAA AATAATTTTC TTATTAATCT TGGATAGTTT CTTGTCACAG TAATTCCATT 76740
TTGAAGATAA TAAATATTAC CATAAAGAAG TGATCAAAAA CATAGATATG TGTGCCAAA 76800
GGTATTTATC ACAATAGTAT TTATAATAGT GAAAAAGAA ACAACTAAAA TGTCTGGCAA 76860
TAGGAGAATG ATTAATAAAG CGATGTTTCA GCTGAATATA GTGGCATGCG CCTGTAAGCC 76920
CAGCTACTCA GGAGGTTGAG GCTGCAAGAT GGCTTGAGCC CAGGAGTTAA TGACCAGCCC 76980
AGGCAACATA GCAAGACCCT GTCTCCAAAC ACACAAACAC ACACACAAGT GCTATGTTTC 77040
AGTCACTGTA TAATAACTAG CCAGATTTTT TGTGTGTTGT GTTTGTTTT TGTTTTTGTT 77100
TTTTGAGAGA GCATCTCACT TGCCAGGCT GGAGTGCAGT AGTACAATCA CAGCTCACTG 77160
CAGCTTGTAG AACCCCTAACC CTCCTGGGCT CAAATGATCC TCCCACCTCA GCCTCCTGAG 77220
TAGCTGGGAC TACGGGTGGG TACCACCATA CCCAGCTTTT TTTCTAAGAG ATAGGGGTTT 77280
CACTATGTTG CCCAGGCTGG TCAGTTTTTA ATGAAGCACA TTTGTGTAGA CAAAGCAGGA 77340
TGTGGAACCG GATAAACACT ATGTTGCCAC TGAAGACCCC TTCAAACCCC TCAAAAATGA 77400
CATAGAAGGG AAATATGAGA TATTAGTTTG GGAAATAATT GTAACTTTAT TAAGACTCCT 77460
TATAAATTTA TCTGTTCTA TGACCTGGCT AAGTTCAATA AAAGTTACAC AGAGTGGAAT 77520
AAATGGTTAG ACATCATTTG TAGTATAAGT AATTGCACAT AAGGAGGTAA CTTTAGCTGT 77580
TTTAGAGATA GACATAGTAT CTGAAAGGTT AGTTATTTTA CTAGACCTGT GATTATTTGG 77640
GTGAGAAAGG CTTTCACTGA GATTTTACCC ATTCAGTAAG TACTAATGAT ATTGTGCTGA 77700
TAGCATATAT TAAGGGAATA TATGGTATAC CACAGAGAAA GAATTAAGGA AATTTTGTGT 77760
TTTGCTTTTT GTCTGTTTGC AAACTTACT GACTCAGCTT TCATTCTTGG GAATGTGTCA 77820
GTTTTCTGTG GGAAGATATA CATTGATGAG GAATTGATAA TGTCTCTGT ATTTCTTAG 77880
ATGGAGATTG TAAAAAATT ACCTCAGAAA TATTTGCAGA GATAGAGACC TGTCTGAATG 77940
AAGTTAGAGA TGAAATTTTT ATTAGCCTTC AGCCCCAGCT TAGATGCACA TTAGGTAAGT 78000
AATTGGTAAA ACTTACTTGT ATTATACTCA TCTACCATAT AGAAATATGT ACCTCATAAG 78060
GAAATATAAT ACTGTTTGAT TACCTTGGAT GATCATATTC TTGGGAGAGA GAATCTGAGT 78120
AGTTTGACTT AGGAATCTAC CACTGGGTAA GTTATTGTAG GGCAGAGCTG TTCCATATAA 78180
ATATGTAGGC TGGTGTCCA CCTCTTGAGA GTGGGTGCAG TTCTCAGAAC CAGGAGAATT 78240
TTAGGGGGCA TATCATTAGT TGCTTCTCTA GTACGTTTCC TAGTAGACAG ATCTAGCATT 78300
TTTAACCTCA ATTGTGCATT AAAAAGCACC GAGGGAATTT AAAAGTAAAT GCCAATGCTG 78360
GGGCATTTGA ATTAGGATCT CAGGGATGGG GCTCAGGAAA TCAGTAATTT TTAGAAACCC 78420
CACATGATTG TTATATGTAC CCAGGGTTTA GAATCTCATC TAAACCAACC ATAGTAATTC 78480
TACTTCCCTA CCAGTGATTG GTTTAGGAAT GTCCTTGTGG TAGAGTTTTG GCCAGTGGAT 78540
ATTAAGAGAA ATATGCTGAT GGCCTTTTGG GAAAGCTTCC TCGCCTTAG AAAGGGCACA 78600
AGGATGGGAC CTCCTTGTTT TCTGTGACTT GGTTTTTGGC CTGTGGGAGT GGCCTGCAGC 78660
AAGTGAGCTA GAGAGTCTGT CCAAACCTTT CTAATTTTTT TTAGTATTGC GAAAAGGAGC 78720
TGCGGGGTTT TTTTGTGTTT TTTTGTGTTT AAAGGGCTTT TTGTTTTATT TTTCTTGAT 78780
CCTTGATTA ACTCTTCTAT TAATGTTATA GTAGCAGAAT ATGATACTCC CTATTAGTAA 78840
TAACCCATAT TATGTAAAT ATCAGTGCCT TCTAGTTTTT CTCTCAATGA GTGACATTTA 78900
ACTTATATTA AAAAATGATA TTTATATTTT ATAATAAAT CAGTTGTTGC TACTGATTTG 78960
TCTAGCATGT AAAAAAGACA CCATGCTTCC AGATCATTAT AAAATATGAT ATTTTATAAT 79020

FIG. 6.30

ATATTTACAA TATATTTATA ACATATTTAT ATACTTAGAA TATATTTTAT AAGGCTGGGC 79080
TTGGTGGCTC ATGCTTGTA TCCCAGCACT TTGGGAGGCC AAGGCAGGCG TATCACAAGG 79140
TCAAGAGATT GAGACCATCC TGGCCAACAT GGTGAAACCC TGTCTCTACT AAAAATACAA 79200
AAATTAGCCG GCGTGGTAG TGTGTGCTG TAGTTCAGC TACTCGGGAG GCTGAGGCAG 79260
GAGAATCGCT TGAACCTGGG AGACAGAGGT TGCAGTGAGC TGAGATCACG CCATTGCATT 79320
CCAGCCTGGG GACAGAGCGA GACTCCGTCT CAAAAAATGT ATATATATAT ATATATATAT 79380
ATGTGTGTAT GTGTGTGTAT GTGCGTGTGT ATATATATAT ATCGGGAAGC ATGGCATCTT 79440
TTGTACATGC TGGACAGCTT TTGACGACT TCTTTGACTC ATGCTTCTGC CCCCTAATT 79500
TCACTTTTTT TCCTACATT TATTAATAAT AATATATAAT AGTTGTATAT CTGCTTTATT 79560
TTTCATGGAC TTATACATAC ATATTTATTC TGTTCTTATA AAAGTCTGAT TTTTCGTATG 79620
CCAAATTTCT GACATTTCTT CCTCTAGGCC TGAAGAACTG TTGTAATTTA TGCATCAGAT 79680
AGGCCCTCAG ATGGAATGAA TATTCTTTTT TCTTTATATC AAGGTGTAAT TTACATATAG 79740
TAAGACCGTT TTTAAGTGTG TACAGCTCTG TAACCCTCAC TACAATCAAG ATATAGGACT 79800
CTGTCACTCT AAAACTTCTC ACCAGGTTCA TCACCCCCAG CCACTGATCT GTTGAGCGAA 79860
TACTCATTTT AAAGGAGCTT TTTCCGTAAG ATCCCTAGAG TTTAGATGGA AGGGCTTTTCG 79920
TGGTGCAATTT AGCAGATACC ATTTCCCTTC TAGACTCCCT ACTTCAGTTC CCAGTTGAAT 79980
TAAAGAATGG TTTCTCCCC AGCCTGAGTC ACTACCCTTC TTATCCCTGA TAATTATTTT 80040
TGGAACAAAG TTACATCTTT TGCTCCACCT CCGCCATGGG CCTGGTTTTT TATGTAACAG 80100
AAGGAATTTT TAAATTATTG TTTTGTGTAA TCATAATAAT TGGGCAAGCA TACAGCTCTT 80160
TTCAGTGCAG GAGGATTCCT CTCTTGTTTT ACTGCCCAT CAAGGATAGG TGCTATATTT 80220
TAGCTGAAGA TCTTACTAAT GAAATGCTCT GTAATCATAT AACTTATTTA AAGATGTGTT 80280
TTGAGCTCTT TCATAATATT TTAATTCATG GAGAACTTTA TGTATTTTAG ACCTGAAGAT 80340
TTTATATTGT CATTATGAAA TGTAATTTGT TTGCTTTTTT AGTTAATATA TAGTTACAAT 80400
AGAATACGGA TTTAAAGGCT GATAATGAAT TACAAAATTG TGCTATATGA CATACTGTTT 80460
ATGCATACAG TGTTGCATAT TTTCAATTTCT AGGATATTGA TTTGTATTTT TACTTACAAA 80520
AAAACTTTTT AAACTTATT TTATGGCTGG GCCCGGTGGC TCACACCTGT AATCCCAGCA 80580
CTTTGGGAGG CCGAGGCGGG TGGATCACCT GAGGTCAGGA GTTCAAGATC AGCCTGGCCA 80640
ACATGGTGAA ACCCTGTCTC TACTAAAAAT ACAAAAAATT AGCCGGACGT GGTGTAGGTG 80700
CCTGTAATCC CAGCTACTCG GGAGGCTGAG GCAGGAAAAT TGCTTGAAAC CAGGAGGCAG 80760
TGGTTGCAGC GAGCAGAGAT TGCGCCATTG CACTCCAACC TGAGCAACAA GTGCGAAACT 80820
CCTTCTCAA AAGAAACAAA AAAACTTTTT TTAATGTTTT TGTTCAAAAG TAGCAGTGAG 80880
ACTATCCCGC AAAGGTGACT ACTAAAATAG CCTTGTAAC TACTGATATT TATAGAATAT 80940
GCTTAGGGTT AGGGTATAAC TCGCTTGAT TATACTCATC TACCATGTAG AAATATGTAC 81000
ATCATAAGGA AATATAATAC TGTTTGATTA CCTTGATGA TCATATTTT GGGAGAGAGA 81060
ATCTGAGTAG TTTGACTTAG GAATCTACCA CTGGGTAAGT TATTGTAGGG CAGAGCTGTT 81120
CCATATAAAT ATGTAGGCTG GTGTTCCACC TCTTGAGAGT GGGTGACGTT CTCAGAACCG 81180
GGAGAATATT TAGGGGACAT ATTGTTAGTT GCTTCTCTAG TACTTTTCCC AGTAGACAGA 81240
TCTAGCATTT TTAACCTCAA TTGTGCATTA AAAAGCACCG AGGGAATTTA AAAGTAAATA 81300
CCAATCATAG GGACATTTGA ATTAGGATCT CAGGGAAGGG GCTCAGGAAA TCAGTAATTT 81360
TTAGAAACCC CACATGATTG TTATTGCTTA GGTAATAACA CCTACTGTCT ACCTTGTTGGT 81420
CCTGCCAAGG TGA CTGTTCC TGGCCATGTT CCAGGCAACT GTAGTTCCAG GCTAGGGGGA 81480
GAACTGGACC ATGGAAGTGA GGCTCTGTCC AGGGTAGGGG AAGGGATGGA AGGTGACTGT 81540
TCCTGGCCAT GTTCCAGGCA ACTGTAGTTC CAGGCTAGGG GGAGAACTGG ACCATGGAAG 81600
TGAGGCTCTG TGCAGGGTAG GGGAAGGGAT GGAAGGACTC AGTCTCTTGG GCCAAATCGG 81660

FIG. 6.31

TAAGGCAGCA TCTAAGCTCC TCTGAGAATA GGAAGGAGAG CAACCAATTG GAAAAAGAAT 81720
GGGAAACATG TAGATTCTCC TGCTTACCTT ACTTTCCAGT CTCAAAGCTG GAAGCCAGCA 81780
TTCAGTGTTC AGTTATTTTC AATGACAACA AGATTCAAAT CTTCAGTTGT AAAGTTGTTA 81840
AAGGAAAGGA TTAGACTGAA AAGTTAAGAA GAACGGTAGA TGAAGAGTCC AAAGAGTTGA 81900
GGCTGGTCAT TTAACCATTG TGTGGCCACG CCCTCTCCAC AGGTGGAACA AGATGATCAG 81960
AATAGAAATG GCCAATTCTG ATGTGTTTCT ACAGTGTTTC ACTGATTACA TTTTAAACA 82020
TCTGTAGCAA ACCATTTCCA TAATTTTTTT TTTTTTTTTT AGAGACGAGG TCTCGCTCTG 82080
TCACCCAGGC TGGTATGCAG CGGCATGATC ATAGCTCACT GCAGCCTCAA ATTCCTGGGC 82140
TCAAATGAGC CTCCTGCCTT AGCCTCCTAA GTAGCTTGA CTACAGGTGT GTAGCACCAC 82200
TCTCAGCTAA TTTATTTTCT TTTATTTTTT GTAGAGATAA TGCCTCGCTA TATTGGCCAG 82260
GATGGTCTCA AACGTTTATA GAAACTGGTT TTAGGTTTCT AGAGGCTGGC AGCAATTCTC 82320
AGAGGTAACG CAAGCAGTCT TCCTGCCTTG GCCTCCCAGT GTGCTGGGAT TACAAGGTGT 82380
GAGCCACCAC ACCTCATCAA TTTTGTGTTT AATATACTCT AAGGCTTATC ATAGTTCCGA 82440
GATCTTTTTT TTTTCTCTGA GAAATCTAGA AAGATGGAAG ACAGTATGGG TCTTTTGTGG 82500
ATTTTTGTC CTAAGAAATT TTCATAAATG TCTGCCAAGG AAAAGGAAAG AGATCAAAGT 82560
GGTAATTAAT TCTTTAGGAT GGACATTTTT AGAAAAATGC TTTATAAACT TCCCCTCTCC 82620
CAACTCTGAG TGAATTATTG TGTCACTCTG TATTAACACA TATTCATGCT GTAAATATAG 82680
TAAGAAAAGA CAATAGTTCA CAATTTTGGT TTAGTTTTTG CCATTATTGA TTATGAGCAG 82740
TAATTCTTCC TTTTCTTTTT GAAGGTGATA TGGAAAGCCC TGTGTTTGCA TTTCCCTGTC 82800
TCTTAAACT AGAAACCCAC ATTGAAAAGC TCTTCCTATA TTCTTTTTCT TGGGACTTTG 82860
AATGTTGCA GTGTGGACAC CAATATCAA ACAGGTTAGT TTCTTTTGT TTTTAAATG 82920
GGTCTCTTA GTTCTCCAC CACTAAGGT AAGAGAACA TTTGAGCACC AGACACTACA 82980
GTTTGCTTGC TTCTTTAAAC TGAAGGGTC AAAACCTCAT CGTTTGATAG ACTGCTAGTA 83040
GGATATTTCC TAAGGAGTTC TTCAGTGGGA AATAGGGACG ATGAGAGGAA TAATACACCT 83100
CCCTCTCCA GAGTCCTTGC TGAGTAGAAT ACCTCTCAGA ATGCCATGAA ACTGTAGGCA 83160
TTTTGTGTTA TTCCTCTATT AGAAATGAGG GGTGTTGCTT GTTACTTTA GGTTTCTAAC 83220
ATTATAGACA CTAGTTTTAG GCTCTTGGAG GCTAGCAGCA ATTCTCAGAG GTAATGCAAG 83280
CTTCCCCATT TCTTCCCGTA GTCCTGTGAA AGACCAGCCA CCTCCAGAAG CCTACACATG 83340
AGTCTTCTCA GCCATACTTT CTGCTTTTCC TAATGCCTCT CAGCAGCGTA TTAGAAAGGC 83400
CATGATCGAT GTACCTGTTA CCTTCAGGCT TTGCATAAGG TGTATATGAA ACATAATGAA 83460
TTTCGTGTTT AGGCTCAGGT CCCATCCCCA GGTACCTCT TTATCTTGA GACACTTCTG 83520
GTCCCATACA TTTAGATAA GAGATATTCA ACCTGTACCC ACCACGTAAG GAGAGGAATA 83580
GGTTTAGAA GAGGAGTCAG GGAGGCAAGG TATCCCAGA GGGATATTCT CACTTGGTCC 83640
ATACCTGAGA AAGTTGCTGG CTGGCAGTTA GGAAGATGAC CAGACTGGCT CAATTGTTG 83700
TGTATCAAA TTATTACAAT AGAAATACT CTTCCACCC CCCCCGCC TTTTTTTTTT 83760
TTTGAGTTGG AGTCTCGCTC CCGTCACACA GGCTGGAGTG CAGCAGCGTG ATCCCGGCTC 83820
ACTGCAGCCT CCACCTCTG GGTTAAAGCG ATTCTCCTTC CTCAGCTTCC TGAGTAGCTG 83880
GGATTACAGG TGTGTGCCAC CACGCCCGGC TGATTTTTGT ATTTTAGTA GAGACAGGT 83940
TTTGCCATGT TGGCCAGGCT GGTCTGAAC TCCTGACCTC AGGTGATCCA GCCACCTGAG 84000
CCTCCACAG TGCTGGGATT ACAGGTGTGA GCCACCATGC CTAGCCACAC TTTTCTTTAG 84060
CTTAAGTGCT TAAGTTAGAA AACTTGAAGT CTCTCTAAGT TACTCAAGTA AAATGTGAGA 84120
TAAAAATATT ACTTTGAAG GCCGGGCACA GTGGCTCACA TCTGTAATCC CAGCACTTTG 84180
GTAGGCCGAG GCGGGTGGAT CACGAGGTCA GGAGTTTGA ACCAGCCTGG CCAACATGGT 84240
GAAACGCTGT CTCTACTGAA AATACAAAAA TTAGCCGGGC ATGATGGCGG ACACCTGTAG 84300

FIG. 6.32

TCCCAGCTAC TCGGGAGGCT GAGGCAGGAG AATAACTTGA AACCCGAAGG TGGAGGTTGC 84360
AGTGAGCTGA GATTGCACCA CTGCACTCCA GCCTGGTCAA CAAGAATGAC ACTCCGTCTC 84420
AAAAAAAATT AAAAAAATT ACTTAGATAT TCATTATCTA AATATGAAAT CCTTTTATAGG 84480
TATTTAAGGA GTAGTCAAGG AGAGTTCAGT CTGGGAGGAT GCTCCAGGGA ATGCAGGCAA 84540
CAAAGGTTTT GTTTTTTTTT TAACTGGTTA ACTCAGATCT ACTAGAACAG GGTAAAGGGAG 84600
GCCACAGAGT AGACACCATG AGCAAAGCTA ACCCTCCTGA GTTGAAAAAA TTATGGACGA 84660
GAAGTTATCA TTGAAATTAA CTGTTGGCAG ACATATCCAA AGAATATCGC AAGGATTTGG 84720
TCCCTTTATG CATCCTGAGA CAGATGAATG TGTGGAATGG CAGCTGGTGG GCAACAGAGC 84780
GATATTGGCA TGGTGGTGAT ACAGGGAAAT AGTTTCATCG TGTTAAAAGC CATGGAACAA 84840
AGATACATAA TGGCTGCTCT GCAGAAAAAT CCACGTCCCC TCTCCAAAGG GCCTGTTTTA 84900
CTCTGATGTA AAAATTGGGT CAGATAAATT TTCATATTAA GCTTTTTGTT GAGTAAACTT 84960
TTGTAATAGT CCCCAAAAT CCCACTAGAA CAGGGTGAGA ATTAACGTTT TATTCATACC 85020
TAGGACTTAA ATAATTTAGT GTAAGCAAGT GAGTATGAGA ACACATCTGT TTCCAGTCTT 85080
CTATCATTGC TTTATATAAA TTCTCTGGTT TTCTCCTCAC AGTAACTCAG TGAGGAAGAT 85140
CCTAGTGTC TCATTTGGCA CGTATGGATA TGACAGCTTG AAAGGGGTTA GATTGATTCC 85200
CAAGATGACA CACTGTAAGT GGCAGAGTCA GGAGACACAC TTAGGCTCTT CTGGCCTCTA 85260
AGACTTTCTT GCTCACTGTG GTATACTCCT TAATCACTAC CTGGGTTTTA AATAATATAA 85320
ATAACCTTGC TGATTAAAAT CAGCTTAATT GTAGCTTCTC TGGAAATCCAT ATCTTAGTTG 85380
TTTGACAGTT TTCGGTTGAG TGTCTTCTGT GTGTTAGGAA CTCAGGCACT GGAAATAGTG 85440
TATCTTTGCC AAATTTACTA ATTAGGTAGA GAGATAATAC ACGAACACAT AATAGAGGTC 85500
CAGTGACTTC GTAATTAATC TGATCTTTGG GCTGCTTAAC GTTAGCTTTG AATGCAAGAT 85560
GTAAATGCG TTTTAGAGAT ATATAGCACA AACTGTGAGA GCTCAAGGGA GGGAAGCCAC 85620
TAGCCGCTTT TGTTTGCTTT TTTGTTTTTT AAAAATAATC TTACTTTGTT CTAAAAATAA 85680
AAGTAGTTAT AGAGGGAAAG CTAAATGAA GTGACGTTTT CTAAATATG TTTAATATG 85740
TCATAACTTA AAACCTATTT CCACTTAATC TGAAGGAGAA CTGTCCAGCA AATTCCTTTG 85800
TTTTTGTA GCTGTTTTTA GTGCCAGCAT AAGGGCTTTT TACTCACTT GGAAAGTGTA 85860
ACCCAGAGTC AGTTAAAAAC ATAGTCTTCA GAGGCAGATC TCAGGTCTGT TATTATCAC 85920
TGTA CTCTAT GTGTCACTTT CCCCATCTGT AAAATGGGGA TAAGAATAGC ACCTGCCTCT 85980
GAGAGTTGTT TGGAAGATGA GTGTCCAGTG CCATGCCCTT TGCACATAGT TTAAGTGTC 86040
AGAAATGTCA GATGTCATGT GGAGAATTAA CACTTACTTG CTGAGACAGT CTCCTTTTTA 86100
TAAACTAAAC AGTAGGAGCC TTTACATAAC AATTATCTTT GAAAATTTAA GAATTTAGCA 86160
GAAATCAGTG CATTTGTTGA TATCTTTATG TTGCTTTGCT TTTAAATGT TAACCTCCCT 86220
GACTACTGAT GTTTTAACA GACAGTGCTT CCTCACAAGA TTTATAAGTA TTTGCTATTG 86280
TTTAGAAAGG AAGCTTGAT CTCTTAAGTA GCTGCTCTTT AAATTACAAA TATTTTATT 86340
AAAGTGGATG CAGTTGAGGT TTAGTGACA TCTTAAAGG TCATCTTTT AGATGGCGTT 86400
GCTCTCAAGT ATTCAGACTA AAGTGCAAAT TTAGAAGTGT GTAACCTGT GAAAACAAAA 86460
TTTGTTTACA ATTAATGCTG TGTGTGTGTG GTTTTTTTTT TTAAGGATTA AAAAAAGTTA 86520
AGTTGTATGT ATTCCTGATT TTATGTTTGG AAACATCCCC TTTTCATTTT TGGTTGTCTG 86580
TAATGGCTAG CCAGTTTGAG TTATTTGAGT AAGGGGTGAG CTCTTAATAA ATTTGACAAC 86640
CTTAGAACAG TGGTTCTTCA CTAAGGGCTA TTTTTCCTCC CTGGGACAT TTGGCAACAT 86700
CTACAGACAA CTGGATGCCG TTAAGTGGCAT CTGGTGAGGA GAGGCCAGGG ATGATGCTTA 86760
ACATCCTACA GTGCACAGGA CAGTGCTTCA CAGCAAAGAC TCTCTGGTGA AAAATGCAGT 86820
GATACCATTG AGGAACCCTG TCTTTTTTTC TTGCTTCATC TCATAGTTGA AAGATATGGG 86880
AAATTAACAT GGAGCATCTT CACAGAGCTT CTTTACTAGA GGTAGGGAGG AACATTGCCA 86940

FIG. 6.33

TATTAACATG ATTTGGGGAA ATAAGAAAGT ATGAATCACG AAAAAGGGGA GGAATACTTT 87000
TAGACATTGG TTAAATTAA TGAAATGCA TTAAACGTTA ATGAATTTGT TATGTCATTT 87060
TTTTATAGGC ATATGAAGAG TCTGGTCACC TTACAAATG TCATCCCTGA GTGGCACCCA 87120
CTTAATGCTG CCCATTTTGG TCCATGTAAC AATTGCAACA GTAAATCACA AATAAGAAAA 87180
ATGGTATTAG AAAAGTGAGT TAAAATTGTC TTATAATTTT TAGTACAAAA TGAAGGTGGA 87240
TTTACATTTT TCTTAATGTG TAGGATTGAA AATGGTGACA ACAACTTACC TTTCTGAAAT 87300
TTGAGTTAAC ATATATTTCT GGGTTGCCAG CTGCCTCGCT CTATCTGGCC AGTGAGCCCA 87360
CTGTCACGGT GAAGCCACTG AAAAGCCAAC TTAGGCTGAC TCTCTGGCCC CACTCTCCTA 87420
GTGTCTTTCC TTCTTTTGC CTTTTTCTC CTTTAAAGGA TATCAAGCTT CAGTTTTTCT 87480
CTCCTCTGCC AAGTGTATGG AGTTTCTAGA ATTCTGGGAT TTCCTTAATC AGATTTCAAG 87540
AACTAAGATG ATTCAAAGAT AAGCCACAGG CTCATCTCTC TGAATTTCCA TCTTCTCCTA 87600
GATCTCAGCA TGCTAATTCC TCATCATCTT GAAAGCTATC TAGTGGCCTT GAGCAGATAT 87660
ATTTTCATTG TATTTTGCCA GCTTTTCTGT TTGTCTCAG TTGGGGAGGT TGGTCAGCAT 87720
TACCTTTTCC AGTATTACCA GAGAACCATC TGTTTAACT CACAGGTCAG TTCCATCTCA 87780
GGCCGTTTCC CTCTGTCTCA TTAATGCACT CACACATGTA CACAACCTCT CTA CTCTTCA 87840
TTTTCAGTCT AATCGTACAT TAAGGAAATG TTTTGAGGTC TAATTTGATG TAATAAGAA 87900
CCGGGAACAT TAACCTTTAT GCCCTTGAAT GTGCCAGAAA CCCTTCAGAA TCTTTCCTAA 87960
AGGTTTATTC TCATTGAAGT AATAAATCCT CAGTTTATCA GTGCTTACAG GCTCAAAAGG 88020
GAAAAAGGGC AGTAGTCCCC TGTTCCCTCC TCCAGGTATC TACTTTAAAC CTTCAAATTA 88080
AGGTAGTATT TACTTTTACT TTTCAAATTG ATGTGCCTAT TCTACCGTAA TGCAGTCTGT 88140
TCTCCTTTTA TAGTAATTGA GACTAGGGT CTCACACCAA CACCTGGGCC CCATCTCTGT 88200
TTAGCCTTTC CCTGTCCTTT CAATGCAATT GCGTATTGG CTA ACTCAGT ACTCGGTGTT 88260
TGCATTGTTA TTAATATACA TGTGTTATTC CCTCTTCAGC CAAGCAGTAT ATATAGTTAG 88320
GTTTCACTTT TACAATTCTT ATTTTTCGG GAATTGTTAT TTGCCTTGTT TCACTTTGTT 88380
TTATTATGTA CTGTGAGTTT TTGCCAAATA CTTTAAAGAC TTATTAATAA ATTTTCAATA 88440
CTCAGATGCT TCACAGTTTT TACTCTGTT CCTCTCCCT TTTTTCCTG GAACTCTTTC 88500
CTGCCACCTT TCACTCTTTG CTGCAGTCTG CGCTGGTTC TCTCTGGGCC TGCAGCATAG 88560
GGTGCTCTTT ATTATGTACA CACTTCCAGT CACTATCGTA GTTTTATAGCC CAAGGCCTCA 88620
TCCCCACATT CTATCACATC TGTTGCCCAT AAATATCCAG TCCTTTAGGG GTTCTCTGGG 88680
AAAAATAAGC TCTTCTTGT CATCAACATA TGCACCTCGT AGTACTCATG TCTTCACTTT 88740
GCCCCTTCTG CTGGGTAAGG TGCCACTTCT CTGTTTGCTT TCTGTCCTCT AAATATTTGA 88800
CTTCTTATTT GCTTATTTTC CTTTCTTGT CTTTTGGAC TCATATCTTT TTGCCCCCTC 88860
ACTATTATTT GATAGCATTG GTGTAGGAGG GCGAAGTGG AAGGAAGAGG AGGTGTCTGT 88920
ATCTGTCTGA AGATTACAGA AGTCTGTAAT CTGTCTTGGC TGCCAGGTGT CAGTTTGTAG 88980
ATGTAAATGT TGATGATGAG GTGAGGAGAA GAGCAGCAGA GCATGGGGTC TGCCATCCTG 89040
CCTTGACCA TGGCCTGCTT TAGGCTGCTT GGTGTATATG ATTTCACTA GCTGTTTCATA 89100
CCTGCTTTTT CCTGTGCCCC AGCACTGAAC ATAGACTCGT ACCATTGTTT TGTGTAATCT 89160
GTAAATTGGT TGCACCTGAG CATATATATT TTTTAACTAT ACAAATAAGT TGCTTCCCTT 89220
AAAGATTCAT GCTCTGATCT GGAAATGGAT TCATTAGGTA AAAGTCTTTT AATGGAAAAT 89280
GTGTTTGTAG TTCCAGTGGG CCAATTTATG AGCAGAATTT ATAATGTGGG CATTTCTGT 89340
TTTCTTCAAA AGTAAATTGA ACTAGTGTAT GAAGTTTCAC TTAAATTTTA AATGCCAAGG 89400
TCTTTATATA AGTCCTTTGT GTTTTTTAA TTTTGAAATT TGTATAACTT GATTTGTTT 89460
TGCTAATGG AATTTAGAAA TAAATTTAAT ATAGTTTTTA GGGCTAACCT AAAAGTAATT 89520
GGGTTTCATCA TGGTGTCTA TGTAATTTAA ACATATAGAA TCCTAAAAAC TAATTAAGTT 89580

FIG. 6.34

CCTTGGACAC CTTATCTCAC ATAACCCACA TCTCTAATGT CTCCCCATTG GGAAAAGAGT 89640
CCATTGATAA ATCAGGTGAA TTATGCCTAG CGGGCCCAAA TCTGCTACTT TTCTTTAAGT 89700
TGTTTAGGAG TTACATTGAG ACCATGGTGA CATGGAGCAC CAAGAACTTA GAATCAGATT 89760
TCATTTTACT TGACAACTC TTGAAAGGTC ACTGCCACAG TCTCTCTTGA GTGCAAGGCT 89820
ATGGCTATGC TTTGTAGCAC AGGGACGCGA TATTTCTCTG CTATCTTTGG GTAGCAGAGG 89880
TTAACACAGC TCCCTTGTGC TTTCTTTCTC TCTTTTCTAT TTTCTTTTCT TTTCTTAAGG 89940
ATAGATCTTT AAATAGGAGG AGTTTAACCC CATGTTAGGT GAATTCAAAT GGATCTTAGC 90000
CTGATGTCTC TTGTTCTCTT TTGGTTCCAG TTTGGTTAAT TCCTTTCATC CAATTTTCCA 90060
GTGGTTGAGG GAGAACCCTAA CTTGCTCTCC TCGACTCTGA GCATCATCCT TCACTGACAG 90120
TTCAGGCATT GTGGGTAGGA AGAAGTCTGA GAACAAAACC TAGGGATAAA GTTTAGTAGA 90180
GATGGGGTTT CACCATGTTG GCCAGGTTGG TCTCGAACTC CCGACCTCAG GTAATCCACC 90240
TGCCTTGGCC TCCCAAAGTG AGGCTGGAAA TAAGACATGC TGAATTGTA AGTAGGACAC 90300
TAGAGTCTAG GGGAATCAAA GAGGAAAATG AACAGAAAAG GGAAGGGGAA GGATATTATT 90360
TGATTGACTC CAAGATGCTA CTGTTTGTA GTTTTACCAT TTTAAAAATA TGCCATTAAG 90420
AAAGAAATGC TGGCCGGGCA TGGTGGCTTA TGCCTGTAGT CCCAGCACTT TGGGAGGCTG 90480
AAGCGGACAG ATCACCTGAG ACTAGGAATT TGAGACCATC CTGGCCAACG TGGTGAAACC 90540
GCATCTCTAC TAAAAATACA AAAATCAGCT GGATATGGTG GCACATGCCT ATTGTCCCAG 90600
CTACTCAGGA GGCTGAGACA TTAGTACTGC TTGAACTGGG GAGGCAAAGG TTTCACTGAG 90660
CAGAGATTGT GCCACTGCAC TCCAGCCTGG GCAACAGAGT GAGACTGTCT CAAAAAAAAA 90720
AAAAAAAAAGA AAGAAATGCT GCTTATTTAA CTGTGTTCTG TCAATGTAA GGTGTATCCC 90780
GACTTCAGAG ATGTTAACAA ATGGGAAAAA ATTTGGAATT CATTAGGCAT TTGGAACCTA 90840
CAAAGTTTCG GCCGGGCATA GTGGCTCATG CCTGTAATCA CTTTGGGAGG CCAAGGCGGG 90900
TGGATTACCT AAGGTCAGGA GTTCGAGACC AATCTGGCCA ACATGGTGAA ACCCATCTC 90960
TACTAAAAAT AAAAAATTA GCTGGGTGTG GTGGCATGCG CCTGTAGTCC CAGCTACTCA 91020
GGAGGCTAAG GCAGGAGAAT CGCTGAACC CAGGGGGCGG AGGTTGCAGA GAGCTGAGAT 91080
CGTGCCCTGC ACTCCAATT GGACAACAGA GTGAGACGCC ATCTCAAAA CAAACAAACC 91140
AAAAAAAAAA AAAAAATTC ATAGTTACAG AAAGTAGTAT GGAGGCCATA CCGAGATTTT 91200
CGACATGGTA GTAAACTCT GCATTATGGC TCTGTTCTGC ATCATCTCTG TTCTGCATCG 91260
TTTCACTCCA CATCAGACCC TGGATAGCTT TGGTGTACTG GTCGATCTTG TGGCAGTAAG 91320
GCTAGTGTA TTAAGAGGAT ATTTTAAAC TTAACATATA ATTGCTCTAG TTGTTGTCTC 91380
TTTTTGTCTG GTTAAGAAAA TCAAATTTCT ATCCTATCTG AATCTCATAG CAGACTTTGG 91440
AGATTTCTGA CAAGTCATTT CTTACTACCT AGGGGAATGT ACTTGACTC AGCTAGAGTC 91500
TGAGTATCTT CTACATCCAG GGAATTGGGC TGAGTGTTGA TTTTGGTCTT GGCAGTTTTT 91560
ACTTTTATTA ATTTGCAAAA GAATAGAAGA CTTGGAATGT ACAAGAAGCA TAAAAATGTG 91620
TCAGGTGGTT TTACATGCGT TATTTATCAC GTTAATATGT CTTAAGATAT TTTCCACGTG 91680
TAAACTTATG TAAAGGCAGG AAAGTAGTGA GATTTTCATAT TCTAGGGATC AAGAGATTGT 91740
TTTAGTAACT AGCCTCAGAA AGTATCTTGA AAGGTATTAT ATAAGGTCAA GGAACCTAAAT 91800
ATTAGTAAAG AGTCAGGCCA GGCGTGGTGG CTTATGCCTG TAATCCCAGC ACTTTGGGAG 91860
GCCAAGGCAG GCAGATCACT TGAAGTCAGC AGTTCGAGAC CAGCCTGGCC AACATGGTGA 91920
AACCCTGTCT TTAATAAAAA TAGTAGTGTG TGGTATGGTG GCGCATGCCT GTAATCCAGC 91980
TCCTCAGGAG GCTGTGGTGG GAGAATCACT TGAGCCAGG AGGCGGAGAT TGCAGTAAGC 92040
TGAGATTGCA CCACTGCACT CCAACCTGGG TGACAGAGCT AGTGTCTGTC TCAAAAAAAG 92100
AAAAAAAAAA AGGTCAGATA GGTGCCTAAA GCCTGTGTGT CTCGCTATGA GAATACATCT 92160
CAAGTTTTAC TGTGGTTCAT TGATTGAGAC ATGTAGTTCA CATTTTAACC TGTCTGAAAT 92220

FIG. 6.35

GGTAATATGT GAAATTGATG TCATGATATA GTTTAATTGG CAGCATGTTT TCATAGTGGT 92280
ACATTTTATA ATTAGTGAAA TCTTAGATTT GATGAAATAG ATATGATTTT TTAAAGTGGG 92340
AAAGTTTAGT GTTATAGACA GTTTGCAGGA CTTTTTATTT TG TAGGTACT TAAATTTTGA 92400
GGACTTAATT ATTCTCTAAT AAAGTGATTG ACAAGGATTA ATGTATAAAT TATACCTTGT 92460
CAGTCTGAAC AATCTGCAGT TTGGACATTG ATTCAAATTC ATTTAGGCTG AATAAATTTT 92520
GATAAACTAA GTAAGTTTTG ACAGCTATTT AAATATTGGG AAAGGGGATA TTCAACATTT 92580
TTCTTACATC CTGAGAGCTT TGTTAAATTT AGTTATTTGA GACCCATTGG GTTCTATTTT 92640
CTGGTTCAGC ATGTTGCTGT AATGGTAAAA TACAATTTTG AAATTATAGT TGTCTTGAAG 92700
TTAATAATAA ATTGACCAAT ATGTTGTATT TTTTCTCTA CTTAGTTACA AATTGAACTT 92760
TTCCTAAGTA GAACTTTTAA TTTGACAGGC CCCCTTTGCT TCCTGAGGTA ACTGAAATAG 92820
GCCAAATTAA TGCTTTTTTG AATATCTTAG GTTTGTGTCT TTCTTTCACA TGTTACCTAC 92880
CCCACTTAAC AAAAGCAATT AATCTCAGCA CTTGATGCCA AAGAAAATTC TAAAAGGTCT 92940
GGATTTTTTC CTTGGATTTT ACAAAGTAGC TACAATGGGA CTTTAAAGAC AAAGCTGCAT 93000
TGCTGCTTAC AGAGCAATTT TTGTTTAATG GTCTGTGTTA GAGTCATACT GCATGATGAC 93060
TTCCAATGT CTGGGATACC ATTCTGAAAA GGGTTTAGTG TTACATACTT CTTAGAGAGA 93120
GTTCTCCATT TCTAATTAAG GCACACATCT GGAGGTGCTC AAGAAAAATT AGTGCAGTTA 93180
GCCTTGGAAG TGTTATGTGT GACTAGTTCA CTTGAGACAT CTTTGTATA ATCAGACACA 93240
TGGCATTAAA TTTATTTAAC TTCTCTTGCT TTTCTCTCCC ACAGAGTATC TCCCATATTC 93300
ATGTTGCACT TTGTAGAAGG CTTACCACAG AATGACTTGC AGCACTATGC ATTTCAATTT 93360
GAAGGCTGTC TTTATCAGAT AACTTCTGTA ATTCAGTATC GAGCAAATAA TCATTTTATA 93420
ACATGGATTT TAGATGCTGA TGGTAAGTGT TTAGAGGTTT TCTTTAAGA TAATTGGCAT 93480
AGAACTAAA TTCTAGCATG TGGGGACTTT TTGGTTTTTG TTTTATAAAA AAAGACAAAC 93540
TTTGTCTGA CTCTTTCTCT CTCCATTCTC GCCTTTGCCT TCTGCCCTC CTCGCATCTA 93600
TTAAAGTGA TGGTTTTAGT ATCCTGTCTC ATTTTTCCT TTCTTACAT CATGTATTAT 93660
AGGTAACAC ATGCGCATGT GTGTATTCT CTTTGTAGACA AAGGATGAGA TTAATACTGT 93720
TAGCTCAGTT TTTTTTCCC TACTTAACAT CTTTGCTTTT ATTTTGTAGA CATATTTCTA 93780
AGACTATTAA ACATTAGACT TACGTAGCCC TTCTGTCAAT GTGAAATACA TAGTTTACTA 93840
ACAGCTACCA TCAAGATAAA GCCTTTATTT AAATAATTAA ACTTCTTAGT GGAAAGCTAA 93900
GTAAGCACAG TTTATGGATT TTGGGAATTT TTGCCTTGCA TTTGTCTGAT ATGGTAAAAT 93960
ATTGAGTTTG TTTTCTCAT AATGTTCACT TTGTCTTAGA CAAGATAACT CAATCCCCTT 94020
AAAGGGTTGT ATCAAGCCAT TGATAAGGGC TCACTTTGAT ATAACCATTT TCTGTTATTT 94080
AGACACTCTT TCACACTTCC TATTTTCCTC CTGGGGATGG TTTGAATGGA TGACACAATA 94140
CCATATTATA AAAGCACTTT ACAAAGTGA ACTTATGTTA TAAATGTAAT TATTACCTTA 94200
AGGTTTTACC CTGTTTCAGA TTTGAGTGGA AGTAGTTCTT TACAATACAA AACAATTAT 94260
TTTAATTTT TTTGCATTTT AAAGAATGAT CAATCCACTT CAGGTGCAGC ATGGTTTCCA 94320
ACCTTGACAG CATGGAAGAA TCATTTATTT AGCTTCTAAA AATGTGCAGG CTGTACCCTA 94380
GACCAGCCTT GGGGATTAGG CCCAAATATC AATGTTGGGT GTTTTTGGTA TTGGTTTTTG 94440
GCCCCCTAC CCGCCCTTCC TTCTTCTGTT CCTCTCTCTC ATTCTCTCTC TCTCTCTCTT 94500
TCTCTCTCTC CTTCTTTGCT CCTTCATTCC TTCTCTCTCT CTCTTTTTTT TTTGAGACAG 94560
CATCTACTA TATTGCCAG GCTGTTCTCA AACTCCTGGG CTCAAGTGAT CCTCCTGCCT 94620
CAGCTTCTG AGTAGCTAGG ACTACAGGCA CATGCTATGG CAATACTGTT TTAACATTG 94680
TTTTCAAGGC TCCCAGGTG ATTCCAGTGT GGGTCATGTG GTAGAGAACC ACTGACACAG 94740
GCAAACAAAG GATACATAAA GTTGCTATT TAATGGGTAG GTGCAGGTAG TAGATAAGAG 94800
TGTAGCCACA TAAACCACAT GCTTAGTGAA CGGTTTTGTT TTGTGTGTAT GTGAGGGATT 94860

FIG. 6.36

AGCATCTCTG AGTATATTTT GTTTTCCCTT TTGAACTTA TCAGAGAATT CATATGTCTG 94920
TTATGTGACT AATGCTCACA TTAATAAAG TTATGTGACT TTTTAAATT CATATGTCTT 94980
TTTAATTCAT TTATTCATT C ATATGTCTGT TATGTGACTA ATGCTCTCAT AAAAAAGTA 95040
ATGCTCAGTT TACTTTTTT ATATCAGATC ATATATATAT GTTTTTTTTT TTGAGATGGA 95100
GTTTTGCTCT TGTGCCCAG GCTGGAGTGT ATTGGCGCAG TCTGTCTCA CCACCACGTC 95160
TGCCTCCCGG GTTCAAGTGA TTCTCCTGCC TCATCCTCCT GAGTAGCCGG AATACACGCA 95220
GGCGCTACCA TGCCCGGCTA ATTTTGATT TTTAGTAGAG ACAGGGTTTC TCCATGTTGG 95280
TCAGGTTGGT CTTGAACTCC CAACCTCAGG TGACCCACCC GCCTCGGCCT CCCGAAGTGC 95340
TGGGATTACA GGCATGAGCC ACCGCACCCG GCCATATCTT ATATTTAAT AAATATTTTA 95400
ATTTGGTCTG TAAATTTTC TTTTGGGGA ATGTGTTTTA AGTCTGTGTT GAGTCCTAGA 95460
CATTTGTTGT TCTCAGATAG TCACTAGTGA TACCTTAACA TTAACCAGCC TGTTGGCAAC 95520
TAAATTGGCC TGAAGTGACA ACTAAGGAAA GGTCTCTTC TCCTTTCTTA ATCTTTGCAT 95580
TCCTTAAGAT TAGTCTTTG TAGGAAGGCT TTGAAGTCTG GTGGCAAGTA CCCTTTATCC 95640
CTCACAATCT TAAGATAAGG TCTTTCTGAG CATTAAAAAG TGAAGTGGG AGATATGTCA 95700
AATGAGTTTT CTGTGTGTGC TCTGAGAAAT CTTTTTTTCA AAAAAGGATA GATGTACTTG 95760
TATAAGGAAA AGAGAACTG AGCGCACTTT CAATATTTAA GTAAGTGTCT CTAACATGTT 95820
TTGCAACATA AAATGATGAC CACTGTGTTG GTCATTACTT CTCTACTGCT AAAACAATGT 95880
TTTCTAAAAT AATATACTCC TTAGAAAAAA ATATAGTGCT TTGGGTGTGC ACTGTTGTAA 95940
TCCAAGGAAT AGGAAATGTT TTGTAGTAAG TCGATGGTG TTTGACATCG TGATTTATTA 96000
ATTTATCACA TTTGGTTTCA TAGAAATAGA GTAAGCTACG TATTTGCTGT GCCGCAATTA 96060
CCATGACATT ACACTTGAT CTATTTCTGT TTCATAGATG TGATAGATATT GATATATACA 96120
GTGGAAGTAT GGATTGTTTT GATAAGTTTC TAATGAAAGT ACAGATATTT GTTGATTATT 96180
TATTAAGAAA GGTTGTTACT CATCCAAGCC CGTGTTAGC TTTTCCCAA TTATCATGTG 96240
GTAGTAAGTA AAATGTAAAG AAATATACCC TCCCTTAACC CCACACCACC TGTTAGCACC 96300
TAGCCACCTT CCTTACTTC TCAGCCGTAC TTTTGTATT TTTTGTGT AGTGGTAAAA 96360
TATAAATAAC ATAAATTTA CCATTTTAAC ATTTGTAAGT GTACAATTCA TTGGCATTGA 96420
ATACATTGTG TGCAACCACC ATCACCATCA GGACTTTTTC ATCAACCCAA ACAGAACTA 96480
CTCATTAAC AATAACTCCG CATCCTTCCA CCCCAGGCC CTGGTAACCA CTATTCTACT 96540
TTCTGTCTCT GTGAATCTGT CTATTCTAGA TACCTCATAG AAGTGAATC GTACATTATT 96600
TGTCTTTTG TGTCTGGCTT ATTTACTCA GCATATTTTC AAGATTCATT TGTGTTGTGG 96660
GATGTAGCAG AATGTCATT CTTTCTAAGG CTGAGTAGCA TTGTATGTAT TATCCATTTA 96720
TCTGTTACGG ACATTTGACT ATTGTGAATA ATGCTGTTGT GAACATTGGT GGACAAGGAA 96780
CTGAAAGTCC CTGCTTTTCA TTCTTTTGG CATAAACCTA CAAGAGGAAT TGCTGGGTCT 96840
TAACGGTAAT TCTGTGTTA ATTTTGGAC GAAGTGGCAG ACTGTTTCCA CAGCAGTTGT 96900
ACTATTTTAC ATCCCCACCA GCGTTACACA AGGATTCCAA TTTCTCTACA TCCTTGCCAA 96960
CATTTGCTAT TTTCTATTT TTTTAATAA TATCCATCCT AATGGGTGTC TTTTTTTTTT 97020
TTTAAAGGAA TGGTTTAAAC AGGTTACCTT CTTACTCCTC ATTCATGCTT TAGTTGACTA 97080
CATAAGGACC CCTCTCCCTA TTGGCACCAT TGAAATTGTT CAGGCAAAAA TAACTGCCAG 97140
CGACACACTG CTTTAAGTAA TGGACTTTTC CCAAGTTTGT TATTAATATT TCAGTATTTG 97200
GTAGTGCATC CTAAGTCTAG TTTTAAACT CTTCCTTGT CATCTATCAT CTCATTCTCT 97260
CTTGACAAAT GTGAAATGG AAGCTCAGAA ATAAACAAG AATTAAACG AATAGTGATC 97320
CTTCAGGTAA CAAGCTTCAT TTATCATGAA AACATATATG TATGAAACAT TCTGTTTTCT 97380
GATGTTATTG GATAAATTAG GTGATAACCA AATTCTAAGT TCCAAAAAT AAATATACTC 97440
TATCTAAGGA CTTTAACATG GCAGACAATG GTGACAAGGT CAAGAACATG TTTAGAGTC 97500

FIG. 6.37

TTCTCCTTTG GTCGGTATTC AATGATACAA CAGTTGAAAA GGCCAGAAGA AAGTTAACCT 97560
AGGATGGTGG TTTTGAATA TCTAACTTTC ACTTCTTTCC CATCTCCAG GAAGTTGGCT 97620
GGAATGTGAT GACTTAAAAG GCCCATGTTC TGAAAGGCAC AAGAAATTTG AAGTTCCTGC 97680
TTCAGAGATA CATATTGTTA TTTGGGAAAG AAAAATATCC CAAGTGACAG ATAAAGAAGC 97740
TGCCTGCCTT CCACTTAAAA AGACTAATGA CCAACACGCT CTCAGTAATG AGAAACCAGT 97800
ATCTTTAACA TCGTGTTCTG TGGGTGATGC TGCCTCAGCT GAAACAGCCT CAGTAACTCA 97860
CCCTAAAGAT ATATCAGTTG CCCCTCGTAC TCTTTCACAG GACACAGCTG TAACTCATGG 97920
AGATCATTTA CTTTCAGGTC CAAAAGGTTT GGTGACAAT ATTTTACCTC TGACACTTGA 97980
AGAACTATC CAGAAAACAG CCTCAGTTTC ACAGTTAAAT TCTGAAGCTT TCCTGTTAGA 98040
AAATAAACCT GTAGCAGAAA ATACAGGAAT.TCTCAAAACC AATACTTTGC TATCACAAGA 98100
ATCACTAATG GCTTCTTCAG TATCAGCTCC ATGTAATGAA AAGCTTATTC AAGACCAATT 98160
TGTGGACATA AGTTTTCCAT CCCAAGTTGT AAATACAAAC ATGCAGTCAG TACAGCTGAA 98220
TACAGAAGAT ACTGTAAATA CTAAATCTGT GAATAATACT GATGCTACTG GTCTTATACA 98280
GGGAGTGAAG TCAGTAGAAA TTGAGAAGGA CGCTCAGTTA AAACAATTCC TTACACCAAA 98340
AACTGAACAA TTAACCAG AACGTGTCAC ATCTCAGGTA TCTAATTTGA AGAAAAAGA 98400
AACTACAGCA GATTCTCAAA CCACAACATC TAAGTCATTA CAGAATCAGT CTCTGAAAGA 98460
AAATCAGAAG AAGCCATTTG TGGGAAGTTG GGTAAAGGC TTAATAAGCA GGGGTGCTTC 98520
TTTTATGCCA CTCTGTGTTT CAGCTCATAA TAGAAACACT ATAAGTATT TACAACCTTC 98580
AGTTAAAGGG GTAAATAATT TTGGTGGCTT TAAACTAAA GGTATAAACC AGAAGGCCAG 98640
CCACGTATCC AAGAAAGCTC GTAAGAGTGC AAGTAAGCCT CCTCCCATCA GTAAGCCACC 98700
AGCAGGCCCT CCATCGTCTA ATGGCACAGC TGCCACCCA CATGCTCATG CTGCTTCAGA 98760
AGTTTTGGA AAGTCTGGAA GCACCTCATG TGGAGCTCAA CTCAACCACA GTTCTTATGG 98820
GAATGGTATT TCTTCAGCAA ACCATGAAGA CTTGGTGGAA GGTCAGATTG ATAACTTCG 98880
TCTAAACTT CGTAAAAAGC TAAAGGCAGA AAAGAAGAAA TTAGCTGCTC TTATGTCTTC 98940
CCCGCAAAGC AGAACAGTTC GAAGTGAAAA TCTAGAACAG GTGCCCCAGG ATGGGTCTCC 99000
AAATGATTGT GAATCAATAG AGGACTTGTT AAATGAGCTA CCATATCCAA TTGATATTGC 99060
CAGTGAGTCT GCATGCACCA CTGTTCCCTGG TGTTTCCCTG TACAGTAGTC AAATCATGA 99120
AGAAATTTTA GCGGAATTAT TGTCTCCTAC ACCTGTTTCA ACAGAGCTGT CAGAAAATGG 99180
GGAAGGTGAC TTAGGTATT TGGGAATGG AGATAGTCAT ATCCCACCAC CAGTACCAAG 99240
TGAATTCAAT GATGTTTCCC AGAACACACA TCTGAGACAG GACCATAATT ATTGTAGCCC 99300
CACCAAGAAA AATCCATGTG AAGTTCAGCC AGACTCTCTG ACAAATAATG CCTGCGTTAG 99360
AACATTAAAC TTGGAGAGTC CGATGAAGAC TGATATTTTC GATGAGTTTT TTTCTCCTC 99420
AGCATTAAAT GCTTTAGCAA ATGACACATT AGACCTACCT CATTCGATG AATATCTGTT 99480
TGAGAATTAT TGAATTAATG CTTGTAACT TTTTTCATAT AATATTTATT ATTATTAGAA 99540
GAACTTACAA TGTGTTCCAG TAGTGTTTAT AACTGGACT TGTGTAATTA CTTGTGTAAT 99600
AACCATGAAC AAAATGCAAG GTTTAACCTT TGGTCTGCC CATGAAGCAT GTAATCTTTC 99660
TTACACATTA AAATCACTGA ATGTGTTCTC CTTTTGGTT TCATTTTGT CTTGTGAGAG 99720
TATGAGGATT TCAAAATGTT AAAGATGAAA AGTGGCGTCT AGTTTCTGAC AGTTTGTACA 99780
GTTGGATGCA TTACATTTTT AGATTGAAG TTTTGTTAT GTTAGTGTA TGAGTGATCT 99840
TTGTGGTGGT TTTCTTCCCC TGGAAACCTG TTGCTCGTGG CGCTTTGCCC ACGGTGCCCC 99900
AGTTCTTGTC CTGTGTCCAG ATATGCAGAC AAATGAAGGG TGAAGAAGAA GAAGAGGAGC 99960
TTTATTTAGT GTTAGAACAG CTCAGAAGGA GACCCACAGT GAGCAGCTCC CCTGTGTCGG 100020
CGGGCAGGTC GTCCCTCAAG TGTTAGCTC TCAGCAGAGA AAAGGCCCTG GAGAGGGTGA 100080
CTCCTCTCAG CTCTCAGCAG AGAAGCAGCC CTGGAGAAGG TAGCTTCTGT TCGCAGGCAG 100140

FIG. 6.38

ATTGTCCAGA GGTCCCTGCTG CTCTCAGACG GGGCCCTGGA GAGGATAGCT TCTATCCATA 100200
GGCAGGTTGT TCTGCCGTCT CTACAGGTCT CTGAAGCTCT TAGCAGAGAG GGTAGCTCCT 100260
CCCTGTTGCT GGTCTGCCA CCCTCTGCTC AGTTCTGGCT GAGCCTGGGG CATTTTACGG 100320
GCCTCGGGGG AGGAAGTGCA TACTTACTGG CCTGGAAAAG GCACCAGTTC CCACTCCTAC 100380
AGGTGGGACT GGCAGCCTGG CCCTCAGCCT TCAGGCCCTC CCTGTTTCATG GCTTCCAGGC 100440
TTACCCCCCT GCTTTGATCT GAGAGCTGGT GCCAATAGCA GGGAGAAGCC AAGCTGCAGA 100500
GGCAAGCACT TCCGAGCCTG CAAAAGCAGG CCCCCAAAAG TGCAGGGATG CCTGAGTCTG 100560
CACCCGCACC CAGGAGGGTG GAGATCTTGC CTGCTCCAAG GCTGCAGCCG GAATGATAGC 100620
AGGCTGACTG GAGCACCTGC CACCATCATT AGTTCAAGAG TTTATGCAGA TTTAAGTTGT 100680
ATACGGTATA TGAATGTGTG ACAGTTTTCC TTATGGTTGT GTGGCCTTCT GTAAGAGCCT 100740
ACGCCTGTTT GTTACACCGG TAGAGTGCTG TGAATGTAA ACTTCCCTA TGCACTTAT 100800
CTCCTTTATC TCTCCATACA GAGGAGGGCA AGAAACCTTG TTAAGTGAAC TTTAGTAATG 100860
TTAAGTGATC AATAAATCTA TAAATAAATG ATAGCAGAAA AAAGTTACCT GTTTTTGTGA 100920
TGATGTACAA ACTTTACATG TTATCACAAA TACCATCTTT CTTCCCAAGA CATTTACTTC 100980
TGTAACCAAA GTGGGACACC ATCTAACAGT TCTGTTTTGG GAGAGAGTAA TAACCAGTGC 101040
TTGTGAGGCT TGTTAGATGT TGGTTGTGAT ATATGAGATA GATGTTATTT CATTTAGACC 101100
TCAACATTCC TGTGCGTGAG ATACTTTTAT CACATCTTAC AGATAAGGAG ACTGTACTCA 101160
TTCAGTTGTG GAGCTGAGAT TGAGTAGAGT GGCTATTACA GCAGTTGAGT GCTGAGCTTA 101220
TCAATATATG TTCCACTCCT CAGGCTTCAT TTAAAGTAGG ATGCCCAAAC AGCACCCTG 101280
CCGTAGAGAT TTGAGTTAAG AGCAGTACTT ACTGAGGTTT AAGGCTGGCA GCCAGTGTCC 101340
TTGCAGTAAA ATTATTTGCT AGGGACTCAG TACTTCATAA TCTATTTGTC AGATTACTC 101400
CTAAGCTTCT GTGTTGTTTT ATTTTTTTTG TGACAAAAGT AGTGCATATT GTCAAGGAAA 101460
AACTAGGAAA ATACCAAAAA AAAAGATTTT TGACCATGCA TTTTAATACT TAGTGACTAC 101520
AAACATTTTC CTATTTTATG CATATAGATT TTAATAAAG GTGAGATCCT ATTGTATCTG 101580
TTTTAATGGA TAAACATTGT TCACTGTTT TAAGATTCTG AGGTGATTTA TACTGTCTTG 101640
CCATTGTAA TTGCAGCAGT TAGCCTTGTT GATAAATTTT TGCATGGATC CAAGTTTTGT 101700
TTTCCAGGAG TGGAGTTGCT TGGTCAAAGG AAATGCACAT TTAAGGTTTT TTGGTGATTG 101760
CATGACTGAC TTCCCTGGGC CCTCGCCAAC ACTAGGTAGT AGTATTGGGA GGAAGGGGGG 101820
AACCAATCCT GGGTGCTCCA AGATTACTAG TGAGCCTGAA CATTTTCTAT AACTATTGTC 101880
CACTTGAGTT GTTGTTTTGT TTTTTTTTG GTGGAGGCGG GGGTGGGTTT AAGAATTGCT 101940
TATCCTTTGC TTGTACTAAT TATCTTTTCA ACAAATATTT CTAGATTACT GCTAAGGACC 102000
AAGCACTGTT ATCAGCCTGA GATAAGGCAG CACACTAGAA GGAAATCCTT GCTCCTTTTG 102060
AGTTTGCCCT CCAAACATGG AGATCAATAT ATAATGTTAG GTAGTAATAG GAGATACATG 102120
CAGTTGATTC ATGTCATTTG TAGTAGTTAT GGTCAATAAA GTTGCCCTGA AACTGAATT 102180
AGTATAAACT GAAATACTGT TCCTAGGGGA AATAGGTTCC TGCTAGCCTG TGGTCATGAG 102240
ATTTTGTCA AACAATCACT ATATAACCTT TTCTGTTTCT GTTTAAAGAC ATGTTATTTG 102300
ATCTATATGG TTGATTCTTT ACATTAACAT GGCCAACAGC ACTGTAATC AGCCTGAACG 102360
AAGCTTATCT GACACATGGT GTTCTCCATA AGGCACATCA TAGCTTTCTG TGCTTAGGAA 102420
CACTAGACGG CACTTCAGCA CTGCACTTGA GGACGTTTTA AACAGTGAAA TCAACAAAAA 102480
GCACAAAAAA ATGCAACAAT AGGCTGGGCA AGGTGGCTCA CGCCTGTAAT CCCATCACTT 102540
AGGGAGGCCG AGGCGGGCGG ATCACGAGGT CAGGAGATCA AGACCATCCT GGCTAACACG 102600
GTGAAACCCC GTCTCTACTA AAAATACAAA GAATTAGCCG GGCGAGGTGG CAGGCGCCTG 102660
TAGTCCAGC TACTCGGGAG GCTGAGGCAA GAGAATGGTG TGAACCTGGG AGGCGGAGCT 102720
TGAAGTGAGC CGAGATTGCG CCACTGCACT CCAGCCTGGG CGACAGAGCG AGACTGCGTC 102780

FIG. 6.39

TCAAAAAAAAA AAAAAAAGGA ACAATAACAA AGACACTAGT CCCCCAAAAA TACACTTGTT 102840
TACAGTGTGA ACTGAAAGAG GAAGGTGGAG TATTGACTTG TTTGACCTCA GCTGGAAATG 102900
TGCACGTCCT GTGACTCAA TTTTCTCTG TTCTGTGCAT GCATGTCCAC GAATAACCAC 102960
AAGAAGCACT GAAAGCATTG ATTTTATAGG TTACAAATTA ATTTTAGCAA GTAAATGAAT 103020
TCACAAATAC GGAATCTGTG AGTAATGAGG ACTGATTCTT TTTTTTTTG GAGATGGAGT 103080
TTCACTCTTG TAGCCTAGGC TGGAGTGCAA TGGCATGATC TCGGCTCACT GCAACCTCCG 103140
CCTCCCGGGT TCAGCCTCCA CCTCCCGGGT TCAAGCGATT CTCCTGCCTC AGCCTCCCGA 103200
ATAGCTGGGA TTACAGGCTT GCAACCACAT GCCCGGCTAA TTTTGTATT TTTAGTACAG 103260
ACGGGGTTTC ACCATGTTGG CCAGGCTAGC CTCGAACCTC TGACCTCAGG CAATCCACCC 103320
ACCTCAGCCT CTCAAAGTGC TGGGATTACA GCGGTGAGCC ACCGCGCCCG GCCGAGGACT 103380
GATTCTTATG TCAGATGGCA CTAAATGCTA TGGAGAAGAG GAGTGGATGA GAGGGAGAAG 103440
TATTTTAGAC CAGGTAGACT TGGAAAGGTT CTTGGAGGTG GGTGATGTT GAGAAGAGGC 103500
TTCAATAAAG TTAGGGAGCT CGCCATGTGA TTGCAGGAAG AGCGTTCCAG GAGAACAAAA 103560
GTCATGAAGA GTGAGTGCTA GGCATGTGTC TGGTCTGTT GGGCTGCTAT AACAAAATAC 103620
CTTAGACTGG GTAAATGTA TAAATAATAG AAGTGTATTG CTTATAGTTC TAGAAGCTGG 103680
GAAGTCCAAG ATCAAGGTAT CAGCACATTC TGGTGAAAGC TGCTCTGCTT CATGGCTGGT 103740
TCTCTCACTG TCCTCACATG GCATAAGAGG GGCACAGAGC CCTCAACCGT CTCTCCAGTG 103800
GCCCCATCTC TTAGTACTGT TGGATTGGGG ATTTAGACTT CACTAATTTT GGGGGGACAC 103860
AAACATTGAG ACCACAGCAG CATGACTGAG GATAAGCAAG AGGCCAGTGT GGTGAGCAG 103920
AGTGATCAGT GAAGGAGAGT TAGGACATGA GTAAAGAGGC TAGCAGACAC CAGATCTCAT 103980
ATGGCTTTGT AGGCCATAGT GAGGACTTTG TTTAAGCTGA GAATAATAGA TAACCTCAGG 104040
AAAGTTTCAG GCAAGAGGGT AACATGATCT GATCTGGGTT TTTAAAGGAT CACTGAAGTG 104100
GGGAGACTGT CTACAGATGG TCTGAATAGG AGTCCTAGTC TATTACAATC TCCTGGAGT 104160
TTAGGGTGGT AACTGGAGGT GTTCAAGAGT AGTTGGATTA CTGTTGGATT TCAAAAGTAG 104220
AGCCAACACG ATATGTGCAT TGGCTGTGAG GTAGAAGAGG AGTCAAAATG AACTCCAGGT 104280
TTTATTGACT GAGCAATTGT GCCATTTCTT GAGATGGGTC AGATTTGGGA AGGAAAGAAT 104340
TTAAAGGGGA TAAGATAATC CCATTAGGAG TGTGTAAAGT GTGAGATTCC TATTAGACTT 104400
TCGAGTGGAG ATGATTAAAT AGGAAGATAG ATCTGCAACA CTGGAGCTCA GCGGAGAGGG 104460
ACACCCTGGA GATAGCCGT TGGGAATTAG GAATGTGTGG ATCATGTTAT AGGATGGGGT 104520
CATTTAGGGA CTTAAACAG CTCTGAAGAA CAAAAATGGT GCCTTGATCT TGGACTTCCT 104580
GGTTTATAGA ACTGTGAGCA ATATATATAT ATTTTTCAT AGACAGAGTC TTGCTCCGTC 104640
ATCCAGGCTG GAGTGCAGTC GCACCATCTC GGCTCACTGC AACCTCCACT TCCTGGTTCA 104700
AGCAATTCTG GTGCCTAAGC CTCCAAGTG GTTGGGACTA TAGGTGTATG ACACCATGCC 104760
CGACTAATTT TTGATTTTTT TTGTAGAGAC AGGGTTTTGC CATGTTGGCC AGGCTGGTCT 104820
CAAACCTCTG ACCTCAAGTG ATCTGCCTGC CTTGGCCTCC CAAAGTGCTT GGATTATAGG 104880
CGTGAGCCAC CATGCCCAGA CTAAATTTCT AACATTTATA AATTATCCAG TCTAAGATAT 104940
TTTGTGATAG CAGCCCAAGC AGACCAAGGC AAAGGCCAAG CACACTTGCT CCTCTGACT 105000
TTTGCTCTTC CTGGAATGTT CTTCTTTAG TCACATGGTT GCCTGCCTAG CTTCAATCAA 105060
TAGGAGTGTG GTGCCCTGAA AATACAAGGA AGAATGCTTT TCTTTTTTTT AAAAGGAAGG 105120
GATGATTATC TGTCAGATGC TGCTGAAAAA GAGTAATAGA GTAATTGGCC ACTGGCTCTG 105180
GCAATAGGGA AGTTAGCTCT GCTAACTCCA CATGAACAGT TTCACATGAA CAAGTGTGAG 105240
TGGGCTCAAG AGAAGGGATG GTGAGAAAGT GGAGCTATGG ACTCACTCTT GAAACATTTT 105300
CTGGTGCCTC GTAGGGCAAT GTGAGGTCAA GGTTTTGT ACTGTTCTGA AGATGGGAGA 105360
GGCTGACACA TGGATGTTGT AGGTGAGAGA AGGGGCGCTT GCGGGGGCAA ACTTCTCCAG 105420

FIG. 6.40

GGATGGGATT CCAGTGTCTA AGAGGAGGCG GTGTGACCCT AAGAGCTAGA AAAATTATTT 105480
TATTAATAGG AAAGACAAAG TACTTAGGCT CAGATGCTAA GAGATTTGCT GATAAAAGAA 105540
TGAGAACGGT CTCTTCTGAT TATTTTCTTG GGGAAATAAA TAGATCATCA GCTGAGGGTG 105600
TGAGGGGAGA AGGAGTTGAA CATGGAGGAA GACAGGTGTG AAATATTGGT CTCAGAATGG 105660
AGAGCGAATT GAATAGGGAC ATGCAGTGGG CTGCTAAGC TGTGCGGAGA GCCCGTGGA 105720
AGTTTATGGT CATCAATTTA ATGGCGACCA GCCAAGATGG TGGTTTATTT TTCTCCAGTT 105780
GTATTTAACT GCTCAGGTGC AGGACAGAGA GACTAAGTGT GAAGTTAATT TCAGCCAACG 105840
TAGAGGAATT GTCAGGCAGA TGGGACAAGG AGATAGAGGA GAAAAGGAAT AAGGCTTCCT 105900
GCAAGGGTAA TGATTGTAGG GATGGATAAG TAAGGAACAC AGGAAGTGGC TGTCTGCTGA 105960
GTGGTGGCAG AGCTCAGTGG GTCAGAGCAA GGTTCAAAGA ATGGCAGAGA GGCACCTGTG 106020
GAGGAAGTAA GCTGGCTAGA AAGTAGTGTG CTTGAAATTA AGCTTCTGGA GATAGCAAGG 106080
TTACAGGTGA TGACAAAGTC TGAGTATGAC AAGGAACTG CAGG GCCAGA GTTGGAAGA 106140
ATTCATGAAA AATGAGGAGA AAGAGGCACC AAGAGGCTGG GATAGCACAT GGATTGTCTC 106200
TGTGTGAGGC AAAGTCATCT AAATGGCAGC AGTGGCCCTA GCAGAAAGAA ATACACAGT 106260
AGCCGGAGCA AAAATCCTCA AGGACAGGCA GAACGCCATG AAAACGGCAG ATGACAGCCA 106320
AAGGAGCAGG GGCAGGGGCT CAGTCCAAAG TGTTCAGAG TCACTGGAGG GTTGAGTGGG 106380
AAGGGGAGGG AGTGGCTGAA ATGGCAACAA GGAAGAACCT CTCTCATCTC CAGGCCCAAA 106440
AGTATGTGGA ATGCGGGAGA TAAGACAGCC ACCACTGGCC AGGGCTGTAA AGGGACATTC 106500
AGCGAATATT CAGGTTCCAT TTAGCACGAC AGCAGGGAAG GGAAGTTGG CAGAAAAAAA 106560
CTGGGGCAGT GGGATTAAAG ACAGACCACA CATTCCAAAA GGCACCGTGG GAGGGTCAGG 106620
GGGCGAGGTT AGGTCTAGGC TTCAGTGTCC TGGGAGACTC AGTCTTCACA GGGTGACAGC 106680
GATCAAGAGT GCAGCTTAGG CTGGGTGCAG TGGCTCATGC CTGTAGTCCC AGCACTTTGG 106740
GAGGCCGAGA CGGGAGGATT GCTTGAAGCC AGGAGTTTGA GACCAGTCTG ACCAACATGG 106800
CAAAACCCCA TCTCTACTAA AAATACAAAA ATCAACTGGG CATGGTGGCG TGTGCCTGTA 106860
GTCCCAGCTA CTTGAGAGGC TGAGGCAAGA GAATCACTTG AACCTGGGAA GCAGAGGTTG 106920
CAGTGAGCTG AGATCGTGCC ACTGCACTCC AACCTGGGCA ACAGAGTGAG ACCCTGTCTC 106980
AAAAACAACA ACAACAAAAA AGAAAAGAGT ACAACTTATG AAGGGGTCTC CTGGGGAGAG 107040
GGTTTTTGGG ATTCTCCTGC CTCTCAAAGT GCTGGGATTA TGGGCGTGAG CCACCACACC 107100
CAGCCGAGGG AGGCTGAGTT CTAATTGTTG TATCTCTCTT GGGATTGGCC TCCTGGGCAG 107160
TTTAAAAGAC AAGGCAAGGA ATCTTTTGA GAAAGAGACT GGGGGCAAGG TGTGTCTGAA 107220
CAAGAAGTGT GAGAAGCTCT GTGGGCTCCC TTCAGACTTC CAGTCGTTGA ATTGGGATCT 107280
CATTTATATC AGCTCTAGGT GTAACGATAT TAAATCTTCT CTGTCATTTG GCAATTTTGG 107340
TTTATGCTTG ATCATCATTT TTAATGTTTC GACATGTAGA AGTTTAACAT TATTTTACAT 107400
TCTTTTCTT CTGGCATCAT GTTTTAGCAA GATTGTTTCC ACCAAAAGAA TATATATATC 107460
TTCTAATGAA ACTACGTTTC TTTTTTTTTT TTCCTTGGCT TTCTCTTTTG GTATATGAAT 107520
CTTTGATTAT TTGTAATGTA TTTTGATGTG TAACACTGAA GTTTCTATTT TGTACTATTT 107580
TTTTCCCCAA ACAGTAAACT TATTGTTCAA ATACTTATTG AACAACCTTC ACTATTCTTT 107640
AACCATTTAG AATACGCCAT TCACATATCT TTCATACTAC ATTTAATAAC ATTTTTTAAT 107700
TAAAAAATAT TCTACTGATT TGTTTATTTT GAGACCAGGT TATGAACTG GCTAATTTTT 107760
GTATTTTGT TAAATACCGA AATTCAGTGT GTTGCCAAGG CTGGTCTCGA ACTCCTGGGC 107820
TCAAGCAATC TGCCACCTT GCGCTCTCAA AGTGCTGGGA TTACAGGTGT GAGCCGCTAC 107880
ACCCGGCCAC ACCCGGCCAA CACATATTAT TTGTTATTAC ATTTAATTCC CACAGTACAT 107940
TGAAATTATC AGGGAAAAGT TTTCACTGAA ACATTATTGA ACGCCACATT AAAAGTGTA 108000
ATTACAAAGA TTTAATGCCA ATTTTTCAGA AGAAAAAGA CCAGGAGGAA GGTCTATGAA 108060

FIG. 6.41

GTTTTAGCCA GTCTCTCATC CACCTACCAT TTCACGATCA TGCACTGTGT AAGTCAGGAA 108120
AAGAGTAAGA AAAGTGAAAG ATACAATTGA TTAGAGAGTT TTGCTGGATA CTATAGATGA 108180
AAAGAACACA AAATGGAACA GCCTCTTCAA GCTTAGAGTC AACGGCTGTA GTCCCAAAGA 108240
CTGTAGTCAG AGGCGGTAGG GCCAAAAGAC ATGACTTATG GCATTGGAGG AAGAGGATGC 108300
TTTGGGAGTT CATGGTAGAA GAGGCGGAAA AAATCTGGTG GATTAAAGAA AGCATCCCAA 108360
AGTGACATTA AACTAATGAC TAAATTCTGA GCTGTTTTCA GGGGCAAAGC CTGTTTGGGC 108420
ACCCCTGCCA CACTTAAAGA GTCACCTAGG TATGGTTCGT GGGCTCTGAA CAGGCCTGCT 108480
CAGTGAACAT ATTTGTGACT GTTCTCCGG CCCTTTTAGC TGTATTGAGT AAAATTTAAA 108540
GAGACCATTG TTTTGGCCTA AGCTCCTGCC CTAGGCCCAA AGAACAGACC AAACCTGAAT 108600
GGCTTCACTT GTCCTAGGTG CTGTGTAATC AAACCTGAACT TTGAAACAGG TCGGTTTTTC 108660
AAAAAAGCA AAAGATTAC AGCAACCAAT TAGAAGAGGC CCGGTCAACC TGAGCCAGCA 108720
TGATGAGGCT CTTCTGCTT AATCCTACAA GGAAAGAAAC TTTGAAATGA CCAATCTGCT 108780
TTCATTCTTG GTTCTGCTT TCTTTGGTCT ATTTCTGCCT GTAAACCTA TCTCCTCTGC 108840
TCAGCTCATT GAAGTACCCT TCTATTTATA GATGGGATGC TGCCCGACTC ATGTATCGCT 108900
AGTAAAAGCC AATTAAATTA TTACACTCGA TTTGTTGGAA TTTTGCTATT TTGACAGCTT 108960
TTCAAAAACA CCAGTAGGTT CACATCCCTA ATTCCCCAGC CAGTGTCCC TCAAGGAACC 109020
ATGGAAGAAG CAAAGGTGGC TGAAAGGCGC CTCAGGATGC TTCTAAGCAC GGCACATCCA 109080
TGAAAGGCA CTTACTAATA TTTGCAGGAT AGCAAAGCAC TGCAGTGACG ATAAATCTAG 109140
TATTGGAGAA GTTCAAATA ATCAGTAGAT TAACACAGAA GCCAGAGCTT ATAGGGAGAA 109200
AAGGAACCCT ATGAAATACT TCAAATCCGA AAACGAACAT GCATTTCTCTG TTTAGTTAGT 109260
GCAGGTACGT AAAAGCTTGG TAAAGTACCC TTCTTGCCAG CTTTCTCTT CTTACAAGCC 109320
TTTTCACTGG GCTGGGAGGC TGATATTATC TAAATATGCT GAGGAGGTT AAGTATCTCC 109380
ACAACCTACC TCAGAGTGAA TGCTCCCCCTC GGCCTTAAGG CAATATAAAC CAGCCCTGTT 109440
TAGCAGGATA GCAAAATGTT TGCGGTTGTA AACTGGTGTG CCATTGGCTG TGGCGCTTGT 109500
GGTGTAAGA ATCCCTGTGC TTGGTAATTA ATAGAGAAAT TCTATATTTT AAACCTCAGT 109560
TGTATATTGG CTCTTATCCA TGGCAGATTT TCACGTATGT GTTATTTTTT TATTATTCA 109620
GAGCCGGAGT CTCGCTTTGT CGCCCAGGCT GGAGTGCAGT GGCGCGATCT TGGCTCATTG 109680
CAGCCTCTGC CTCTGGGCT CAAGCAATTC TTCTGCCTCA GCCTCCCTAG TAGCTGGGAC 109740
TACAGGTGCA TGCCACCACG CCCGGCTAAT TTTTGTATT TTAGTAGAGA TGGGGTTTCA 109800
CCGTGTTGCT CAGGCTGGTC TTGAATTTCT GAGCTCAGGC AATCCGCCCG CCTCGGCCTC 109860
CCAAAGTGCT GGGATTATAG GTGTGAGCCA TCATGCTCGG CCCTATGTGA TATTTATTAC 109920
AATGAATTCC AATGATCAGA CCTATACTCA AGTATAAGTG AATATATCAT TCAATGAAGT 109980
ATAAATGATC ATTATGTTCA TATTCACACA TACAATAATG TACTCAAGTT TATTGCTAAG 110040
GTAATTCAGA ATCTCCTTAT TTTGAAGTG GCATTTGATA TACCTGTTTG GGAATAACTA 110100
GTTTCTTATC TTTGACAGAA AATAATTTTG TTGTTTTGTT TTTACTAAAA AAGCATGGTG 110160
AAAAATGGCT CCATTTCTAA GAGAGGTAAC TAAAATATCG CAATTTGCTG GGTGTCATTA 110220
AAGTAACTCA CAAGGGAAAA AATGCAAATT GGTATCTGCT GATGGAGTAA ATCTCCGCAG 110280
AAGTGATGAC CCTGAAAGGA TCAATATATT AAAGCCCTC CCAGCTGGTC ATTCCAGATT 110340
GCAACAATAA AGCATTAACT GTTAAACCT CAAGGCAGCT TTTTTTTTTT TTTTTGTCT 110400
CAAGTCCTTT ATTATTAATT TTATAGACCT ACTTAATTAC TAAGCCAAAA AAAATCAAAC 110460
TTGTTTCTCT TTGTGACTTG TCAATAGTAT TAAACTATTC TGGTTTTTTA TTTTTGTGTT 110520
ACCTTAAAGT CTCCAGTTTA GTAATTTTTT TGTACCTAAA CACTTCGGAT TTGACATGCT 110580
TTGTGGCCTT TATCAGTAGT TAGAATGTAA ATCCAATAAA TAAAGTAAAA GCCAGGTCTT 110640
CAAAACCTGG GGGCCAAGAA CTCTGTTTTA GAGGGCCTGT GACTCTCTTG GACACTGGAC 110700

FIG. 6.42

AAAATCTCAT CTCTAAATAT GGATATTTTA GGGAGAGGGT CTTTAGGCTG TCATTGGAT 110760
TTTCACAGGG CTCCATGTAT CCATAAGGTA GTCTCTTGGG AAGTTTGACT TCAATAAATG 110820
AAGTTTAACT TAAACCTAAA ATGAAATTTA ACTGAAAAAC AAAATCCAAT GAAAGATGCT 110880
TTCTTATGCA AAAACAAACA AACAAAAAAA AAACAAAAAA ACCCCAAAAA ACCCAAAGCC 110940
AAAGATTGTT TCTGAAATTA GGTCTAGGT TCCAGAGCAA CTCCATGGTG GGAATCAGC 111000
CACATGTAAA GTAAGCTAAG AGTTTGGACA ATTTGTAATA TTTATTCCTA GTTTTCTTTA 111060
AGACCCTTTC AGATTTTGAA TTCCTATTAG TAGCATCAGC CAGGTTCTAA ATGTAGGCAT 111120
CACCATAGAC ACTTCCCCAC TGCTGCAGTC CCCAACACTT GCCCAATTTT CCCTTGAATT 111180
GCACCCATGC TGCCTTCTCC AGGCCTATTT GAACCCAGAA CCTCGTTGTG CCTCGTTTGA 111240
AATATAATTT CCTCCTAACT AGTCTCTGAT CTAATTTT CCCTACATTG CTGCCACACT 111300
AATCACCTAA AATAGATTTC ATTCTACCTT GAAACAGAAA TCTCTAATAA GTTACTCCCT 111360
TCCCTTACGG GGTAAAGTTA GCCACATCCT AGGTATTCAA GGACCTTCCA GGAGCTAAGA 111420
ACATTTCCCC TGCACCTTCT TGAAGTACAC TTGTCTATG TACTGGTTAT GTTCATTCT 111480
TACCCTCGCT CTCGTTTTGT CTGGAATTTT CCTTGGCCTT AAATGCCTCT CACCTGCCTG 111540
CCCACATCTC TCAGGGTTGT TTCAAATCCT CAATGAAGGC TCACAGCCCC AGTCTATGTT 111600
GGCCACTTAC TTCGTGGCCT GGGAACATTT TTCTTTGGCT GACTTGCTGA CACTCCATCA 111660
GATGCATTTT TATCTGGTTG TCCATCTGTG AACCATACCC TGAGAAGGCA GAGAGTGCTT 111720
CTGCACTGAA CATGTGCTAG GGGACAGGTC TGTGCTAGAG GGGCAAGCAC TGGGAATGAA 111780
GAACTGGTCC CTAATCCCAA GGAGTTCATA TCTCAGTGGA GGTGACAAGC AACTCACTGT 111840
TTCCGGGGGT TGTGGTGAAT GCTGGGAGAA GGGGTGTCTA TATTAGATCG AAGCAGCATC 111900
AGGGGAGGTT CCCTGAGAAG GTGATGCCTC AGCGGATGTC TCCAGCTAA GTGGGGTGGA 111960
GGTGGAGAAG GGCAGAGCAG GGAGAGGATC TAGGTGGGGC GTGTAAGTCT GCATGGGTAA 112020
CTCAGGGAAC CCTTGGTAAC TGCATGTAAC TGTGTGAAGC TTTCATGAAG GAACATGGTA 112080
GGAGACTAGG GTATGGACTA TAGAAGCOCT TTTGCTAAGC TCAAGAATTT GAGGCCGGGA 112140
GCGGTGGCTC ACGCCTGAAA TCCAGCACT TTGGGAGGCC AAGGCGGGCG GATCACGAGG 112200
TCAGGAGATC GAGACCATCC TGGCTAACAT GGTGAAACCC CGTCTCTACT AAAAAAAG 112260
TACAAAAAT TAGCGGGGCG TGGTGGCGGG CGCCCGTAGT CCCAGCTACT CAGGGAGCTG 112320
AGGCAGGAGA ATGGCATGAA CCCGGGAGGC GGAGCTTGCA GTGGGCGGAG ACTGTGCCAC 112380
TGCACTCCAG CCTGGGCAAC AGTGCAAGAC TCCATCTGAA AACAACAACA ACAACAAAAA 112440
ATTTGAAGTG TATCTGAAG GAAATCCCTT GGAGCCTAAA AATGATCATT GATAACAGAA 112500
AATGATCTCT GCTCTGCCT AGGGTAATAT ATTCAGCTTC AAAGTGAAG GGCATGTTTT 112560
CCAAGGGCAT GTTTTCTAAG TCCCTGTAAT TGTAGTGATA GCAAATATAT GCCCTGCATC 112620
TTGAAATGTA AGACTAGGTT TGAACAGTAT ATAAATTATC TTATGATCTA ATTTCCCTC 112680
ATTTTGTGGT TTCTACTATA AGCTACCCAG AAGTGATAGC AGGACGTTTG GAATTTGATG 112740
GGCATCGGAA AGATTCTAC CTAAGAACAT TTTTTTTTTT TTTTTTTTTT CTGAGAAGGA 112800
GCCTTGCTCT GTCACCCAGG CTGGAGTGCA GTGGCACGAT CTCAGCTTAC TGCAACCTCC 112860
ACCTCTCAGG TTCAAGTGAT TCTCCTGCCT CAGCCTCTG AGTAGCTGGG ACTACAGGTG 112920
TGCACCATCA TGCCTAGTTA ATTTTATAT TTTTAATAAA GGCAGGATTT CACTATGTTA 112980
GCCAGGCTGG TCTTGAATC CTGACCCCAT GATCTGCCCA CCTTGGCCTC CCAAAGTGCT 113040
GGGATTACAG GTGTGAGCCA CTGCGCCCGG CCTCTAAGAA AATTTTGTAG AGCTACTTGT 113100
TCTGTTGCCT GGAATTCCAC CGTAAGTACG ACGTTGTGTC TCCTTCTCCA GGGCTACTAA 113160
CTAAACAACA GAGGGTATTG TGTTATCGAC AATTATTTGA TTGATAACTA TCAGCAAACA 113220
TTTGCCAAGG CATTCCTTTA AAGATAGCCT AGTGACTCTA TTAATACTC CTTCTCCAG 113280
GCTTCTAAGT TCTGTTGGAG GTAAGTAGAT CCCAGAGATA AAGCACCTAC CATAGGACCT 113340

FIG. 6.43

GAATCTTGGT AGAAATAAAT TATATCATCA TGTTATCATA TTATCATGTG TTTTCTATC 113400
TTTAAAGTCT TATGTGAATA TTCTGCTTGA AAAATATGTG TCCTCTGTGA GACCAGAGTT 113460
GAAAATATGT TATTCAAGAA CTTGTAACAG GAACCCGCAC AATTTCTGCT GGAGTTTAAAT 113520
TTCAGGGTTA ATTCTGTCAG CAATCTAAGG TAAACATTAA CATTTTCCC TAGATTCAAG 113580
TCCGTTGTCC AAAAGCTGTA ACAGAACTTA ACTGAATAAA TAGTTTCTTA AGATGGTAAG 113640
CTTCCATATG CTTATAATGA CTCCTCTACA CGTTTTCATC TGAAGGCTG CTCATGCTTT 113700
TGGAAGCAAA GAAGACAATC TTAATAACT ACATTGCTT TTTGGTGGTG CCAGATT.TTT 113760
CTGAGAAACA CCAATGGAAT TTATAAATC ACCAGTCAAT GGGCAATTGA GTTGCTGTTT 113820
TGCTATTACC ACTGCCGTTT GTGAGCATTG TTGGGAAGGT GTCTTGAAGC ACACGTGCAA 113880
GTTTCCCTTG GATAAGTAGT AGGAATAGAA TTGCCAAACC ATGGCTTCCA GTGCAGACAC 113940
AGTCTCTCCC TTGGGCCAG CCACTAGGCA CCACACATTA AGAGGATATT GTCTGTCCAT 114000
GTCCTAGAAA CGTTGTAGCA TCATGCTCCT ATTCGATTAA AAATCTCATT ATTTAAATGA 114060
ACCATCGGGT AAATGTTGTC TCGGGAAAAG AAGCACTGAC CGTCCCTGGG TGGGCTCGAA 114120
CCACCAACCT TTCGGTTAAC AGCCGAACGC GCTAACCGAT TCGGCCACAG AGACCCAGTT 114180
ACTCAGGCG CGCTGCGGTG TGTACAGATT TCCGCGGCGC CGGCAGCCGC TCTAGCCACC 114240
CTGGGCGTCG CCACCCAGG CGTTGCCACC CCAGGCACGG GCTGAGAAGT CGCGGGGCGC 114300
GCCGAGGAGG CAGCGGAAGC GGCCGAGGTG CCCAGCGGCC GCCGCGGGGG GAGAGGCTGT 114360
GCCCCGGCGC GCGGGAGGGG GCGGGCGAGG CCGCGTGA CTGGGCTTCT CTGGGGACGA 114420
AGCGCGCCCC TCGTGGCGGC AGCGGCCAGT GGTCCGCACT CGGCCCGGAC TCGGGGTAGG 114480
AAAGATCCTC TCAGCAATGG CTGCGCGCCA TCGTGCTCT GCGGCGGGGA CCGTGCCGGC 114540
CGGGCGCGCC ACCAGTAACC AGGGACCCAG GGGAGAACCT GCCAAGGGGA ATAGGTGCA 114600
CGGAGAGAAT ACGACACGCT TGGAGGGAAG AACACGTGC TGTACAGGT TAAAGGATGG 114660
AGAGTCACGT GCGCTTAGGT CCCAACTTA AGGGACCTAA CCCTTTTCT GGGTTGCCGC 114720
TATTGCCCT TCTCCTTAGA CAGTTTTCA TCTCATCACC TCTACCCCG TAAATGCAA 114780
CGAACATAGA TAGGCTGTGT ATCAATGTAG ACTGTATGTA TATCTGTGCT TCGTACATAA 114840
AAAGAATATG ATTTTGCCA CCTTCTAAGA ACCAATTGTC ACCCATTTT GAGGCATATG 114900
GCCTCTGTTG AGATTGCATA GTTTAGGGGA CATCAAAAA GCCTTATAGA GGGACTGGCA 114960
ATTAAGATAG CCTTTCAGTT TGAATGGCC ATTGAAGGCT TCTCCCTTC CCTGACTTCT 115020
GAATTTTTT TTTTTTTTT TTTTTTTTT TTTGAGATGG AGTCTTGCCC TGTGCTGGA 115080
GTGCAATGGC GCGATCTCGG CTCAGTCAA CCTCCGCTC CCGGGTTCAA GCGATTCTG 115140
CCTCAGCCTC CCGAGTAGCT GGAATACAG GCGCCTGCCA CCACGCCAG CTAACCTTTG 115200
TATTTTAGT AGAGGCGGGG TTTCGCCATG CTGGCCAGGC TGGTCTGGTA CTCCTGACCT 115260
CGTGATCCGC CCGCCTCCGC CTCCCAAAGT GCTGGGATGA CATTACAGGC GTGAGCCACC 115320
GTGCCCGGCC AATTTTTTA GGCGCACTGT TCAGTGGCAC TAAGTACATT CACATTGTTA 115380
TGCAACTATC ACCGCCATCC ATTTCCAGAA CCTTTTCATC TTCCGAAACA GAAGCTCCCT 115440
ACCCATTACA CGGTAATCA CGATTCCCCT CCTCTAGTCG GAACAATCAC CATTCTACTT 115500
TCTGTCCCTT TGAATTTGAC TACTCTTAGA GACCTCATGT AAATGGAGTC ATACGGTGTT 115560
TGCCTGTGGC TGGCTTATT CACTTACCAT ATGTCTTCAA GGTCCATCCA CGTTGTAGCC 115620
TGTGTCAGGA TTTCTTCCT GGATAAGGCT GAATAAGCTG CACTGTATGC AGGTATCGCA 115680
TTTTGCTTTT CCATTCTCT CTCCGTGAAC ATTAGGGTTG CTTCCACCTG CAGCTATGAA 115740
CATGGGTCTA CAAATAACTG ATCCCTGCT TTCAATTCTT TTGGGAATAT ACCCAGAGAT 115800
GGAGTAGCTG GATCACATGG TTTGCTATTG GCTGTACCAT TTTACATTG CACCAACAGT 115860
GTACAAGAGT CCCTATTTCT CCTCATCTAT TTTTTTTTA AATAATGGGC ATCCTAATGG 115920
GTATGAAGTA TCATCTCATT GTGGTTTTGC TCTGCATTTC TCTAACGATT AGTGGTGTG 115980

FIG. 6.44

GGCATCTTTT CCAGACACCA CCAATCTGAA TTCTATGGCC CTTCGTTTAC TCACTTCCTC 116040
CCAGCAAGAG CCATTTCTGC TTCAGCAAGG AGGAAGCTGC GACTGATAGA GGGAAAGGGC 116100
CCAGGGGGCT TGCAGAGTGG GGCCTGTGCC ATGCAAGGAG AGGAGAAGAA GGTGGATCTT 116160
TGAGTAGGAC TATCTGGAGA TCCTGCTTTC ACAAGGTCCT TGCTTGTGTG CTGGGCAGCT 116220
TTTGAGCTA GTTATCTTTA TTTAGCCCT TGAGGGATAT TTAGGCATGT GGTGCTTGTG 116280
AGCAGCCAAT CCATGAAGAA GGAAGTATG GTCTCCACCT TGGAAATATT GGAAGAGATA 116340
ATGCCGTCCA AATTGCAGTT TTAGAAGTTA ACTTAAATT ATGCTATTTT AATGGAATTT 116400
TGGGTGCATT TCCATTTTCT TCTTAAGAAT TGCTGGAATT TCTTAAGTGT TTAGGTGATG 116460
ATCTCTTTT GTGATTCCTT TTTTAAAAA CAACAACAAA ATCTTTCAA TACATAAGAA 116520
ATAGGCCGGG CACGGTGGCG TAATCCCACC ACTTTGGGAG GCCGAGGAGG GCCGATCATG 116580
AGGTCAGGAG ATCAAGACCA TCCCGGCTAA CACGGTGAAA CCCCCTCTCT ACTAAAAAT 116640
ACAAAAAATT AGCGGGGCGT GGTGGCGGGC GCCTGTAGTC CCAGCTACTC GGGAGGCTGA 116700
GGCAGGAGAA TGGCATGAAC CCGGGAGGCG AAGCTTG CAG TGAGCCTAGA TCGCACCCT 116760
GTACTTTAGC CTGGGCGATG GAGCAAGACT GTCTCAAAAA AAAAAAAAAAG AAAAAAAAAAG 116820
AAAGAAATAG ACCTTTATTT TTCTGTAAT CCACAAAATT TCTATTTTGA TTCCCTATTA 116880
TTTTGCTATT GTCAACACAG TCTCAGTCAA TTCAAGATCC TGTGTGTGCC TTCCCTGGA 116940
GTCATTTCCA AGTGCTAAGG CTTTGGTCCA TGAGTCGCAT GTGCACACTC ATGGCTGTAG 117000
AGGGAGTTTT GCTCCCGGTG AAGGTCTTGG TGGCTCTTCT ATACCTTGAT TGAGGGAAAG 117060
GAATCTTATG TGAAGTTAGC TTTGTTGTAT CAGATATTCC ATAAAGCCAT TTCTGGGACA 117120
GTCCCCTCTG TTTATCGGAC CACAAGCTTC TCTGTCTCA TCAAGCCCAC CTTTATACTT 117180
CATTTCCTCA GACTTCATGT CCAGACTGTG GGATGAACAA GTGGTTATAA GGTTTTAGAG 117240
GCTCCTGTAG GACTAGATGG AAGGCAAAAA AAGGAAATAA CCTTTAAGCA TGCTCTCGAT 117300
TCCTTAAATC CCATCTGAAA GTCTTAAGGA TGTCTTCTCA GTCATACTTA TTTGACAATA 117360
TTACCTAATT TTCTCCATTA GCCCAAGCTC AGGGGTCTTT CTTCTTCCAT ATTCACATGG 117420
GTGCAATGGT TTTCTGAAAG GAAAACAGCA TTAGTAGGGC AGTAACATTT AATTAATCAC 117480
AGGTACTTAT CAACTACAA AACAGGCATT CCAGGAACTG GGTGTTTCTG TTTGTAAAT 117540
TACACTCTCG TGTACATGCT CCCACTAAAA TGAAGTTCTG CTGAGGATGG AGGTTTTGGT 117600
CTCTTTGCTC TGTGCTGTAA CCCCACACT GCAGCAGGGC CTGGCACATA GCAGGCATGC 117660
AGGGACTATG CACTGAATCA ATGAGGAAAT GAAAACCAGG ACCATGAAGT AAAGTGGACA 117720
AAATAAAATG TGATAGAAAA TCTAAATTCC TAATACATAA GGAGCACTTA TCAATTGATA 117780
TTTACAAAAT CTTTTTACAA TTCAATTAAA GACAACATAA AACAAATAAG AATGGGGACA 117840
GGAACAGAAA ATTCCCCCAA AGAAAAAAT ATATATACAT GGTACAGCCA TTGTGGAAAG 117900
CAGTATGGAG TTCTCAAAAA TATTAATAA GAACTATCAT ATAATCCAGC AATCCCATCC 117960
CTGGGTATAT ATCTAAAGGA AATGAAATCA GTACCCCAAA GAGGTGTCTG CACTCCCATG 118020
TTTATTGCAG CATTAGTTAC AACAGCCAAG ATATGGAATC AACCCATCAG CAGATGAAAG 118080
GATAAAGGAC ATGTGATACA TATACACAAT GGAGTAGTAT TCAGCCTTAA AAAAGAAGAA 118140
AATCCTGTCA TTTGCAACAA CATGGATGAG CCTAGAGAAC ATACTAAATG AAATAAGCCA 118200
GGCATAGAAA GACAAATGCT GCATAGTCTC ACTTAGGTGT GGAATCTAAA AAAGTCAAAT 118260
TAAAAAATAA TGTCAAGCAG AGAATAGAAT GGTAGTTGCC AGGGACTCTG GGAAGTAGCA 118320
GGGGTGGGGG TGGAGGGGAG GGGATGGGCA GAAGTTGGTC AAAAGGTACA AAGTTTCAGG 118380
TAGACAGGTG TAAGTTCTGG GGATCTATTG TACAGCGTGG TGACTGTAGT TAATACTGTA 118440
TTGTGTACTT AAAAATTGCT CACCAAAAAT GTTCTACCA AAAAAATGAT GTTTGGATAT 118500
GTAAACAGT TTGATTTAAT CATTTTGACG TGTGTGTGTG TGTGTGTGTG TGTGTGTGTG 118560
TGTATACATC AAAACATCAC ATTATATACC ATATACAATT AATATATACA ATTTTGTCA 118620

FIG. 6.45

AAGAAAAAAT GCACATGACC AATATGATAA AAGTTTAGTC TCACTAGTAA TAAAAATCAA 118680
AATTAAATGA AATAAAAAATT TCTTTCCCCA AATCGCAAAA GAGAAAGAAA GGTAATACTA 118740
AAACACAGTC ACGGTGTAGT GAGAGGGCTG CTCTCACACA GGA CTGATGA GAATAAAATT 118800
GGAGAGCAGT GTGGTAATAT ACATATTTAA CAATGTATAT ACCCTCTCAT TTTAGAAAATT 118860
CTATATTAGA AATCCATCCT AAGAAAATAA CCAGGGATGT GATCAAAATT TTGAATGCAG 118920
CAGCACAGTA TTATTTATAA TAGTTATAAA TAAGAAACAA CCTGAATGTC CAGCAACAGG 118980
CAAAAATGAT AAATAAATTG TGGCATATTT AAGCTGGTGG CTCATGCCTG TAATCCCAGC 119040
ACTTTGGGAG GCTGAGGCAG GAGGATCTCT TGAGGCCAGG AGTTTGAAAC CTGTCTGGGC 119100
AACATAACGA GACCCAGTCT CTACAACATA TTTTAAAAA TTAGGTGGGG CATGGTAACT 119160
CATGCCTGTA ATCCCAGCAC TTTGGGAGGC TGAGGTGAGC AGATCACCTG AGGTGAGGAG 119220
TTTGAACTA GCCTGGCCAA CATGGTGTA CACCATCTCT AAAAAAATA CAAAAATTAG 119280
CCAGGGTGGG GTGCGTTCT GTAGTCCAG CTA CTGCGCA GACTGAGGTA GGAGAATCAC 119340
TTGAACCGG GATTCGGAGG TTGCATTGAG CTGATATCAT GCCACTGCAC TCCAGCCTGG 119400
GTGAGACCCT GTCTCAAAAA AAAAAAAAAA AGAAAAAGAA AAAATTAGCT GGGCGTGGTG 119460
CTGTACGCCT GTAGTCCAG CTATTCCGGA AGCTGAAGCG GGGGGATTGC TTGAGCCCAG 119520
GAATTTAAGG CTGCAGTGAG CTATGATTGT GCCACTCCGC TCCAGCCTGA GTGAGAAAGC 119580
AAGACTCTGT CTCTAAAAA AAAAAAAGTG ATATATTTT AAAATAGAGT ATATTACTTA 119640
TATAGACATC AAAACAATA TTTCAAGGG ATATTTAAAA ACATAGGATC ATGACAAAAT 119700
GTAAAGTTCA AAGGTAAGAT GGAGAATGGA GAACTGTGGG GAACTGTATA ATCTGACAAT 119760
TCGTAGTTGC ATACATCTTT CTGTGTGCTG GTGCTGTTAG AACACTTTGT ACGCATCACC 119820
TCATTTAAGT TCAGCATCCC TAGGTGGCAG ATACTATTAT TATATTCCAG TTTTGTTC 119880
CGTTGTATAT GCGGTGTGAG CCCCAATATG GGATGTGTGT GTGCACATGT GCAGTATTTG 119940
GAAAGTTCTA TGAAATATTA TTAGTGTTA TCTCTGGGAG GTGATTTTTA TTCCTTTTCC 120000
AGTATGTTCT CAAGCATTTG CTGCAAGCAG TCTTTTGCGG GGCCAGGGTT GAGAGGCAGC 120060
AGCAGTTTCC CTAATTACA GATAGAGGGA GGTAGGTGGT TATGCTTGGC CAGATCTCTG 120120
TCTAGGGGTA GAGGAGTGCC TGTGTGTGGG TAGGGACACC GGCGGGGGGC TTTGCCAAAC 120180
ACAGTGGAAC TGTCACGCTG GTCTCTCTC TCAACTCTT CACTCACCTG AGAAAAGGGT 120240
GTCTATGGAC CATGCACACT TCTGTGGGGA ATTTTACAAG ATGTGAATCA TCAGTGATGA 120300
AGATGCTTTC ATTTAAAAAG AATTGGAGTA CCTGAGATTA GAGATAACTT CTACCCTTTT 120360
AAAATATTTT TAAAAATTC TTTGCACTGA TTTTTTTCT TCGTTTTAT GAGTTGTTT 120420
CATTTGGGTG GGATAACTCA ATCTACAGGA GAATATTAAG ACTTTTTAAA TTTTAAAAA 120480
TATACTTTCA AATACTTAAT ACATTTTGTG TTAATGACA GCCAGCAGAT ATTGACTGAA 120540
TTGGGCTAGA TGCTTCAGGG ATCTCCCTTC CATTTAAGAC TCTCCGAGAG GCCATTCTG 120600
ACTGCAGGTC ACTGTATTAT TTTAATTTT AAAATTTT CTTACTTATT TTATTTAATT 120660
TTATTTTTTG AGACAGAGTC TCACTCTGTC GCCCAGGTTG GAGTGCAGTG GCACAATCTC 120720
AGCTCACTGC AACCTCCACC TCCCGGGCTC AAGCGATTCT CCTGCCTCAG CCTCCTGACT 120780
AGCTGGGGTT ACAGGTGCAG GCCACCACAC CCCGTTAATT TTTGTATATT TAGTGAGATC 120840
AGGGATTGCG CATGTTGGCC AGGCTAGTCT CAAACTCCTG ACCTCAAGCG ATCCTCCAC 120900
CTCAGCCTCC CAAAATGCTG GGATTACAGG CCTGAGCCAC CCCACTCGGC CTACTTTATT 120960
AATCCACTTG CAGAAACAGG ATATACACAA AAACGTTTCA AGGCTGTAAG TGCCACTGCA 121020
TGGCACCAAT GGTAACGTT TTACAAATTT GAGTCAGGAA CAATCATTAG TGCTACTAGC 121080
AACAAAAATC AAAATTAAAT GAAATAAAAA ATTTCTTTCC CCAAATGGCA AAGGAGAAAG 121140
AAAGGTAATA CTAACACGCA GTCAGGGTGT AGTGAGAGGG CCGCTCTCAC ACAGGACTGG 121200
TAAGTACAGA GCCATGGAGT AAGCAGGTCT TGAGCTGACA CTGGAGAGGA TCCTTTTTT 121260

FIG. 6.46

TTTTTATTTT TATTTTTTTA GAGTCAGGGT CTTGCTTTTT TACCCAGGCT GGAGTACAGT 121320
GGTGCCATCA TAGCTCACTG CAGCTTCAAA CTCCTGGGCT CAAGAGATCC TCCTGCCTCA 121380
GCATCCCCAG TAGCAGGGAC CACAAGTGAG AGGATCCTTT AGTGTGTGCA AGGAGAAGGA 121440
ACAGAGGTGT GGATGGGTGG GCACAGACAC AGGAGCACAG CTGAAGCAGA GGATTACAAA 121500
GGGTGGAGCC TGATGTAAAG AAACCTAATA GGTGACAGAG CATGGAGGCT CTTGAATACC 121560
AGGCTGGAAA CTGCATTAGG AACGGTGCTC ATAATTGCAG AAAATTTTAC ATGGCCTAGA 121620
TAGTCATCAA AGGATGATGT ACAAACAACAT ATGGCATATT TATACAATGT GCCGACAGGA 121680
TGCACTGAAC ATTTTGAACA ACAAAGAGAC TTGATAATGG CGAGGTTTTG AGGAGGTGAA 121740
TCAGGATGCA AAAAAAGCAA ACAACTAATA AAGTTGATTG ATGACAAACA CTATCAAAAG 121800
GCAGCCAGGA GAAAAGCTAC TGGTTACCTC CAGGGAGCTG GTGAGGGAGG CTGGGTGGGA 121860
GGATCTACCC TTCTGAATTC TGAGGGCACC TCCAGTGTGG CCCTCAGAAA GCAGGAGCTT 121920
CCAGGCTAGA ATCAGATCCC GACATCCCTG TTAATTCCAC GGATTCCACA CCGAGTCAGA 121980
TTTATGATTT ACTATAGGGT TTTAAAAACC AAATTGCAGG GATGCTAGCC TATCACAGCT 122040
TATCTCAGAC ATTGTCCACT AAGGTATACA GAGTGCTGCC TGTTCCTTTG GTACCCCTAAT 122100
CAGGAAACCC CATCAGATCT GCTCCTTCCT ATGGGGTAGT GAGTAACACG AAGGCTTACC 122160
ATCTCACACA GATAACTGGT CATAGGTCCA GCAGAAGTTT AAAACAGAAA ATGAGGAAAAG 122220
CCATGTGATT AACTGCTGCC AGACTGTTT TGTACAAAC AGCAGTTCCT TAGGCATTGC 122280
CTGGGACATG CAATAATTTT TGTACACAA TCTGTGGTAG TTAATATGCT GCACGATGAA 122340
AGCTATCTGA TTTGGATTCA TTATTAGGTG AGCCATCTCG TCTGCAATTT GGTTCCACCA 122400
TTTTCATTTA ACAAATGTAA AAAAGTTTAT TAAGCTCTTA CAAAGTTATG CTGGGCAAAT 122460
ATGCAAAAGT CCAGATCACC TACCGCAGGA ACTAATCTAG CCTCCTCTCT GGGCACCCCTG 122520
TTGTTTGGGG CTGGGCAGTT CTTTCCTGTG TAGAACCATC TAGGGCTGAA TAGGTCATTG 122580
TGACACCTGG GCACCTCTGC CTGCTCGTAA ATGGGACAAT CAGAAAGGGC CTTATGTTT 122640
CCAAACTTTC TTTAAAGTAG CTGTTCTGAA AACATGGTCC AGGGACCCCT GATTGTCCCT 122700
GAGACCTTTG AGGGGATCTT CAAGGTTAAA ATTAATGTCA TAATAATACT AATATGTTAT 122760
CTGTCTTTTT TCACTCTCAC TTTCTCACAC GTGAACAGTG GCATTTTCCA GGTGACAGAG 122820
TGTGTGATAA TGAACCTAAC TGAATGCAGA AGCAACATG AGAACCTAGT TTTTCAATC 122880
AAACCAGACG TGAAAGAGAT TTGCAAAAAT GAAAAACAA TGCTATCCTC CTCACAATAT 122940
TTTTGTTTTA GAAAATAAAG TTATTTTCC TAGAAATGTT TTTGAGTTTA TCAGTCATAG 123000
GTTTATTATT ATAATTAAAA AATGAAATAT ACATACACAG ACATATTTT TAAAGTTCTC 123060
AGTTTAAATC TCTTTTTTTT TTTTTTTTTT TTTGAGACGG AGTCTCGCTC TGTCGCCCCG 123120
GTTGGAGTGC AGTGGTGCGA TCTCAGCTCA CTGCAAGCTC CGCCTCCCTG GTTCGCGCCA 123180
TTCTCCTGCC TCAGCCTCCC GAGTAGCTGG GACTACAGGC ACCCGCCACC GCGCCCGGCT 123240
AATTTTTTGT ATTTTGTAGTA GAGACGGTGT TTCACCATGT TAGCCAGGAT GGTCTCGATC 123300
TCCTGACCTC GTGATCTGCC CACCTCGGCC TCCCAAAGTG CTGGGATTAC AGGCGTGAAC 123360
CACCACGCCC GGTCTCAGTT TTAATTTCTA ATACAGTAAG TATTGATCAG TGTGCCCCAC 123420
ATTAGTAAAA GCTCTTGGGG TCCTCAGTAC TTCTTTTAA GAGTTGTCAA GGAGTCCTGT 123480
GACCAAAAAT AGGAGAGCCA CTGCCCTAGA AGGACAGCCC CAGCCCGGGT CAGGAACAAC 123540
TGGGACAGAA CCTACTGCTC CTAGTGGATT GTAATATGAT AGGATTTAAC CTTCAAGGTT 123600
TCAACTCTTG GCAAGAGTCC ATGAGGGGCC ATGGTTTGTG CTGAGCATTG CTTACTGTTA 123660
ACAGGAGCAA GTTCCTTAGG CTGGTGAGCC AAGCCAGCCT GACGCTGGCC ATGGACATCT 123720
TAGTGGGCTG CTTGTTCTAG TGTGGGTTTT CATTTTATGG GAAATGTCAT CTGCTCTAAG 123780
GCTCTTCTCA TTTGGGGAAA TCACAAGTTC TCAGAATGTT TGTCTCTCTT GGTTGGGGCC 123840
TCTATAATTA AATTATAAAA CAGAGGTAAT GGTTAAGTAA TGCAAGATTG GACAGAAAAC 123900

FIG. 6.47

ACAGAGGATT TAGGGTTTAA TTTGAGTGAG GCAAAGGGGG GATGAAGATG AGCGGTCCTG 123960
GAGACAAGAA AAAGATTGGA TGAAGCTGGG CACGGTGGCT CACGCCTGTA ATCCCAGTAC 124020
TTTGGGAGGC CAAGGTGGGC AGATCACTTG AGGCCAGGAG TTTGAGACCA GCCTGGCTAA 124080
CATAATGCAA CCCCGTCTCT ACTAAAAATA CAAAAATTAG CCAGGCGTGT TGGTGTGTGC 124140
CTGTAGTCAC AGCTACTTGG GAGGCTGAGG CATGAGAATC GCTTGAATCC GGGAGGCAGA 124200
GGTTGCAGTG AGCAGAGATC ATGCCACTGC ACTCCAGCCT AGGCAACAGG GTGAGACTCT 124260
GTCTTCTTTT TTTTGTAGAC GGAGTCTGTC GCCCAGGCTG GAGTGCAGTG GCATGATCTC 124320
TGCTCACTGC AAGCTCCGCC TCCCAGCTTC AAGCGAGTCT CCTGCCTCAG CCTCCCGAGT 124380
AGCTGGGATT ACAGGCATGT GCCACCACAC CCAGCTAATT TTTATATTTT TAGTAGAGAC 124440
GGGGTTTCAC CATGTTGGTC AGGCTGGTCT CAAACTCCTG ACCTCGTGAT CTGCCCGCCG 124500
CGGCCTCCCA AAGTGCTGGG ATTACAGGTG TGAGCCACCA TACCTGGCTG AGACTCTGTC 124560
TTTAAAAAAA AAAGAGAGAG AGGGAGAGAA AGATTGGATG AAACAACAGA GTGGGGAGGA 124620
CCTGTGAGCT TGGTAGCTTG GTGAAGGCAG GGCTTTATTG GGGGCCTTAG AGGGGATCCA 124680
ATAAAGGTTT CCAGTCATGG TAGTGACCTA AAGAAAATAG CATTTTAACA TCTTTCATTT 124740
CATAATAGAC AGTCACAGTT TACAAGACCC TTTCCATACA TTCCTTATGA CATCCATACT 124800
ACAGCCCAGA GGCAAGTTGT GCACTCTCTC CTCTCACAAA TACAAAAACT CAGCCTCTAG 124860
AGGCCAGCGA CCGTCTCAGG GTGATGTGCA ATTCAGGGAT GACAGAGTCG AGGCTCCCAG 124920
CCCAGTGGTT ATCCCTCACA GGCACGTTGC CTGTCACTGT GCAGTATAAA ACTTTGTACA 124980
AGAAATCAAG TTGCATTAGT CAGTCGGATT CCCCAAATGA TCACATTGTA GATGGTGTAT 125040
GCTGTGGGCA GAGCAAGGGC TGCTGTTTCT TGGGCAAAAC AATCAGTCCC CCTCCCCCCC 125100
AAAATAATG AATGCCAATG GTGTGACTTT ATTTTATTTA TTTTATTTT ATTATTATT 125160
GTGAGACAGA GTCTCACTCT TTCACCCAGG CTGGAGTGCA ATGGCATGGT CTCGGCTCAC 125220
TGCAACCTCT GCCTCCTGGG TTCAAGCGAT TCTCCCGCCT CACCCTCCCG AGTAGCTGGG 125280
ACTACAAGTG CATGCCACTG CACCCGGCTA ATTTTGTAT TTTTTTAAG TAGAGACAGG 125340
GTTTCACTAT GTTGGTCAGG CTGGTCTTGA ACTCCTGACC TCATGATCCA CCTGCCTCAG 125400
CCTCCCAAAG TGCTGGGATT ACAGGCATGA GCCACCGCGC CCAGCAATGT GACTTTATAA 125460
TTACAGAATG TAGGACTCAG CTCCCCTAT TGTATGACT CAATATTCTC TTAGATAATG 125520
TTTGGGGCAC TAGCTTACAG GCAGCATTGC CCGGTGGTTA ATGTTGTAGC TTTGCAGGCA 125580
GACTGACCAT ATTAATTC GATCACACCA TTTGCTAAGC CTGTGGACTC GGGCACGCTT 125640
CTTTCTCTGC GTTAGTTTCC TCCTCTGTAA AACACGGATG ATGCTATAAA CACACCCAAG 125700
TCCTAGAATT GTTATATGAG TTAGAAAAGA TAGGCAATA CAACTCTCAC AAGACAGCCT 125760
GGCCTCCAGT AAGTGCCACT GAGTGTTTGC TCTTATTGTA CAGTGGCTCC AAGTGCTTCT 125820
GTCTTGGATT ATTTCTGACC AGGTGGCTAT GTCTCCTAGT AACCTACCAA TCCTGTTGAG 125880
TCTTAATAAG CACGTCTTTG ATGCCTACAG TCGACTGAA TTTCCAGGCC TCATTACTGG 125940
AGACACAATC ATCCTATATG CTTTTTCCA TTTGTTTTTA ATAAAGTGGT ACATGTGTAT 126000
GGCACCAGAT CAAACAGTAC AGAACAAGTT ACAATGGAAG AGAATGGCCT CCCAGCTTTC 126060
CTGAAATCCT CAACTCAGAG ACAACTTTTT TTTTCTGAC GGTTCCTTTA TACAGCCCTT 126120
TTTGTGGTTA CCTTCCTAAC TCTAGAAAAA CTATTCTTAC CTCTGTTTAT TACTTAGAA 126180
ACATTAGACG TTACCTTTCA ACTCCTCAGT ATGAAGCTTT AGTTTTCAGC ACCCAGGCC 126240
ACCAACCTCT TTCCAGGACT TACTACTTAT ACTGGTGGTA GGTGGAATTT TAAAATTCAT 126300
CAGCATTCTT TTGTGATTCT CTGTGTGTTT CAGTTTACA GCAACCCGTA CTTGTTGCAT 126360
GAGTACAGTA GAACTGGGAG GCTCATAACT TAGCCTGCAG GACTTTTCAC TTAAAGCCTG 126420
GCCCTCAGGG TGATGTCACC CACCTCATTG TGCTGGCTC AGGAGTTTAG TCCCTCAGTT 126480
GCCTGGTTGT ATAGTTTGA TGTCAGCAC CTCCAAATCT CACATTGAAA TGTGATCTCC 126540

FIG. 6.48

AATGTTGGAT GTGGGGCCTG GTGGGAGGTG TCTGGGTCAT CAGGTGGGTC CCTCTTGAAT 126600
GGCTTGGTGC CTTCCCCATC GTAACGAGTG AGTTCTTGCT CTGGCAGTTC ACACAAGAGC 126660
TGGCTTTTTA AAGGAGCCTG GCACCTCCG CTCTTTCTCT TGCTCTTCCT CTTCCCTTCC 126720
TTTGTACTA AAAGCTTCCT GAGCCCTCAC CAGAAGCGGT GCAGATGCTG GTGCCATGCT 126780
TGGACCTCCT GTAGAACTGT GAGCCAAATA AACTCTTTCC TATAAATTAC CCAGTTTCAG 126840
GTATTCCTTT ATACAATGCA AAACAGACTC ACACATCTGG TAAACCCAG TTGTTTGCTT 126900
CTAGGTAAGA CGGGAGGAGT GGGGAGCTGG TGAGGGTTTC CACTGCATTG TCTATTTTCA 126960
GGCAAGGTGT CTCCACTGAG TAGGCTTCAC ATTCAGAGCT CTGGGTAAGG TGGGCAGGAA 127020
GAGGGTTGCA GGCTGCCCAA AGGAGGGAGA GAAGAAGGCT GAATCCTTCA GTGACAACCT 127080
GTGAACCAGA GTCTTAGCTC TCTTTGAATA TTTTGTTTCA TATCTTTGGG TTTTGTTTTA 127140
TTTTGCCTAG GGGTAAATGC TGAAGCTGCTG TTCTCTGGAC AGGAATGGAG AAGATGGTGC 127200
TAGCAGGGTT GCTGTTTATA TGAGACATT CATGCAGTCA CTCTCTTTTC AGCACACTTC 127260
TTACTTCTGC CCTGGGTTCA GTTGCTGACT CTGAGCCCAG AAACCTTCTA GGGTCTGTT 127320
AGGTAGATTG GCTTCCACCG TCTTTGCGAC AACCACAGAA AATTCTAGAC TGTTTTCTCT 127380
TCGGGCTTCA TTAGTCAACT TGCTTCAGTC TGTCTTGCAT CTTCTAAATA TTTATAGATC 127440
TCTCTTTTT GTTGGAGTGG CAGAAAATGC TAGTTGACCA CCCAATATTC AAATTATCCT 127500
GCCTCCTTAA TAACAGAATA TCATTGGATG TGGTGGGTAA ATAATATACC CTAACCTTCC 127560
TTGCAGAGAG GGGTGGCCAA TGAGATGGAA ATGAAAGTCA TTGGGAAAGA CTCCTAAGAC 127620
ATCTCTTTAA ACAAGACAGA CTGAAGCAAG TTGACTAATG AAGCCCAAAG CTAGCAGTTG 127680
TTTTTGTTA TCTTTGCCTC TTTCTTCTTC TTCCTGTGGG GACAAAGGGC AGTGATATCT 127740
GGAGCTGCAG CAGCCATTTT GGCATAATGT TGGAAAAGCC AAGAGACTCT CAGAGACCGC 127800
AGCTCCAGCA GTTTTTTATT TTTTCCAAAT ATTTGCTCCA CTGCAGGAGG ATGAGATATT 127860
CGTGTTTGTT GCCTTGAGAC TGAGGAGGA CTGCACCTCC CTGCCTTGTT GTCAAGTTTC 127920
CCCATGTGGT CTGCTTTGGC CAGTAAACA TGAGTGGGAG AAGCTTGGTG AACCATTGCA 127980
TGTCTACCAG CTTTTTTGCT CTCTCCCTT TGGCATTAGA AAGGCATGTC CAGGATGGAG 128040
TTGTTCTTC AGCCTAGATT GGGTTATGAG AAGCTAGCTG GGGGAGTCCA GTAACATATA 128100
AAGCGAGTTA GAAATAAAAC TTTGTTGTTG TAAGCTATAT ATATATATAT ATATATATAT 128160
ATATATATAT ATATATATAT AATATGTATG TAATATATAA ATACATATTA TACTTTAAGT 128220
TCTAGGGTAC ATTTGCACAA TGTGCAGGTT TATTACATAG GTATACATGT GCCATGTTGG 128280
TTTGCTGCAC CCATCAACTG CTCATTTACA TTAGGTATTT CTCCTAATGC TATCCCTCCC 128340
CAGCCCCCCA CCCCTCAACA AGCCCTAGTG TGTGATGTTT CCCTTCTGT GTCCAAGTGT 128400
TCTCATTGTT CAATTCCCAC CTATGAGTGA GAACATGTGG TGTGTTGTTT TCTGTCCTTG 128460
TGATAGTTTG CTGAGAATAA TGGTTTCCAG CTTCAATTCGT GTCCCTGCAA AGGACATGAA 128520
CTCATCCTTT TTTATGGCTG CATGGTATTC CATGGTGTAT ATGTGCCACA TTTTCTTAAT 128580
CTAGTCTATC ATTGATGGAC ATTTGGGTTG GTTCCAAGTA TTTGCTATTG TGAATAGTGC 128640
CGCAATAAAC ATATGTGTGC ATGTGTCTTT ATAGTAGCAT GATTTATAAT TCTTTGGATA 128700
TATACCCAGT AATGGGATCA CTGGGTAAAG TGGTATTTC AATTCTAGAT CCTTGAGGAG 128760
TCGCCACACT GTCTTCCACA GTGGTTGAAC TAATTACAC TCCCACCATC AGTGTAAG 128820
CATTCTATT CCTATGTCTC CACATCCTCT CCAGAATCTG TTGTTTCCTG ACTTTTAAAT 128880
GATTGCCATT CTAATTGGCC TGAGATGGTA CCTCATTATG GTTTTGATTG GCATTTCTCT 128940
GATGACCAGT GATGATGAGC ATTTTTTCAT GTGTCTGTTG GCTGCATAAA TGTCTTCTTT 129000
TGAGTAGTGT CTGTTTATAT TGTGTTGTTT TTTTGTGATG GGGTTGTTT TTTTCTTTCT 129060
TGTAATTTG TTTTCTTCT TTTGATATC TGGATATTAG CCCTTTGTCA GATGGGTAGG 129120
TTGCAAAAAT TATCTCCCAT TCTGTAGGTT GCCTGTTTAC TCTGATGATA GTTTCTTTTG 129180

FIG. 6.49

CTGTGCAGAA GCTCTTTAGT TTAATTAGAT CCCATTTATC TATTTTGGCT TTTGTTGCCA 129240
TTGCTTTTGG TGTTTTAGAC ATGAAGTCTT TGCCCATACC TATGTCCTGA ATGGTATCGC 129300
CTAGGTTTTC TTCTAGGGTT TTTATGGTTT TTAGGTCTAA CATTAAAGTC TTTAATCCAT 129360
CTTGAATTAA TTTTGTATA AGGTGTAAGG ATGGTTTCCA GTTTCAGCTT TCTACATATG 129420
GCTGGCCAGT TTTCCAGCA CCATTTATTA AATAGGGAAT CGTTTCCCCA TTTCTTGAGC 129480
TACAGATATT TTGAGTTTGG TTACCACAGT ATTATCTAGT GGAAGTTGAC TTATACAGTA 129540
TGTAATAGGA TAAATATAGG TGTGTAACAG AATATTAAGT GTTCGTGTTT CAAAGCTGAG 129600
GGGAAAATGT TAAAAGTGT CACACACTCT AAAAAGAGAT TAGCTAAAAC TGCTTCATTA 129660
ACCACACTTT GGGGAAACCA GTTCTGAGAT TCTTCTCCAT TACTCTGACA GGTGAGACCC 129720
TCTGGGGAGC AGATCTCAAG ATCAAGTTAT GAGTGCAAGA GGTGTGTTGG GAAGCGATGG 129780
TTGTAAAAGA ATCCTGCAGT AGCACCAGGC ACAAGTCTGT CCAGGGAGAG GAGGACTTCT 129840
ACTCTTACC AGCATCTCTC CTAAGTCCCC TTAGGGGACG GGGGCAAGGA AGTGCTGGGA 129900
AGGGCAGGGC ATGGTTCTCT GCTAGGACTC CACCCCCCTG GGGCCTGTAC CCACGGACCT 129960
AGGTGAAGAC AGGCACTCCT GCCTTCTCGC CCAACGGTTG CGTTTCCCAA GATCATCCTG 130020
GCCTGCCACG CCCCCATCTA CCTATTAAAC TCCCCACCT TCCCCAAACC CTAGCAGGCA 130080
GACACACATC GGTGGAAGAA GACAGGAGCG GCTGGACATT GAAAGGACGT CGAGAGGAGC 130140
ACACCTGCAC ACCATCGACC AGCGGAACGA GGCAGAGTGT GGCTGGAACA GTCGGAGGGA 130200
AGCCTGGGCC GCTGACTCCA GGGGAAAACC ATCTCCTTTC TGGCTCCCCC CTCTGCTGGG 130260
AGATACTTTC ACTGAATAAA ACCTTGCACT CATTCTCCAA GCCCACCTGT GATCCGATTC 130320
TTCCTGTACA CCAAGGCAAG AACCTGGGAT ACAGAAAGCC CTCTGTCTT GTGATAAGGT 130380
AGAGGGTCTA ACTGAGCTGG TTAACACAAG CTGCCTATAG ACAGCGAAAC TGAAAGAGCA 130440
CACAATAGCA CACACTCATT GGGGCTTCAG GAGCTGTAA TATCCACCCC TAGACGCTGC 130500
CATGGGGCGG GAGCCCCACA GCCTGCCCGT CTAGAGGTTT GAGCAGCGGG ACACTGAAGA 130560
AGAGAGCCAC ACCCTCATCG CAGTCTCTGC GAGGGAGACA AGGGAACCTT TCCGGTTTCA 130620
CTTCTGCTTG GCTTGAGCTG GCACTGAAGC ACCCTTTTCC CTCCTCACTG AGGGAGCAGA 130680
GGGGAAAAGC GGTAGAACTA ACAGGCTAAC AATGCTCCTC CGAAAATATA TCGTATTTTT 130740
GGATCCCTAG AGATAGGTGA TCACGGCAGC CGCGGAGTGC ATTTGGGTCT CCTTTCAGAA 130800
AAGAACTTGC TGCTCAGCGT TGAAGAATGC AGTTGGCCAA CAGCCTCCAG CTGCTCTGTC 130860
TTCAGCATCT GCCATGGCAT CTGAGCTGAG GTCATGTTCT TCCTGGGAGG TCCCAGCAG 130920
AAGGATCACG TGGAAGCTCC ACAAGCTCCA CAGATGTTCC AGGAGAGGAA TAGGCAGCAT 130980
TTGGAAGACA TATCCTGCCA TAACAGAGGG CATTGCTAG TAGAGACAAC AAACAGCAAC 131040
AGCCAAGTAA ACAAACACAC AAGCACAAAG CACTTTCTCC CATTTCCTCT CATTGATCCT 131100
GTCCGGGTAG AAGCTGGGGA GGAAGTAGAA TAGGGTGAGG CGGGGTGGGG CTGGGGGGCC 131160
TACACCTTCT TCCTTCCCCC GCAGGTCCTG TCCCTGGGCC AGGCTTGAAC TAGGGGAATG 131220
GGAAAAGCTG TGAAGTGAAT GAGAATTAGG AGTTTTTATT TAGACTGGAC TTGAATTTTT 131280
TTTTTTTTTT TTTTTTTTTT GAGACAGAGC CTCGCTCTGT CACCCAGGCT GGAGTCCCGT 131340
GGCGCCATCT TGGCTCACTA CAGCCTCTGC CTCCCGGGTT CAAGCGATCC TCCCACCACA 131400
GTCTCCTGAG TAGCCGGGAT TACAGGTGCC TGCCACCATG CCCAGCTATT TTTTTTTTTT 131460
TTTGTATTTT TAGTAGAGAC AGGGCGTCAC CGTGTGAGCC AGGCTGGTCT CGAACTCCTG 131520
GCCTCAAGTG ATCTGTCCGC CTCGGCCTCC CCAAGTGCTA GGATTATAGG AGTGAGCCAC 131580
CACGCCTGGC CTGGACTTGA ATTTTAAATT CCTAAAAATG AACTACCAGT TAAAATTAA 131640
AAATGACCAA AAAAGCTATG GGATATGCTG ATGTTTTGCT TTGGGGATAA GGAAAAGATA 131700
TCTGGTTGAG CGGCATTGAA AACAGTGTAG GGAGAGAAAA ACTCATTCTT GGCTCACCCT 131760
TTTGAGTCCC ACTATCTCAA TAATCTGATG TTATATGACA CACACACACA CACACGGAGG 131820

FIG. 6.50

AATCCTGGAA GACTCCATAT CAAGGTGGTG ATGAAGGTGA CCAGTGGGTG ATAGGATTAT 131880
AGGTGTGTGT TTATTTATTT ATTTTAATTA CCTTTTTTTA GAGACAGGGT CTCTGTCATC 131940
CAGGCTGCAG TGCAGTGGTG TGATCATGGC TCACTGCAGT CTTGCACTCC AGGGCTCAAT 132000
CCTCCTGCCT CAGTCTCCTG AGTAGCTGGA GCTGCAGTCA TGCACCAACG TGCCCAACTA 132060
ATTTACTTTA TTTTATTTTT TATTTTTTGT TAAGATGGAA TCTCACTTTA TTGCCTAGGC 132120
TGGTCTTAAA CTCCTGGTTT CAAGCATTCC TCCTACCTCA GCCTCTCAA GTGCTGGAAT 132180
TACTGCACTT GGCCCTATTA TATTTTTAAA AAATTCAAT AGTTTTAGGG GTAAAAAGTGG 132240
CTTTGGTTAC ATAGATGAAT TGTATAGTGA TGAAGTCTGG ATTTTTAGTG TACCCATCAC 132300
CCAAATAGTG TACATTGTAC CCAATGAGTA GTTTTTCATT CCTCACCCCC AACTGTCCC 132360
CACTTCTGAG TCTCCTGATG TCCATTATAG CACCCTGCTT TTGCGCACTT AGAGCTTACC 132420
TCCCACCTAG AAGTGAGAAC ATGTGGTAGT TGGTTTTCCC TTCCTGAGTT ACTTCACTTA 132480
GGTCAGTGGC CTCCAATTC ATCTGAGTTG CTGCACATAA CATGATTTC A TCTTTTTT 132540
GACTGAGTAG TAGTCCATCT CTCTCTCTCA CACACACACA TACACACACA CACACACACA 132600
CACACACACA CACATTTATC CACTCATCCA TTGATGGGCA CTTAGGTTGC TTCTATATCT 132660
TTGCAATTGT GAATTGTGCT CCAATAAACA TACATGTGCA AGTGCTGTTT TTTCTCCCTT 132720
TTATCCTTCT TTTCTCCCT ATGCTCCAT AGGTACTGAG AAAGAGTCTT TTTTATATAA 132780
TTATTTCTTT TCCTTTGGGA AGATACCCAG TAGTGGGATG GCTTGATCCA ATGGTAGATC 132840
TGTTTTAGT TCTTTGAGAA ATCTCCATAT TATCTCCATA TTGTTTTCCA TAGAGATTGT 132900
ACTAATTTAC ATTCCCACCA ACAATGTATG TGTTCATTT TCACTGCATC GGCACCAACA 132960
ACGGTTGTTT TTTGACTTTT TAATAATGGC CATTCTGGCT GGGGTAAGGT GGTATCTCAC 133020
TGTGGTTTTA ACTTGATTT CCCTGATAAT TAGTGATGTT GAGCATTTAA GAAATATATT 133080
TGTTGGCCAT TTGTATATCT TCTTTAAGA AATATCTCTT GAAGTTGTTT GCCCACTTTT 133140
TAATGTGATT ATTTGTTTTT TTTCTTGCT GATTTGTTG AGTTCCTGT AGCTTCTGAA 133200
TATTAGTCTT TTGTCAGAGG TATAGTTTGC AAATACTTTC TCCCATTCTG TAGGTTGTCT 133260
CTTTACTCTG TTGGTTATTT CTTTGTCTAT GCAGAAGCTT TTTAGAATAA TTAGGTCCCA 133320
TTTACTTATT TCTGTTATTT TGTTGCAATT GTTTTGGGG TGTTAGTCAC AAATCTTTG 133380
CCTAGACCAA TGTCAGAAG AGTTTTCTT AGGTTTTCTT CTAGAATTTT TATGGTTTCA 133440
GGTCTTAGAT TTATGCTTTT AATCCATCTT GAATTAATTT TTGTATATGG TGAGAGATAG 133500
GAACCCGGTT TCATTCTTTT AACTACATG TGGCTATCCA ATTTCCCAG CACTGTTTAT 133560
TGAATAGGAT TTCCTTTCCC CAGTGTATGT TTTGTTTGT TTGGCTGAAG ATCAGTTGGT 133620
TGTAGGTATT TGGTTTTATT TCTGGGTCT CTATGCTATT CTACTTTTAT ACCGGTTCCA 133680
TGCTGTTTTG ATTACAATAG CCTCGTAGTA TAATTTGAAG TTGGGTAATG TGATGCCTCC 133740
AGATTGCTC TTTTTTGCT TAGGATTGCT TTGGCTATTT GGACCCCTCT TTGGTCTCAT 133800
ATAAATTTTA GGATTGGTTT TTCTAATTCT GTGAAAAATG ACATTGGTAT TTTGATAAGG 133860
GTTGCACTGA ATCTGTGGAT TGCTTTGGGT AGTATAGTCA TTTTACAAT ATTGATTCTT 133920
CTAATCCATA AGCATGGTAT GTTCTCCAT TTGCTTGTGT CATCTATTAT TTCTTTCATT 133980
AGTGTTTTGT AATTCTCCTT GTAGGGGTCT TTCACCTCCT TGGTTAAGTA TATTCCTATG 134040
TATTTATTTT TTATTTTTTG CAGCTATTGT AAATGGGATT GAGTCTTGA TTTGATTTTG 134100
AGCTTGGCCA TCATTGGTGT ATAGCAGTGC TAGTGATTTG TGTACATTGA TTTTGTAAAC 134160
TAACACTACT AAATCACTT ATCAAATCTG GGAGATTTT GAGGATTCCT TAGGATTTTC 134220
TAGGTATGAG ATCATATCAT TGGTAGAGGT AGTTTGAGTT TCTCTTTCC AGTTTGGATG 134280
CCCTTATTT CTTTCTCTTG CCTGATTGCT CTGACTAGGG CTTCTAGTAC TATGTTGAAT 134340
AGAAATGGTG AAAAGTGGGC ATCCTTGCTT CATTCTAATT TTTAGGGGGA AATGCTTTC A 134400
ACTTTTCCCC ATTCATTTTG ATGTTGGCTG TGAGTTTGTG ATAGATGATT CTTACTATT 134460

FIG. 6.51

TGAGATATAT TCATTTGATG CCTAGTTTGT TGAGGGATT TATCATAAAA GGAGGCTGGA 134520
TTTTATTGAA TGCTTTTCT GCATCTATTA AAATGATTAC GTTTTTCATT TTTAATTCTG 134580
TTTATGTCAT GAATCACATT TATTGACTTA TGTTTATTTG TTGCTTACAT CTACTTTCTA 134640
ATTTTACTAT AATAACATG TATAATTTTG TTATCAGAAA AGTAAATGTA AAAGTGAGTT 134700
TTAATTTTAA AACTTGGGCC TAAGTCTTCC TGCCCTCCAA GCCCATTCCC TTCCTGATAT 134760
CTGGGGCTTC CCTCCTCAAG CCTGCTCTGC AGGATAAGGG GATACAGTCC ACATGCCTGC 134820
TGCTGGTTTG GCCCATGATA ACCTCCATGG GCAATGTCTG AGCCTCTGCT GTTGAGTTTT 134880
GCTTTACACA CTCCTGGCAA GGAAAGGATG GCCAACATGG CTTGGACATG GGTGCTGAT 134940
AATTGGTGAT GTCTCATGAC TGGTTCTGCC TGGAGGGCTT GCTGTAAGTC CCTGATAGGA 135000
GGAACATGGA CCTGCACAAG AGCAGAACTT ATCTGACACT GAAGAGGACA CTTCAAGAAC 135060
AGATTATCAA AGTCTAGCTC AGGGAGAAAT ATACTTTAGA GCAGAATGAG GAATGGCGAG 135120
GCAGCTGAGC TTAGACACAA GCAGAAGGAA ATCCATGGTG AGGGCACAGG CAAGGAAAGG 135180
GGCTGAGAGA GCATTAGTGG GGGCAGTCAG GGGCAGTGGT CAGGATGCTC GGATGCCAGC 135240
GTGAACAATC GCATCAAGAT TAAACACCAT GAGGATCGTT AGACTTCCTG TCATATGTCT 135300
CCAGGTGGTG CTCCAAATAT CCTAAACCAG ATGACAGCAC CCTCCACCC TCTGCTGTAT 135360
AAGCACATCT GCTCTCCTAT AATCATTCCC ACATAGCAAT TTATCATTTT TATTGATTTT 135420
TCTTCATTTA ATACAGTAT AAGTGTGTCT TTTATTTTAA AAAATTGCA TTCCTTTAAT 135480
TGCTTTGGAG ATTGTGCATT TTTCTCTCTG TTGATTTACT CTGCCAATAA ACATGTAATC 135540
CTACCATAAG CATGTTTTAC TTGTGTAATC AACCAAAATA AAAAATTTAA AAAGGAATCA 135600
CTGACTATGA ATTAGACATG TGGATAGGCA CCAGGGTTGC AGACATGGCC CACGTTCTTG 135660
CATTAACTTG CACTGTGGCT GGGGCATTGG ATGGGTACAT TAAAAGGATT AAAGTAATAT 135720
AAGGCAGTAT TTATTAAGTG TTGAGTGAGC ACTACAGAAC CCAAGTGCTG AGGGAGTTTC 135780
ATGCAGGAAG AGATCAAGAG TAACACAGAG AAGAAGAATA GATCAATTTA GCGCATTCTAT 135840
TTAAAAATTC ACCTTTTGCA TAAGGGGATG TGTCTTTTGT GGGGAGGAGG GGAGTTCCGA 135900
TTGGCAGTTT GTTCTCAGGG AGCTTGAAGA AGAGATCTTG GAGAGGAGAC GCAGAGAAAA 135960
CAAATGAAGA AAATGTCAAA ATGGAAGGGG TTGGCCCGGC TATGCATACC TTAGTTAGCT 136020
TAGGTAGAGT CTAACTTTT ACAAGTGGTT TCAATAGGTG TGTTTGGTCT GGGTTCTTTG 136080
GGAGGTATCA TAGGAGAATG AAGGCAGGGA GGACGCTTCC AGCACCAAAA TTCAAAGGGA 136140
AATGTATTTT ACATGCATAG CATTGTTTTA CTCTCTTTCC ATTTGGAGCA TATCTTAAAA 136200
ATTCCATTG GAGCATATCT TAAAAACCC ATTTCTCTGA CAATGGTTCT AAAAGGGGGA 136260
AACATCCTTT GCAACAGAAT CATTCAATTCT CTCATTCTATC AACCACTGAT TGTGTACTAA 136320
GTGTCAGACC TGATCTCCAT CCTGCCTGGT ATGGCACTAG CTTCTGTCTT GAGACAAGCA 136380
TTGTGATAAA CCATGACCAA AAAAAGGGCA GTTTTATAAA CACAAGTCTG CCAGGCTTTC 136440
AGCAATTCTA AATTCCTTT TGCAAGTCAG GCTGGAGTTA ATGGCTCTTT CCTGCAGCGG 136500
CGGAGATGAC AGGGCTCTCC CACAGTGCTG AGCAGGCAGT TTGAAAGCCC CACTTCCTGT 136560
CTCTGCATGG GCGAGTGTC ACTGGAAGCC ACTGAGAGGA AGGAGGGAAA CCTCAGAAAC 136620
CGGCCCTGCTG CTGGCTGCTT CACCCTAGAA AGCCCAGGCA GAGGAGGGAA AGGTGAAGTG 136680
CTGAAAAAGA ATAAAAAGG GGGAACATGA AAAAGAGCAA GAGCAGGAAG GAGGCAGGGA 136740
CGGGAAAGGA GGGGAAGCAC GGAACAGCC AATGTCAAGG AGAAGAAAAG ATGGCTGGTG 136800
GAAAGGAGCT TCCAGGAATT GGGACACAGC CCTGTCTTAT TGCAAAAGAT GGAAACCCTG 136860
AAGGAGAACA GGAAGGAAAA AGAAAACAAG TCCGTCTGAG CTGGCAGGGT CCACTTTCTC 136920
ATTCTACAGA TGAGGAAACA GAGGCACAGA GAGGAAGTGG CTTGCCCAAG GGGGCAGATT 136980
CTTGAAAGGA TCATCTGCAC TCTCTCTCC TTAATGCATT CTTACCTCTT CTTTACTCGT 137040
GAGTCAGTCC TGAAGGACAA GCTGCCTGAA GTCCACACA GATGGGCCTG GGGCAAGCAT 137100

FIG. 6.52

CAAACATCCT GGGGGCCCTG GGTGAGGTTT GCTTTTAAAT TCCAGGTCAG GGAAAGGAAG 137160
GTCTTTAAGT TGCTGCTCT AAGCTTAGTA ATCCCCCTCA GAGTTATGGG TGCGGTGTCT 137220
GGGGTAGCCG TTGCGTCTCT GGGCAAATAC CCTGGAGAAT GCAGTGTGG TTGTCTGAGC 137280
TGGGGACAGA GTGACAGCAT AGTTGCATGC AGAGCTGGAG GCTCCTGCAG CTGTACAGGT 137340
AAGGTGCTGA AATTCTCCAC CAACCCTTCC TCTTTGCCCC CAGCACCACG AAGATAACCC 137400
TCTTTGAATA TGTGGAAGTC TGTCTCCAA ACTTTCTAAC ATTCTCATGT CAGTCTTAAT 137460
AGATTGAGCT CAGTTACTGC CTCCTCCAGG AAGTCCTCCT TGTCTGCAA TCGGCTGCC 137520
ACCATGCCGG CTCACTCATA GTTTAACTC TGTATCTTTC TAATATGCCT TAGCCCACTC 137580
TGTCAGGATT CCAGTCAGCT TCCTTCTCCT AGACTAGGAG TTGCCTCAGG CCAGGAGGAC 137640
CAGCCTTGTT CATATCTGTA CCCTGCAAAC CTGTCAATGC CCAAACCTGC TCAGTGCTTT 137700
GGAGTATGGA ACCAGCCGTC AATGCAGGAA TGTTACACTC TAAGAGTTCC CAAAGGTAGA 137760
GAGATGAGGG ATTGGTGCTG GAAAGTGGAG GTTATTCTAA GGATGGGTAT GGCAGGAAAC 137820
ACAATTATAG TTCAGGGAGT GGAGTGTCCA GGAGTGGAG GAGAGGAACT GGGAGAAAGA 137880
GCAGAGAGTG AAAGTGAGAG CGGGCACAAA GAAAGGGAAA AAGAGTCAGG GATCAACCAA 137940
AGTGCATGCT TCCTTTTCAG CCCTGCCAGG ATGTGCAGGG CGGCTGCTGT GGACGCGTCA 138000
AGGCTCAGCC TCAAACATGT CTTCTCCTT GACTTTTGTC TATCATTCTA AAGCTAGGTC 138060
ATTTAAAAAG TTCTTTTGTT TTCTTTCCAC CGATACTCTG ATTTCTGACA TCGCCAAAA 138120
AGAGGTCAAG ACCCTGGCAT ACCGCCCTAC TAAGATTAAT ATAAATATTA TCCATTGAAA 138180
CTGTTATTTT TTCCTTAACT GTTATTTGTA GAGTTAAAGA TTCCCATGAT CGCGCTGGCT 138240
CTAACATCAT TTTTGGCTCT TTTGAGATCA AATTTGCAAT TTGATGCAA AATAGCTGTG 138300
ACGCATATGT GTCTGTATGT GTGTGGTAG GAGATTTTTT ATCATTACAT CTTCTTTTGC 138360
CCTGCCCTTC TGCTTTCTG TCCTTTTAAAT TTGCGGGCTT TTGGCAACCA CAGCACGGGT 138420
CTGGTTTCT AGGAGTTTCT TTTGTAGGAT CAAACCGCTA GTTGGCTCTT GGCCCTGTGA 138480
TAGGGCCCTG GGCTAACTTA TTGGGAAAAT GTTGCTGTAA CCCCTGCCCA GAGGTGCCTG 138540
TGACATGGGC CGCCATCTTC TCCTCTCCC TTGGCTCAG CCCACCTAG AACCTGAAC 138600
AAACATTTTC CTTGACATT CATAAAGTG CAGTGGCTCC TCATTAGCA AAATACATCC 138660
CAGGGAAGTT CAAAAGTGAA AAAAGGCCGT AACTTCTTCT TCTTCTCAGG GACCTACAGA 138720
AAATATGTGG CACCTCGGCA GCCTGGCCTG CAGCACTCCC CTCCCCATCG GTGAGTCCTG 138780
CTACAGTGGG TCCAGGTGTC TGGACGCCCG GCACGCACGG CTCTCTGCAG ACCTCTGGAC 138840
AGTACCATGG GAGCCGCACA GTCCCTGCCT GTTCTGTCCG GCAGTTCTTG TTTCCAGCA 138900
CCCTGTCTCA GGTGAGAGGT TCCCTCTTCT GCTGGGCTTC TCCTCCCTGC TGTGAACCCC 138960
AAATATCTGA GGCAGGTCAA TTAGGAACC TTATTTTGCC AAAGTTGAGG ATGTACCCAT 139020
GACACGGCCT CAGGAGGTCC TGAAGACAAG TGCCCGAGGT GATCGCGGCA CAGCTTGCTT 139080
TTATACATTT ATACAGACAT CAGTCAATAT ATGTAAGATA AACATTGGTT CGGTCCCGAA 139140
AGGCCGGACA ACTCCAAGTG GAGAGGGGGC TTCCAGTTCA CAGGTAGATA AGAGACAAAA 139200
TGTTGCATTC TTTGAGTTT CTGATTAGCT TTTCCAAAGG AGGCAATCAG ATATGCATTT 139260
ATCTCAGTGA GCAGAGGGGT GACTTGGAAT GGAATGGAAG GCAGTTCTCA GTTTAAATTT 139320
TCCCTTTAGC TTAGTGATTT TGGGGTCCCA AGATTTATTT TCCATTCACT CTGCAGACAG 139380
GGGCTTCTGT GCATCCAGGG AGCCCTCCT CACAGAAGGA AGCAGGCCAT TAATGAGACC 139440
CAATCCAGCT TCAACCACCT GGTAACAATT AGGACATCAC TTCTCTGAGC AAGAGCTCCT 139500
GCCTGTCCAT GAGTTATCAA GACATTCCAA TTGTTCTTCC ACATCTTTGA CATGAAGACT 139560
TGAGGGGGTC AGATTTTCCA GGGGGCTTGA TGGCATGTTT TCTTCACTGT TCCCTGCCCT 139620
GGTCATCCAA GTGACCCTTG GCAGGGAAGA GGCCCCGAGT TGCAGAATCT CTGTTCTCAC 139680
AAGCCATTGC CAACCCGGAG AGTGGCTTTG CCACTATTCC TAGCATGTTG TTGGCTATTT 139740

FIG. 6.53

CAGGAATGGG AGTATTTGAC TTTTCCCTTT GCAGTGATTG CTGCAAGGAG AGGAATTGAG 139800
AGACTCAAGT CCCTGAGATA AATATTTATC AACTATTACT GAAAGGGAGT ATGTCAAAGA 139860
AAAAATGTGG AGAAACTTCA GCTTGAACAC ATAGTTTAAA TCCAGCTTGG GTGTACTCCA 139920
GTGGGCATGG ATGTATTACT GTTTTGCACT GCATTCTTCT ATGATCAATA CACAGAAGCA 139980
AACAGGCCAC GTGGGTAAAC AGTAATTTTC ATTTACCAGG GTGAATATGG AAGTCCTCTT 140040
GTTTCCATGT CATGATGAAG GAAAGCAAGG ACCATCTTTT GCCAAGGAAC AGTGGCTGTG 140100
GGGGAAGTGA GGAGATGGAA GGACAAGGCA GTCAAAAGCT TTGGAACAAC TCTTTTTTTG 140160
AGATGGAGTT TTGCTCTTGT TGTCCAGGCT GGAGTGCAAT GGCACGACCT CGGCTCACCA 140220
CAACCGCTGC CTCCCAGGTT CAAGTGATTG TCTGCCTCA GCCTCCCGAG TAGCTGGGAT 140280
TGCAGGTATG CTCCACCATG CCTGGCTAAT TTTGTATTTT TAATAGAGAC GGGATTTCCTC 140340
CACGTTGGTC AGCTGGTCTT GAACTCCCGA CCTCAGGTGA TCCACCTGCC TCGGCCTCCC 140400
AAAGTGCTGG GATTACAGGC ATGAGCCACC ATACCCGGCC CTTTTTTTGA ATAATTTTAT 140460
AGGTTTTCAA ACTATTACAC TTACCTTTTT ATATAAGAGA CAGGACATAG TCACTGAACA 140520
ATCACTCCAG ATTTTAAGTA AGTCCAGGAT GGGATGACAA TGGAACAACC ATGAAATGAA 140580
AGGAAGAATG TGTCACCTGT ATGTCCACAC GTCTCCAAAT CTCTCACCTC TGTCAGCTGC 140640
AAACAGAGCC TGAAATAAAT GTTTCCTCTG TGCACAGCCT CCACAACCTC CTCCCTCCAC 140700
GTTTCTCACT CACTCCTCTC CAGCACTTCT CTCGGGGTTC TGCTTACAAA CTTGAAACCG 140760
GCTATGCAAA AATTATAACT GTGGAAATTA TGACAGTGAA AGAGATCAGA CCTAACCGAC 140820
TCCATCTTGC TTCTAACCTT TAAGCTGTCC TTGTTCACTT TTGGGCTGAA CTAACCTTGG 140880
GAAGGAATTC AGTTCATGGT AGAACTCTGA AACAAAATTG ATAATAGCCC TTTCCTGAAA 140940
AGACCCCTT CTGCTCTGGG GACAAGTCTG CCATTGTAGG ACTAACAAT TAACATAAG 141000
ATTAGAAAT AAGGTTTAGG GTTCATGCAG CCTCCAGTTC CAAGAGTCTA AACCTCCCCA 141060
AATTGCTCCT GGGGATAACA TCACTGTTGT AAAAGCTAAG ACCAGTGCTT GAGATATTTT 141120
GTAGACCTG CTCTGGATGG ATCAGCTGAC ACCATCCAGA CTGGTAATTT GGCTCAACCA 141180
GCTCTGCCAT CCCACCCAGG AACAGAAAAA TACTCACTTC ATCACCCCAT GAGTCCATCT 141240
CTAACCTGAC CAATCAGCAC TCCCTACTTC CCAGGCCCTT ACTCGCCAAA TCTGCCTTTG 141300
GAGGCAGATA ACAACTTATC TTTAAAACT CTGATCCCTG AATGCTCAGG AGACTGATTT 141360
GAGTAATAAT AAAACTCCGG CTCTGCATGA ATTAATCCTT TTCCATTGCA ATTCTCTTGT 141420
CTTGATAAAT TGGTTCTGTC TAGGCAGCCA GCAAGGCGAA CCCTTTGGGC GGTTACAAAC 141480
TCATCCTCTG TGGAAGAGTA GGAGTTCATG GAGAAATTGG TTGCAAATTA CAAAATTTTA 141540
TTGTAAGGTC AACTTGTCCT AGTGTCCTG TGTGCAGCGA AGGGCCCCTG CATGGTTTAG 141600
TGATTGCAAG TTGAGCCTCT AGGGTCAGGT TGTCTAGGTT TCCATCCCAG CTCATTCACT 141660
TATTATCTGT GTGTTCTTGA GCAAGCTCCT TAATCAATTG AGGCTTTGTC CTTCTGTTTG 141720
TATAATGATG AGAATAATAA CCTCCACAAT AACCTCATCA TAAGGTTGTT GTGAAGATGG 141780
ATCAGATAAT ATATATGTAG AGTGCTTATA ACAGTGCTTG GCACATAAAA AATGCTCAAA 141840
AATCTTAAGT GTTATTAATA ATAACTGAC ATATATTTCT TGAGCAGGGT GGTGGTAAAT 141900
GGGTGTTCTT TTTATTAAGC TTTAAAGTGT GCATAGATCA TATTAATTCT TTTTATGCAT 141960
ATGATATATT GCACATGCAT GAAAATACAT GCATTAAAAA TAAATGAGCA TTTATGAGAT 142020
TTAGTTTAGC AGTCACATGT CCCAGGATTA CAAGCCAGCA ATAATGGGTT GGAAAACATT 142080
CCAACCCATT CCAACCATG GAAAACATTC CAACCCATCA CTGGACCCAT GTGCCAAACA 142140
ATGGAACCGC CCACAGGTTT TCATTCTTGG TTAATAAAT ATGATTATTA CGGGAATAAT 142200
ACTGATTCCC TAAGAATTAA TATCTGAGCA AGTTTCTTTT TTTTCTGTC TTCTTGAAG 142260
ATCAGCAGGT TCTAGATTCA ATGGAGTCAC TAGGATTGAG CCACCAGTAT ACGCCAGTCC 142320
TCTCCAGAAC GGCCACCTGG TGGTGGGCAC TAAGGCAGTC TCAGATGAGG ACTGATTGAC 142380

FIG. 6.54

TTTTGTGTGA ACTCAAACCTG CCAAAGTCCC TCCCTCACCT TGCAAACCTC AAAGCACAAAC 142440
TTTCAAAGCA CTACTTTCTT TCTTGGCTCT CAATTCTCTG CCTAGAAAAA GGGAGGTGTT 142500
GGCAAGGATG TTTGTTTAGT TCTGGGCATC AGTCAATGGT ACCCAGATCT TGCTGAACAG 142560
AAAAGACACA GATTTGTTTC TCTGAGGCAG TTGGTAGTGC TTATTGCTTA TTGCTCTCAG 142620
GGGCTTCTGC AGCAGTAGAA GGGCCCTCTT CCCCTGCCAT GCCACACTGA GAGGAGCATC 142680
CTTGGAGTCA TGGTTGGAAT CTGTTTTTGT TATGCTAGTC CTCTCCGCA TGCTAGCTGT 142740
TGCATTGCAG GGATATGTGT ACCTGTTTAT CTCTCCACT AGGCTCTAAG AAGCCAGGTT 142800
TCTTAAAGGA AGGAAGCTGA TCTTGTATTAT CTGGAAGTCC TCACAGTGAC ATTGCTCAGT 142860
CAATGTTGAG TGTATGAATG AATAAACGGG AACCATCACG AAAAAGCCGA AAATACAGTG 142920
GAAAGACTGG ATCATAAAAT CTCTAAGCA AATTTTTTTT CCTCTTACAC TCCATTTCCA 142980
AATAGATAAA GTATTTTTTA AAATCCTATC AGAATATTCT AACACACTGA GTTGACAGAA 143040
TAGAGATTTT TAAATGCAGT GTCATTTGGC CAGCCATTTG TGAGAATTTA TAAATGTTTC 143100
AGTAGGTTGA AAACACTATA AAAGCAAGGA CTATGTTTAT ACCCAACAGC TGGCACTTAG 143160
TATGAATGCT AAATGAAACA TTCTCTTCTC TTTCAAGAGT CAGTCCAACC AGTGACCCTG 143220
ACAAGAAGGA AGGCACATTT AACTCAATTT AATGAACTCT TATAGAGCAT CTCCTTCTCC 143280
AAGTGCTTTG CTAAGGATGG GGTA AAAACA TGAATAAGTC TTGGATTCTG TCCTTCAGGA 143340
ATTTTCAGTC TTTGGAGGCA GATACATTTG CACCCAACTA TTATCCTAGG CAGAGTGTGA 143400
TAAGTACGAT AATAGCAGTA AAAGCTCTAA GTTAGGCAGG AGAGGAGGAG CTGTTAAAG 143460
CTTATGGGGC CTGGGAGGCT TTCGGCGGAG TAACTCCAG GGGGACAGCT AGGCATCTGG 143520
CTGCTGGAAT TGGGAGGAGG ATCATTTTAA GTGGCTACAA CTCTGGGTGC ACAGGACTAG 143580
AGGGTGAGGG CCAAGATGGG AAATTGTGGC AGCCATCTTC CACACTGGGC GCCCGCCGAC 143640
CCTTGCTTCC TGGTATTCAT ATTATTGTGT AGTGTCCCCC AACATTGTAT CAGGGTTGGC 143700
CTGTGTGACC AATTGCATAT GGTGGGAATG ATGGTGTGTG ACTTCTAAGA CCAGTTCATA 143760
GAAGATGTGG CCAATTCCCT TACTGTCTTT TTTTTTGGCA GGGGAGTGCC GAGTTTCACC 143820
CTTGTGCCCC AGGCTGGAGT GCAATGGTGC GATCTCTGCT CACTGCAACC TCTGCCTCCC 143880
AGGTTCAAGT GATTCTCCTG CCTCAGCCTC CCAACTAGCT GTGATTACAG GTATGCGCCA 143940
CCATGCCTGG CTAATTTTGT ATTTTATAGTA GAGACGGGGT GAGATCAATG AGGCAGTCAA 144000
TTGGCCAGCC TGGTTTGA GCTCCTGACCT CAGGTGATCC ACCCGCCTCG GCCTCCCAAA 144060
GTGCTGGGAT TACAGGCATG CGCCAACCGC GCCTGGCCCT TACTGTCCTT TGGATCAGCT 144120
GCTCTGGGGC TAGGTCAATC CTTTATGTGA CTGCAGCCCC AGCCAACATC TGGACTGAAA 144180
CCCATGAGAC ACCCTGAGCC AAAAAAGCCC AGCTAAGACT TCCTGCATTT CTGACCCACA 144240
GAAACTGAGA AAAGAAATGT TTTGTTGTTG CTTTAAGCCA CTGACTTCTG GGGTCATTTG 144300
TTTTGCAGAA ATAGATAGCA GATACAGAAA AGCAGGCTGG TGGAACAGTG TGGGAAACAC 144360
CTTGATTTTC AGGGAGTTGC ACTTTGTTTA TGTGCAATGG TGCAGTGTTC TTAGAAAGAC 144420
ACAAAGATGA TAATACTGGT GATGGGCATA ATACGGGTTG TCAAGAGGAG TGAAGGAGGC 144480
GGGGATAATT TAAGAGGCCA CAGCAGTAGT GTGGCAAGAG GTAATGAGGG AATTGAACCT 144540
GGTGGGAATG GGTGAGATCA ACGAGGCAGT CAATATGGGC AGTGAGTGTG AAGGAGCTGC 144600
GAAGGATGAT TCTTTGGTTT TGAGCTTAGG AACATGAGAG AACCAAGATC TCATTTATCC 144660
AAAGAGGAAA CACAGAAGTG AGCCCCTGTT TGGGGGCAGG GCTGGGTAGG AGGAAAAGAG 144720
TGGAGACGTC TATCTCCCCA GGAAGAGAGC CCCTGCTTC CAGATCCAG TGGATGGCAG 144780
GGCACTCGGC TCATTACAG ACTGGGCTCG TTGAGAAACC TTTCCCTGGA GGGCAGGGCT 144840
GCTCTGTTTC ACAGCCATA TCCCTCATGG CCAAGTGTTT CTCGAGTGAC AGTCTCTGCC 144900
ATCAATATTT TTAGCATGTG GTCTTTCAGA GACTAAAGAG TGGCATCCAT CTCCTGAAAC 144960
TCCTTCCCCA GCTGACAGCT GGTGACCCGT GGAGGAGGGA GCTTCAGGGA GCCTGATGGG 145020

FIG. 6.55

CGAGAGTCTG TTCCAATGCC AATCCATTGG AAGAGATGAA GTCAGACCCG AGTTTGATAG 145080
AAAGCCTACT TCCTCCCTTG TATCCAGCTG TGGAGACCTA CCAACATCAA TGCAAACCCAG 145140
AAGCTAACAC CCAGTTCATA TATCCCAAGT GGAAGGAAGC TTCTCGTGGA ATTGTCTTAC 145200
ATGACAGTAA CATAAATCCT GAAGGTAATA CTTGGCCAGG TAATGTTAGA AAAGAACCCG 145260
AACATAGGCA TTGCTATTAT AGATCCTAGG ATAGGCCTGA GCAAAACTG TCTGGGATTG 145320
ATAACATGCT TCGTTGCAAT CTGATAGAGG GAGTGAGATC CACTCCAAAT GGAGTCTGAT 145380
TTGGGGCAAA GCAAAGAGTA TGGGAAGGAAA CTTGAGAAAAG GGGGACAGCT TCTCAAATGG 145440
AGTCTGGCCA CAGCTGGGGC TGGAAAAGAG ACATGACTGC GCTTGACAGAG TGGTGAGAAT 145500
TTGCTGCTAG AATTTTAAAG TTGTGTGTTT TCATTTTAT GATAATGTAA ACTGAGATAA 145560
GCATATTCTC TGCTATCCCA ATGAGCCCCT CCTCTAGGAG GACTACCTTG CCACCTTATC 145620
CATAAATGTG TTTATAAATT ATTTTGATGC CAGCTGGTAT TTTTAAAAA GTGGTTTTGG 145680
ACTCACAAAA AAAACCATGA TGGATTTAAT ACATAACAAA GCATTTGTGT CAAGTGAAGG 145740
CCAAGTAACA TCTTAGCGTC CTGTGTGAGC GAAGGTGTCTG TGGCAGTTCA AACAAGAATG 145800
CCGATGAAGC TGCCCAGGAT GGCCAAGGCC ACCTTGGTGT GTTTGAGGGG AATTAGAGTT 145860
TAGAAAAAAA AAAAAAGGCA CCTGACACTC TGAACATG TGGTTACCTG GAATTTTGGG 145920
GTTTTGAAGC TTTGCATTTA ATTTGCAGCT TATGGCCTGA AGGAAAAGAC AGGTGAAATG 145980
CATATCCTGG GATGAGTCAC CTGGAGGAGA GGGCTGGGAA GGGGCTGAGC TGCACATGCT 146040
CAGATCTTCT CCCAGGCTTA TCGACCCAGT GAGTCAAGTC TTCTTCCAAC GGGATAGAGT 146100
GTGAGAGAGA GCAGGGAACA GAAGCCAGAG TCTCTGTAA ATTTCTCGGT ACATTTCTGT 146160
TAGAGAATGG AAGTTTCTCT ATCGTAGGAG ACCTTGAGAG CCTGGGATAG AAATTACCCC 146220
TTTGTGATGT ATTTTCTCC CAGAAATAGC ATGGCCACTG TCACTGCTAA GCTGGAGTAT 146280
CATGAGCACA ATTTCTCTCA CTTTCTATAC CCATGCCTTT CTAGGAGATT GGTGGCTCCA 146340
TCAAAAAGGA GTTAAAAAGA AGCAGCACTA TTTTGTGGAA TACAATCATC ACCATTATCA 146400
CCATCAGCAC CACCAACCAG CACCACCATT ATCAAAAGCA TTCACCTGGT GTCTGCCTTA 146460
CAAAGTCAA ACTGCAGTAG GTATTTGTAA TAGAATGTTT CCTTCCCCC TTGGGATCTG 146520
CAGAAAAGCT GGAGAATGTT TTGGTATCAA CACACTAGGT TGCATTGCTA ATCATGTGAT 146580
GGCCCCATGA CAGTCTCTGT TGGCTGGTGT AGTTCAGGTG GACGACTGCA GGATTTTGT 146640
CTTGAGCCT CAGTTCTGAC TGGGCTTGGG GTGTAAAAGG TTTGGGAGCC AGATGACAAG 146700
AGTATTTGAT GGGTAGAATA ATGGGTTTCT CCAAAGATC ACCAGAATGG TTATTAAATA 146760
GTACAAAGGA GGAATTTACT GGTAATACCA GTTTGCAAAC AGAGAAGAGA GTCTCCAATG 146820
TGGACTGAAA GTGCTCTCTC TTTGAAGAGG GGAAGGACAG ATTGGGTTT ATGCCTCACA 146880
GGACTGGTAC CACATATATT CAGCAGGTTT TTGGGGAAAA TCTATACATA TTTATAAGGT 146940
GAGCTGATGC CTGCATAATA GATAAACATA TATGTAACAT ACTTTTCATA TTCATTTTGG 147000
GACTGGGTTT TGGCACTAAA ATTTGTGGAA TTTGGCTCTT TATGTTAAAA GGTGAAGTATG 147060
AGGACACAAA GACGGTTTGT GTGCACCCTC TATAAACTGG CTGAACTGG CTTAAGGTCT 147120
GCAACTGCTT ATCCAAAAAG AATGTTTGTG AGGCCAGGCC TCTGTCCAGT CAGAGTTGTA 147180
GTGGTCCAGG TTGTAAATCA AAGTTTATAG CTCTTTTGT TAGAGAGTTC AGCTGTAGGA 147240
ATTTAGAAAT TTGCCATGCC TGCCAGGCCC TGAACCTTTG ACCCATAGGT AACTTTATTT 147300
CCTTAACCTT AGGGTCAGTC TTAGTTGATA TGGGGCATCT ATTCTGGTAT CTCAGATCCT 147360
ATGGTCAAGA GAAAAGATCC TCCACAAGAG GGTCTATGT GGCTGCAAAA ACTGCTCTGA 147420
GCTAAATCCA CTCAAAATCA CTGCAGGATG TCACTACTAG AAAATAGGGC AGGGATAGGG 147480
ATCCCCTTCC CATGCTGCCA GAAAATGCCT GATAGCTTAC CTCCCCCGGC CCTTGAGGCT 147540
CCCTTGGAAT AGGCACATGC AATCCCATCT CCACCCAATA GAGCTTGTCC TAGAGCTCAG 147600
TTTTTCCCA TAGTTTCCC ACCCACTTGC ACCAGAAAAT CTAATAAAGT CATGTGATTA 147660

FIG. 6.56

ATACAATTCA TTTTATCACG CTTCTGAAGA TTTAAGAGAG AGCGGTCACA TTGGATTCCA 147720
CAGTACCGAC CTTCTGACGA TTCTTCATTT CACCTTTATC TATTTTTATT TTTATTTTAT 147780
TTTTTTTTCG AGACGGGGTC TCACTCTGTC ACCCAGGCTG GAGTGCAGTG GGGCAATTAC 147840
GGCTCACTGC AACCTCTGCC TTCTGTGCTC AAGCAATCCT CCCACCTCAG CCTCCCAAGT 147900
AGCTGGGATC ATAGGTGCAC ATCACCAAGC CTGGCTAATT TTTTGTATTT TTGGTAGAGA 147960
TGGGGTTTCA CCATGTTGCC CAGGCTGGTC TTGAACCTTCT GAGCTCAAGT GATCTGCCCCA 148020
CCATAGCCTC CCAAAGTGCT GGGATTACTC ACGTGAGCCA CCTCGCCTGG TCCCTTTCAC 148080
CTTTATTATC TTTGCCTTTA ACTCTAGTGC TTCCTCCCTG AATCAGTTAA GGATTGCATT 148140
TGGCTGCATT AACAGAAACC TGA CTGCAGA AGCTTAACCA AATAGGGTAG TTTTAAAGA 148200
GAGATTGCTT ACATCACGCA AATTGCACAA ATTTAAGTG CATAGTTCAA TGAGTTTGA 148260
CAAATGTAGA ATAACATAGC TATATAAAAC CATTCCATCA AAAAAATTTT ATCACCATAG 148320
GAAATTGTGT CCTGTCCCTT TCTGTCAAT CCAACTCCT CCCACAAGG CAACCTTCAT 148380
TCTCATTTCT CTCACCATAG CTTAGTTTTA CATGTTTCTA TAATACAGCA TCATATAAAT 148440
GGAATAATAC AGAATGCAAT CTTTGTATG AAGCTTCCTT TGGCTCAATG TAATGTTTAT 148500
GAGATTCATC CATGTTATTG AATGTATCAG TAGTGTTCCTT ATTTATATTT CCTAGTGTTT 148560
TATTGAATAA ATATACTACA ATTTGTTTAT CCACCTATTT GTTGATGAAC ATTTGGACCG 148620
TTGGCAATTT TTGCCTATTA TGCATAAAGC TGTTAAAAA CATTCTTGTA CAAGTCTTTC 148680
ATTTCATATG TTTTCTTTT TCTGAGGTAA ATA ACTACAA GTAGAATTGT TGGGTAATAA 148740
ATAGGCATCC ATCTAATATT ATAAGCAACT GCACAACAGT TTTTCAACGT GGCTGTACTA 148800
TTTCACTCTC CCAATAGCAA CGTATGTGTT TTCCAGCTAC TCCACATGCT CACTGGCATT 148860
TCCTGTTGCC AGTTTAAACA TTTCAAGCCAT TCCAGTGGAT ATGAAATCTC TCTGGCTATA 148920
ATAATTGTAT TTCTCTGATG ACTAATTATG TCAAGCCCCT TTTCAAATGC TTATCAGCCA 148980
CTTCTATACT GTCCTCTGTG ACATGTCOGT TCAATCTTTT TGCTCATTCT TAAAAACAT 149040
TGGGTGTTTT GTCTTTTCT TAGTTTGTCT TTTGCTTTTC ATTTATAGGA GTACATATCT 149100
TCGGAATACA AGTCCTTTGT CAGATAAATG TATTGTGAAT AATTTTCTCC TAGTTTGTGG 149160
TTTGCCTTTT CACATTCTTA ATATCTTTTG ATGAGTGGA ACTA ACTTTC AAATTATGTT 149220
CAGTAGATTA ACTTGTTTTT GTTTTGT TTTTGT TTTTGT TTTTGT TTTTGT TTTTGT TTTTGT 149280
CACTTGTTGC CCAGGCTGGA GTGTAGTGGT GCCATCATGG CTCACTGCAA CCTCTGCCTC 149340
CTGGACTCAA GGGATCCTCC TGCCTCAGCC TCCAAGTAG CTGGGACCAC AAGCACGCAC 149400
CACTACACTT GGCTACTTTT TTATATTTT GGTAGACACA GGATTTCGCC ATGTTGCTCA 149460
GGCTGGTCTG GAGCTCCTGA GCTCAAGCGA TTCACCCACC TCAGCCTACC AAAGTGCTGG 149520
GATTACAGGC GTGAGCCACC ACGCCAGTC GAGTAGATCA AGTTTAAATT TTATGGCCAG 149580
TAGAGATCTA TTTCAAGGCT CTCTATTTTG TTCTGTTGCT CTATTTATCT ACCTTTATGC 149640
CAATTTTCTT CTCTTTTGAT TCAGATAGGG TTATAATAAT AATTATTTT TCCAGGGATT 149700
AGATGGACCA GGGCTGGTGA AGTTGTTCAA GGGAGTGATC AAGAGCCTGG CTCCTTTCAT 149760
CCTTCTGTTT CATCTCCTT GGCTCATGGA TTTGTTTTC CAAGTGGCAA GATGGCGCCT 149820
CCACCTTGG TATCCTATTT TAGTTCCTGG CAGAAAGAAA GGAACAGGCT AATGGCCCTG 149880
ATGAGTCTAC CCCCTTTTAA CAGGAGAAAA TTTAAAAAAC AAAAACCATG AAACCCTTTC 149940
CCAGAGGCAA CAACCAGAAT TCCATTTATC TTTTATTGAC CAGAACAGAC CACATGGTCA 150000
CTGGTGGTGG CAATGGAGAC TGGGGAGATG AATATTTTAA AGGTGGCATA TTCCAGAAGA 150060
ACACTGTGCA CTGATTGCAT TAATGAACCC ATTAATGTGC CAAGGGGAGG TTTACCTATG 150120
AGCATGGGCA AATTAGAACC CACTCTTGA GCTGCAGGTG AGCCAATCCC ACCTAAACAG 150180
TGTGGATGCT ACAAGATGGG GAAGTAAATT GATTCTATTC CATACCCTAA CCTCTCTCCA 150240
AGATGTATTC TAAAAATAGA AGAGGGAAGA CAGAAGAAAA CATCCAGAAT ATATTTTAT 150300

FIG. 6.57

TGTCTTTTAC TTCTTCAGTG CATTITAGAT CAGTGCTTCT CAATCTGGCA AGGGGCATGC 150360
AGGAGGATGT GAGTTTTATC AGGAAAACTA CACAACCCCC CAACCACAAT GCTACCCCCA 150420
CTCCTGTGGA CCTTCTTTAA GAGAGACTCA CTATTATAGA TGGAGTTGAT ACGATTTTAA 150480
GAGAGGCCAT ATATTATTG CTTTCTGTCT TGAAAACTT GTGATTTTTC TGTATTGTGC 150540
TACTGCCAAA GAGAATAGAA ACCTGACTGA GGTGTCAATG TTTATGTAAC TGATTTTCATG 150600
TACTTTCTGT AGTTCTACCA TTTCTGATGG TTAATAATTT CTTGTGTGTG TGCAGTTGGG 150660
GAGTGTGTCC TCCTCCTTCT GCTCTTATAC CACACATTAG CACATCAAAA TGCTCTAATC 150720
TTTGTATGAT TATGTGGCAT GTGGTGATGC AGCCTCACAG TGGAAAACT TCTCTTGGGC 150780
CATTGCAAT GTAACATTTT TTTCAATCAG ATAGTGCCAT TAAGGATTTT ATTATGGCCG 150840
TCACATCCTG TGACATCTCT AAACATGCAG CATTAGGGCC TAAGTGCAGC CCTGCAGGTA 150900
GAGTTGCCAG GTTTAACAAA TAAAAATTAC ACGCTGGCCA GCGGGGGTGG CTCATGCCTG 150960
TAATCCAGC ACTTTGGGAG GCTGAGGCAG GTGGATCATT TGAGGTCAGG AGTTCGAAAC 151020
CAGCCTGGCC AACATGGTGA AACCCCATCT CTAATAAAAA TACAAAAATT AGCTGGGCAT 151080
GGTGGCAAAT GCCTGTAATC CTAGCTACTT GCGAGGCTGA GGCAGGAGAA TCACTTGAGC 151140
CCTGGAGGCG GGGGTTGCAG TGAGCAGAGA TCACACCATT GCACTCCAGC CTGGGTGGCA 151200
GAGCGAGATT CTGTCTAAAA AACAACACCG TATTGGGGGC ATGCTGATAC TAAAAATTA 151260
TTCATTGTTT GTCTGAAATT AAAATTTAAA TTGGGGGGCC TGTATTTTAC TGGGCAACCC 151320
ATTTGCAATA TCAGCAACAA TCTCTTATTC AGACCACTGA TTAAGTGTGC AAAATTTGAA 151380
TCTCTGAACA GTACCTATGT CCTTGATATC TTAATTAAT GAGTGTCTTA GACACTCAAA 151440
GCAGGAGGAA GCATTATGGC AGATGTTTGA GCCCCAGAGA TGTCCATGAG CACAGCATAG 151500
AGCTCAGAGC CTTCTTTATT ATTTGCTTCA CGACAGAGCA AAGGACTGCA GCAGGTTGAC 151560
TGATATAAAA GTTTTACCAT GTCTCACAGC AGGCCTTTGC TCAAGTTTCC AGTAAGGATA 151620
TTGTATCATT TCTTGCCTGC AGTACTTGTA AATCCACTTA CACTGCCTGC TGTGAGTCA 151680
TTTGTTCGT CTTGAGTAGC ATGTCATCCT TGTTCTAGA AGATAGTGAG TTTAGAGACA 151740
GTAGCCAAAGC AACAGCAGAG CAGCCTCAAC CAAAACGATT TTCCATTTTG GTGGGATGAA 151800
TTGAAACACA AGCATCTTCT ATCCAGGGGA GATTGGGGA TCATAAAGAA TCAATCTGAG 151860
CTGGTACCAC CATATTGGCT GCTGCATTTT CTAGAGTTGC CGTAACTAGT CTCACAAGCT 151920
GGGAGGCTTT ACACAACAGA CATGTATTGT CTCATAGTTC TGGATGCTAG AAATCTGGAA 151980
TCAAGGCTCC AGGGGAGAAG CTGCTCCATG GTTTTCTCTT AGCTTCTGGT GTTGCCAGCA 152040
ATCCCTGGTG TTCCTTGGCC CGCAGGCGGA TCACTCCCAT CTCTGCCTCC ATTGTCACAC 152100
GGCATTTTCC CAGTGTGCCT GACTCTGTGT TTCTTCTCAT AAGAACATCG GTCATATTGG 152160
ATTACAGGCC CGTGCTACTC CATTATGACC TCATCTTAAC TTAACAATT ACATCTGCAG 152220
TGATCCTGTT TGCAATAAG GTCACATTCT GAGGTTCCAG GAATTAGAAC ATAGACATAT 152280
CTTTTGGGAA CAAAATTCCA GTGATAACAG TTTCGGAGAC AGACTAGTCC TGGAGTTTGT 152340
AAGGTGAGCC AGGACCAAGG TGCCAGGATT CTCATTTTGT AAGGTCCAGG AACAAAGTGA 152400
TGTTAATAGA AAGAACATGT TTTTGTGTGT TTATTTGTTT TTGAGACAGT CTCCTCCAT 152460
CACCCAGGCT GGAATGCAGT GGTACAATCT CGGCTCACTG CCGCTGCCAT CTCCCAGGTT 152520
CAAGCGATTG TCCTGCCTCA GCCTCCTAAG TAGCTGGAAT TACAGGTGTG TCCCACCATG 152580
CCCAGCTAAT TTTTGTATAT TTGTGTGTGT GTGTGTGTGT ATATATATAC ACACACACAT 152640
ACATACATAT ATATACATAC ATATATATAT ACACACACAC ACATATATAT ATATATAAAA 152700
TATATATTTT TTTTAGTAGA GACTGGGTTT CACCATGTTG CCCAGGCTGG TCTCGAACTC 152760
CTGCGCTCAA GTGATCCACC TGTCTTGGAC TCCCTAAGTG GTGGGACTAC AGGCACAAAC 152820
CACCACGCCC AGACAGAAGG AATATGTTTC CTTCCAGTCT CACTTGACTG GCTGCTTCCC 152880
TAGATAACAA CAGAGGATGT CTGTTGCAGT TCTCATTGCT GGGGAGTCTA AACTGGAATA 152940

FIG. 6.58

AAACACCCAC TATCTCCATC AGGCTTGCAC TAGAGCCCAG CTCTAGCTGG AGAGAAAGAA 153000
GCTAACCCGC ACAGACACAG GACTGTAGGC AGGGAGCATC CGGGGGTATT TGGGTCCTGG 153060
CTCTGATGTG CCTAAGGCCA ACTTCTCTCT GGCCATGCTG GCGTGCATGA GCTCACTAAT 153120
CTTCCTTTTT GCCTTCCATT TTCTCCAATC CTGACTTAGC AAAGGTTGGG CAAAAGAGAC 153180
TCTGTGTGAG TCGAGCAAA GCCTGAGATG CTGGATTTTC CAAGATACGA GAAGGGGCTG 153240
GGGGCTGGGT GAACTGGTGG TGGAGGAGGG AAGGATTAAT TTCCAAGGA GGGGAAGGGG 153300
CCAGGACATC AGGCCCGGG GACTTTGAAG AGAGGGTCGT GGGTAGGAGG TAGATCAAGT 153360
GGAGTGACAC AAAGGTCAGG AAAGAGGAAG TGTCCACACT GTCCTTCGAC AGACTTGAGT 153420
CTATGGGACT TCCTCCCTGC ACGGTACAAG GAAATGAGTA AGTGAGATAA TGTTGTAAGT 153480
TCTGGCCCTC TGACATTGCA CTGCCCCGAT GTCACAGTTG GAACTGTAC CTGCCCCCAT 153540
CCTTGCTCTG GGTGTGTTT GTCTGGGGAG GGCTGGTGAA GCAAGAGGTA CTCAGAAAAA 153600
GGACAGAAAT TGCTTCCTAT TATCTGGGCA TTTGGAGGTG AAGGGGTCAC AGCTCTGGCA 153660
AAGATGGGGT TGAAAGGGCC CGGACTCCAG GGAGGGGCAG CTCTGCATGG CCTGATTCCCT 153720
GCACCCACC TTTGCCCTT CACACCTCCT CTCATCTCCG GTTTTTGAAG AGGAGGACCC 153780
TGTCACATCT GGACAATTCT GCAAGAACTC TGTAGAAGT ACTTCACTGT GAACCAAGGCT 153840
CCAGAAGTCA ACAGAAACAA AAATGCTCAC ATTTAATCAC GATGCTCCCT GGCATACACA 153900
GAAGACTCTG AAAACTTCTG AATTTGGGAA ATCCTTTGGC ACCTTGGGGC ACATTGGGAA 153960
CATAAGCCAT CAGTGCTGGT GTGTGTGTGT GTGCGGCAC ACGCGCATGT GTGTGCATCT 154020
TCTACCATGC CTCCTACAAA TTTGACCTGG GCCCAGGGCC ATGTTCCGGT GTTTTTAAGA 154080
ACCGAGGCTC CCAGAAGCAG TATTGGGCAG CTAGAGTGGC CCCAGGATCT ATATCAAAT 154140
CTACCTGTTT CTGAACCAAA TTTCTTCTAG AATTTTATTC CATAAATCTG AATTATGGTG 154200
TCAGACTCCT AGCATACT AAAGGAACTC TCTGCCTTGC ATTAAATAAC AGGAGTTACC 154260
CCTGGAGGTA ACTCCTAGCC CTGGCTCTTT AGAGAACAGA TGCCGAATAG GCATTAGGGG 154320
ATGTGATGGA TGTGCTAACT TTCAAAAAA AAAAAAAA AAGGCCTGAG CTGAGTGCTC 154380
AGAGATTCAC AAAAAGCTGA CAGCATCTCT CTGTTCCATT GGAAGCTGGG TGATCCTTTC 154440
TACTCTTCC TGAGAAAGGC AGTTGGGCAG GAAAAAGCTG TATCTCTGTC CTCCTGAGA 154500
GGGTTTCCA GTCTGAGGGT GAAGGATCAG GAGAGGGAGA CCTGACGGGT CGATGTGGGG 154560
CATCATCCAC TTGAGTGAGA ACCAGAGGGA TCCCGTCATT GCCCAGGGCA GATGCTCCAT 154620
TTTGGGGGGC ATCATTCAAT CTTTCTGTT CTCCCTGCAT TCCTCTGGCT CCTGCCAGG 154680
AGAGGTGGCC GCTGGCAAGA GAGCTTGGTG GAGGTGGGAG GTGGGAGGTG GGGGGTGGGG 154740
GGTGGGGAGT TCTTGAGCCA GGACCTAGCG CATAGTCTCC AGCCTGCTGA TGGCTGTCTT 154800
GGATGCTTCA AAGGGGAGAA GATCCTAGAT GTGGGAAACA TTGGTGGGCG TTCTGCTGGG 154860
GCATCTGTAG CCTCTGAGAA GGCTACCACT CTCTCCTAAG CTTACGCCGT CACACCCTGG 154920
GCACTTGTTG AATGACTTTA CTTAGCTTAC AGCCTCTGGT TCCTGTTGGG AAACCTAGGG 154980
CTTGCCACAG TGTTCATTTT CCTTTGCGGG CAACTCCGTT CCTGGCACTT ATCATATTAC 155040
CCACTGTACT CCCCCTTAG AGCTGTGTCA AGGTTCTGAG AATCTATCCC TTGGCTTGGA 155100
AGGGGTCATC TCTCTGGCCA GATCATTTCC TGATAGGTCC TGAGGCACCA CAACACATAG 155160
GAGGCTTGTC CTCTCTCTGG GGTTCACTGC CTTGCTCCTT CTCCAGGTCA ATATGTGACC 155220
TTGGACCGGT TGCTTGAGTC CCCTGGTCAT TCAGAAACAA TTGGGTTTCC CTGGCTTTGG 155280
AGCCTGGCAG CCTGGCTTTG AGAACCGGGC TTTAACTTGT CACATGACTA TGGCCAAGTT 155340
CCTGGGGCTC TCCAAGCTTC ACTTCCTCTG TAAAAAGGGC AATAATATAA TACCTGTCTT 155400
ATTGGGTTTT GTCCATGTTA GATGAGACAT TGGGTACAAA GCACTTGGTC CCGTGCCTGG 155460
CACATTTACT GCACTTAATG TATGATAGTT TTCTTATTAT TCTAATAAAC AATATGGCTT 155520
TGGGAGTATA GTTCTGCCAC ATTGCAGTGG CCAGAGTGAA GGTGGTGAGT GCCTTCTGGG 155580

FIG. 6.59

GCCCTGGGAG TCAAGGTTAT CCGCATGCCC TTTCTTGCTT GCTCCTCAGT GTGGCTGCCT 155640
CTATGTCCAC ACCATGCAGA TGCAACAGGT AGTTTGAACC TCTGAGGCC ACAGTGGGAT 155700
GGGGAGGCAG GGACATCACT TATGGGGTGG GAAGTCACCC ATTCCCAGG AAATGGCCCC 155760
AGCTGCCTTT TCCATGACTC CTCTTGAAAC CCTGTGGAGG CCACATTCGT GTTGGGGCGG 155820
TCTTTCCCAT GAGGATATGT TCAGATGCCG AGGCATTTTG AAAAGCCCTC CATAGAGTTT 155880
CCTTTCATAA CACATGATCA TCCCCTTGGG CTCTGGTTT TTTTCTTTC AGGACCTTAT 155940
TTTCAGGCAA GTGGCCTTGG ACCTCTAAGG CTGTCCTTTC CTAGCTACCG AATCCAGCAT 156000
TCAAAGTGAT GGAAATATGT ATATATAGTA ATAGTAAAAT ATCAGCACTT AATGGCCTGA 156060
TAAGAATGTC ACTGCAATGC TGAGTTTGA CCAACATTTG CCTGCTCCTG CCATTGAGCC 156120
CGGGCTCCCC TCCAGAGCTG AGCTGCTGCA AGGGATCTGA GTAAGTAGGG CTGTGTCAGA 156180
GTGGCGATGA CAGCCACCAC ATGCTAAGGA AGAGATCCCC AAGGACAAGG AGAATCCCAC 156240
GTGGAGCTAC TTGCTTCTTT GTCAGTCTTG TTTTCTTAT TTCACAACCT TCTAAAACAC 156300
AATCTCTCAA CCTCTATTGT TAGCTTGCA TTTTCAATCA TGAGCACAGC TTTACCTGGC 156360
TCCATGCTTT GATTGACTCT ACCTGCCAAC ACTGCAACAA CAGGGAAAGG GACACCGGCC 156420
TCATACCATT AGATGGTGTG TAGCCTGGGC ATGAGGATAA TTAATACTC CCAAGGGGAT 156480
TTTAACATGT AACACAGTTT GGAAACCATT GATGTAAGAT CTTCTTACTC AACATGTGCT 156540
CCAAGGAGCT GTTGATCAG CTTATCAGAA ATGTAGATCA GGCCGCACTT GGACCTGTAG 156600
AATCAGAATC TGCATTTTAT CAGATCCGA CATTATTTGT ATGAACATTA GCTTTTGAGA 156660
AGTGTGCTT TAAGAGACTA AGGGGGTCAA TCTACCTCAC TTTGCAGCTC TGTGTTCCCT 156720
AGTCATTGGC TAAAATATCA GCCCCCTGC AATGAGCCAT CCTCCCTTGT ATAGTCAGTG 156780
ATGGCCTGTG AACCTTTAGC CAACTGGAAG TGGGAGGGGA CACAGTCCAC AAAACACTAT 156840
CCTGACTTTT GACACCAACT ACAAGTCAAG GGGTCCCCA AACCACCCTG AGTTGTGATA 156900
ATTCGCTGGG AGATCTGACA GAACTCACTG AAGGTTGTTA TACTCATGGT TGTGATCTCT 156960
TATAGGGAGG GAATACAGAT TAAAATCAGC CAAAGGAAGA AGCACACAGC ACAGAGTCCA 157020
GGACAGTGCC TGACATGGAG CCCCTACGGT CCTCTCCCGT GGAGTCACGG ACAGCGCCAC 157080
TCTCCTGGCA TTGATGTGTG ACAACACAGA GGGAGTGTTT CCCACCAGGG AAGCCTTGGT 157140
GTCCAGGGTC TTTACTGTGG CTCTGTCACA TGAGCACAGC TGAAGGCCA TGCAGCCGAT 157200
CTGTTCCCAG ACTCTCCACC GCTACACATC ACTCACAGTC CCTGCTCTAA ATCACACACC 157260
ATGACCCAAT GTCCCCGGGC AAATGAAAAC ACCTCTAGCA GGCAGGACGT TCCAAAGCCT 157320
TAGAGATCAC CTCTCAGAAG CTGAGGGCAG AAGCCAGACC TCTTTTGGG CAGGGTTAAA 157380
TTCTTTATTA CTGTTTTTGA AAAAATCCC AAATTGAGTT TTTCTCTTC ACTTACAGCA 157440
GCATAACAAC AATCATCAAT GCAGAAGACT TCTGCGAGCA AAGGTGTGGG GGAAAACCCC 157500
AAGCAGTGGA CACTAGCTGG TGTCCTCCAA TTTGATTCTG ATGCTGTCTA CTGGGAGATA 157560
GTGTCAGATC CTCAAGCCTA AACCCTCCTT CTCCCAGTCA GAGGGCTGGC CTTTGGAAC 157620
TCTGACCAAT CCACTTCAAG TTGAGGTTCC AACCCTCCG CTCTTGGGT TTGGTTGATT 157680
TGCTAGAGTG GCTCACAGAA CTCAGGGAAA CACAGCTACC AGTTTATTGC GAAGGACATT 157740
TTAAAGGATA AAAGTAGGCA GATAAAGAGA TGCATAGGGC GAGGTGTGGA AAGGTCCCTA 157800
GTGCAGGAGC TTCTGTCCAT GTGGAGCGGG GGTGCACCAC CCTCTCAGTA CATGAATGAG 157860
TTCTCCTTCA CCTGCCTATC AGCCTCTACA TGTTCAAGTC CCAACCCAG TCCTCTTGGG 157920
TTTTTATGGA AGCTTCAAGA CACCCACATT CTTCCCCAG AGTATAGGGC AAGACCTTCT 157980
CTGGGGAGGG TTTTAAGACC CACAGTCAGA AAGGTGGGGT GGGGTCAAGA TTAGAGTCCT 158040
GCCTTGACGG GCAGGTGAAA GGGGTAGGGG GAGTAGGTGA GAAAAATTCT GTTTATTTT 158100
TCTTTTTTTT TTTGAGACGG AGTTTCACTC TTGTTGCCA GGGTGGAGTG CAATGGCACA 158160
ATCTCAGCTC ACTGCAACCT CCGCCTCCCA GGTTAAGCG ATTCTCCTGC CTCAGCCTCC 158220

FIG. 6.60

CGAGTAGCTG GGATTACAGG CGTGTGCCAC CATGCCTGGC TAATTTTGTA TTTTAAATAG 158280
AGACAGGGTT TCTCCATGTT GGTGAGGCTG GTCTCAAACCT CCTGACCTCA GGTGATCCAC 158340
TTGCCTCAGC CTCCCAAAGT GCTGGGATCA CAGGTGTGAG CCACTGCATC TGGCCAAAAG 158400
ATTCTGTTTT TGAGGCCTGC CTCTGAGGTC TAACACACTC AACATTATAA CAAGACTGTA 158460
GTAAGGGGCTA TGGGAGTTAT GAGCCAGGAA CTGTGGATGA AAACCTATCA CAGATATGCA 158520
TATATATATA TATATATATA TATGCATATC TATAATAACT CCACAACCTAC AACTGCCTT 158580
ATTGCTCAGT TCTTCTCTCC ATGTCTCTGA CCCACCCTTG CCCCCTTCCT CCATCCTTTT 158640
CTCCATTGCA TACCCATCCA CTGTGCCCTT TGGAAATGCTC ACACCATGAA CTGCAAACCTC 158700
TCGTGTGGCT TCAGCCTCTT CTCTGAAAGT TCCTCTCACC TATTACTTTC TCTGGAACCT 158760
GCCATCCCTG CCACCTTCTC AAAAAAGGCC TTTTATTCTC TTCATTCCAC AAAGCTCAGT 158820
GTCAAAACAT GGGGTTTACA CTGGAAGCTG AGGTACATC AGTAGCCGGG ATCAGGGTCG 158880
CCCTAGCTGC CCAATGCAGC TCCCAGGCCT CCTGTAAAC CTTGACCTTT GAGGTCATGA 158940
CAGCCCTCTC CTGCTATGCT CATAGCTGAC CACTGAACTC CTGGACACTC CCTCCCCAA 159000
GTTACAGAG AATGTGGCA CATGCCTTAC AGTCTTCCCT TGATCCAAAC TACTGCCTTC 159060
ATCTTGAGTG ACAGCAGCAT CTTTGGATG TCTTGGCCTG TCTAGCTTTA TTTTTTGTG 159120
TTCTGCCATC AAGTTGCTAC TTCTGTTGCC ATCGTGCTG TCAGCGCAGT GCAGGCTGTG 159180
GTGAAATCCC ACGAACTCAG GCATCACACT GACCGGGTCT GAGTCCTGTC TCAGTTGTCA 159240
GCTAGTTGTG CAATGAAGGG AAAGGGACCT ACACCTTCCA AGCCTCAATT CACTCATCTA 159300
TGGCATGGTG ACAATAATGG AGGTTGATTT AAAGTCCTTT GTAAGAATTA AGAGTTATAA 159360
TAGACATAAA GTGCTGTATC TGGTATACCT AGAAAACATT CCATAAAAGT TAGTAATTGT 159420
TGGTCATGTA ATGATGACTC TCTAGGCTAG GATTTCAGCT TCATTGCATG CACATGCTGC 159480
ACTCACAGGG CGTGACCTCT CTCTGTCTCA GTAACCTCAT CTGAGGACCG GGATAATCAT 159540
ACCGCTCAA AGGGATGTCA TAAAGATTAA ATAATATGTG TAAGGCTGCT TGCATTTAGC 159600
TGCATTCAAC AAATATTTCT GTATCTTTCT CCTCATTTCT CTTACTTTC TTGCTTATTA 159660
TCTGCTCTAG GTATAGATTT CAGAGAACTA AGCTTGTTAC AATCCTTCAT AAAATAACCA 159720
GGTTGGTTAG GGCATTTCOA AGAGTCAATA CTGTTTAGTG ACTATTCTCT GTTTAATCTA 159780
TTTTGATTGT CCAGGGTCAT CTTTGTCTAT GTCATAGGTT GTTGGCTTCT TCTAGAGAA 159840
TGAGACGATG GACAAGTTCC AAGTGAGTGA GGCGACTGGT CAGGATATTC CGCTGAAAAA 159900
CTCATGTCAG TTCTAATTCG TGATTGTAAT TCAATCACAG CCTGAGAACA GTAGGACTGT 159960
AGTTCAAATG CTCTGTTCCC TTTTTTTTTT CCCAGAGGAT AATTTTTTTT TTTCTTTGAG 160020
ATGGAGTCTT GCTCTGTAC TAGGCTGGAG TGCAGTGGCG TGATCTCGGC TCACTGCAAC 160080
CTCCGCCTCC TGGGTTCAAG CAATTCTCCT GCCTCAGCCT CCCAAGTAGC TGGGACTACA 160140
GGCACATGCC ACCACGCCCC GATAATTTTC GTATTTTATG TAGAGACGGG GTTTCCCCTT 160200
GTTGGCCAGG GTGGTCTTGA TCTCTTGACC TCATGATCCG CCCACCTCGG CCTCCCCAAG 160260
TGCTGGGATT ACAGGCGTGA GCCACCGCGC CCGGCCTCTA GAGGATAATT TTTAAATGTG 160320
CTTTTGCAAT TGGAAAATGT GATTGGCATT TTTTCTAAT TTTCTAATAT GATACGCTGT 160380
CGGATGCTAT GGATTACTTA AACCTCTGG CTACCTAGAA AGATCTTTAA GTGGTTCTCA 160440
ACAAGCTTCA TACGCAATGT AAATTGTATT ATCTCTCAGG ATGTGTGAGA ACATCTGTTT 160500
TTCTTCTAAT GCAGTAAACA TATAAGGGTC TCTTGGGATA TCTTTTAAAT AGACTTAATA 160560
CAACATTGAG GAATGATAAC AAAATATAAT CACAGTTGTA AGGGAATGTG AGCATTTCAT 160620
ATTAATAACA TTGGAACCTT ATGTTTAAATA CAGTGTTAAA AGTTGACAAA CATGTAGGAG 160680
TCAGAAAATT CAATTAATAA TATCACAGTA ATATGAATTT AGCCACATCC TGTGTTAGTT 160740
ATGAAATCCA TTTAACACCA CAAACAGTAA TATTTTATAGC CAGTTTATTC AAAAGGAAAA 160800
CAGGAACTAA ACCACTTTCA TGCAATATAT ACTCTGTAA TGTGGTCAGG CTAATTTTGC 160860

FIG. 6.61

TGGGGGAAGG AACTTAACCTT TTGAATATTT GAATGCCCAG TCATTTAATC TGAATATCCT 160920
ATTCCTTGCT ATGTTGCAAA ATTTTGTCA ATAAAAGGCA GAAAAAGAAA TCTCTTCTCC 160980
ATGCTCATCC CTAAGAGAAT GGGTTGTCTG TACCCTGAGA GCATTTTATG GAGGGGACAA 161040
CCACTTTTCT AATTTTCTTT CCCACTTCTC TGTGGGCACA AATGCTCTTT GGTGAAAGA 161100
GTTGTAATTC AGTCCCAAGA TGAGGTGTGG TTAAGTGCATC CCTAACCTAT ATCTGGGGAC 161160
CCCACAGCCA CACACATGGG GGAAATGGAG CTTGTCTATC AGTTCTCCAG CCATTGCACA 161220
GGGTTCTATG ACTCTTCGTT GATCCACCCC CAGCTTCTT CTCTCTGCTA GCCGAACACA 161280
CTTCTCTCTT CTTTATCAGG AGGCCATAGG AGAAGGGCAT TCATTTTAA TACACATACA 161340
TCTGCATCAA GTCTAATTTT GCCATGTCTC AATCCAACCTG TCAAATGGGT TGTTGGGGG 161400
CTATGGTGCT TATCAAACAT TTAAGTCAAGA ATAGCCAAAA TTAGCCAAGC AAGGAGAACT 161460
TCAGCAACGT TCCCAATGG CCCCAACCAA GTACTGTAAG ACTGAGGATA GCTAAAGGGT 161520
CTTGAGAGGG ACTTCTCAGG CAGTGGCCCC GACATTTATC TGTTTTTTA AGTGAGAAAT 161580
CTGAGTACCA TTCTTGACTC CTCTTCCTTA CCCCCAACCC CTCCTAAGC CTTGTGCTAC 161640
TATTTAGTAA ACAGACCTC AATGCACAAA CTTCTGTCTA AGGCCATGGC CACCACCCTA 161700
GTCTAATCCA CCATCTCTTC TCTGGAACAG ACCCCAGCTG CTCTCCCTGT CTCTGTGCTG 161760
GTCTCTCAAT CCATGCTCCA CACTGCAGCC AGAGTGCTCT ACAATGCAA TCCATTTGTG 161820
AGACTCCTCC TCTTAAATC CTCAAGTGGC TTCTCTTTCG CCCCAGGATC ATTTTGAAAC 161880
TCCTTAATGG AAGAGGCATG GCCCTTTGGG ATGTGGTTCC CCAACCCCTC CCACATCATC 161940
TTTTCAATCA GATTTCCAC TAAATGGAAA TTTTTCAGG TCCTCAACTT TATGGTGAAT 162000
TTCTCTTGCT CAGGATCTTT GAACATACTG TTTCTTCTT CTTTTGTAT TTGCCAAGAC 162060
AACACTTCCT CTGGTAAGAT TTTCTGACA TCCTCTATAA AAAAAGATTG AGATAGTTGA 162120
CTACCCAAAA TGTTCCCAT TCATTCCAAG CTCTATTCAA GGCAGTAAAG TGCCCGGCTG 162180
ACAGATTGCA TTCCTCATCT TTTCTGAAGC TAGCAATGGC CATGCAACAG CATTCTGGCC 162240
AATAAGATAG AAGTCGAAGT TGAAGGGTGG GATTTCGAAG AAAGCTCGTT GAAGACATAA 162300
TTCCTCATTT CACTTCTTAC TCTTCTCTT TCCTGCTTCC TAAATGCGG TGCAGATGGC 162360
AGACACTTCA AAGCTGTCTC AGGCAATCAG GTGATGTTAA GGCAGAAACC AGCTTTATGA 162420
TGGGTAGAAG AGGAAGAAAG AAGGCACCTA TGTTCTTGT CACCTTGAAC CACACCAGCA 162480
CTGCCTTGCC TACCCCTGGA ATTCCTTTAA TGAGAGGCAA ATGAGAGCTT ACGTGTTTAA 162540
GCCATTGCTA TTTTATTTT TTTTGTAT ATGCAAAAGA ACTTAATCCT AACTGATATT 162600
AACACTAAT GGGTCTATTG CTTGGTACCA AGCCAATGCA TGACACATGG TATATATGCT 162660
CAGTAAGTAT TTGTTGAATG AGTGAGGCAA TGAAAGAACA TAGAGGATAT ATATAACAGT 162720
CCTCCTGCCC AGATGTCATC TGATCCTCTT TAGGATCTGG GCCCATAAAA CTGTATCTGA 162780
TATAGTTTGA ATATTTGTTT CCTACAAATC TCATGTTGAC ATTTTATCCC TAATATTGGA 162840
GGCAGGGCCT AGTAGGAGGT GTTTTGGTCA TAGTGATAAA TGGCTTGGTG CCGTTCTCAC 162900
AGTAACGAGT GAGTTTTTAT TCTAGTGGT CCTGCAAGAA CTGATTGTTA AAAGAGCTTG 162960
GATCCTTCCA CCCCTCTCTC ACTCTTGCTT CCTCTCTCTC ACCTTGTAAT CTCTACAAGC 163020
TCTTCACCTC CCCTTCTCCT TTTGCCATAA GTGGAAGATT TCTGAGGCCT CACCAGAAGC 163080
AGATGTTGGT TCCATGCTTC TTGTACAGCC TGCAGAACCA TGAGCCAAAT CAACTTCTTT 163140
TCTTTATAAT TATCCAGTCT CAGGTATTCC TTTATAGCAA CACAAATGGA CTAAGACAGT 163200
TTCTAATGCT ATGGTTCCTT TAGTAGGTCA GTGTAAACC CTGGATCACT CCTGTAACAA 163260
ATTACTTGA ACTCTTCTCA CCATACATAT TAAAAATAG TTGCCATGTT GAAATCCTA 163320
TAAGATCATA TTTTATTTC AATCCAACAA CTCATTGCTA AGGAGATACA AGAAGCAGAA 163380
AATACAGAGA GACTAATGTG TTGATGATTT TTGTGAGGGA CATAAGGTCT GTGTCTAGAT 163440
TCATTTTTTT GCATGTGGAT GTCCAGTTGT TCCAGCACCA TTTGTTGAAA AGACTATCTT 163500

FIG. 6.62

TGCTCCACTG TATTGCTTTT TCTCCTTTGT CATAGATATC TGGTCACCTT ACCTTAGAGT 163560
CACAGATGAA TGGTCCTATT ACTTAACTAC TGAAAATACA GGCCAAAGCA AACAGAGGAA 163620
TAAGGGATAT ATAATAAAGT ATTTGTGTAC TTGACTTGGC TCTAAAGGAA GCATTGCGTG 163680
TCTGTGTAAA AAGAATGGGT GAGAGTTTTC CACCATTCAA TATTTCTAAT CTTTCTGAAA 163740
TACAAAGCCA GGACATCCTC TAATCCATAC ATTCCATAGT TTGGTTAATA TAAATTCCTT 163800
TATTAAATCC TTATTAAATA AAGTTATTTA TGTTTCTATG AAATCATT TAACCTCTAA 163860
GTGAAAAATA CTAAGTGGCT AACTAAACAT CAAACATTTT TAATTTTTTA AATTTTTTTA 163920
GAGACAGGGT CTTGCTATGT TGCCAGGCT GGCTTTGAAC TCCTGTGCTC AAGCGATCCT 163980
CCAACTCAG CCTCCCGAGT AGCTGGGACT ACAGGTGCAT GCCACTGTGC TCAGCTAAAC 164040
ATTTTTTTGA AATGCTCTT TAAATCAAT TTTATTGAAG TATAAGTTAC ATACCATAAA 164100
AGTACTCATT TTGAGTGTAC AGATTGACAA GTTCTGACAA ATGTGAACAA CCATGTAACC 164160
ATCACCAAAA ATAAAGATAT GAGACATTTT CATTACCCCA AAAAGTTCCC GTGTCCCTCT 164220
CCAGTCAATA TCCAGCCCTA GCCCCAGCTC CAGGCAACCA CCAATCTGCT TTCTGTTGCT 164280
ATAAATTGTA CTTATCTTTT CTAGTGTTC ATACAAATGG AATCATACAG CATTACTCT 164340
TTTGTGTCTG TCTTCTCTG CTCAGTGTA TGTCTTTGAG ATTCATCTAT GTTCTGTGCC 164400
TCAGTAGTTT GTTCTTTTTA TTAAGTGATA ATTCCATTAT AAGAATATAC CACAATTTGT 164460
TTATCCATTT ACTGCCTGAT GGGCATTGG TTGTTTCCAG CTTTGAAC TA TTTGAATCC 164520
TAAAAGACTG CCAGTTTGA ATGAGACCCC AGAACAATGA ATGTAGGCTC TGTATACAAG 164580
TTCAGGCTGC TGGGCAACTT AGGCCTTAAG ACACAACCTT GCCACTTAGG CCTTAAGACA 164640
CACTGACAT GATGGTGCTT AAAGTGGCTG TGATGGAAAA GGAGGCTGTT TGGAGCCTTT 164700
GGAGTGCCTT TATAGGTGAA CCCCAGCATA GCACCTAATG ATTTGGAGCA AAGCTGTGTC 164760
ATTCCCCAAA GATAACTATT CGCCTTTTGA GAAACATCTT CTAGCTACTA TCAATAATAA 164820
ACACAGAATG CATCACCATG GGCCACCGTG TTGTCTTTT ACCTGAGTTT CCATTGTGAA 164880
CAAGAGTCAT TTGATCCAAG GCAGAAAGT GGGTGCACAC AGCAGTGTTT CATCATCAAA 164940
TGGAATATGA GATTGGGCCC AAGTAGGTCC TGCAGACACA AATAAGTTGC AAGAGCAAGT 165000
AGTACAGGCG CTTGGCCTGG CCACTACTGT TGCCAAGTTG ACTGCTTCCC CTCAGTCTGC 165060
ATCTGTGGCT TCATGGGGAG TTTCTATGA CCACTTGATG GAGGAAAAA CAAATTGGAG 165120
CATAGTTTAT AGTGCTGGTA CTACCCAAAG TGGCTAGCTG AGGCACTACA TCTCCACTCT 165180
GGGGTGCCCC TGAAGGACAG TGCCAAAGGA AAACCCCTC AGTGAGCAGA ACTTGGAGCA 165240
ATACAAGTGG GTGTTCAATTT TACCTAGAAG AGAAGATGTC CGTGAGTTAC AGATCTACAC 165300
AAAATCACAG AGAGTGGTTA ATCGTTTGT CTGATGGTCA GGGACTTCCA AGAGACATGA 165360
TTAGAAAAT GGTGACAAGG AGTCCTGGGG AAGAGGCATA TGGATACCTC TGAACACACA 165420
CAAAACATGA GAATATGTAT CCCATATGAA TGTTAACCA AGAGCAGCCA CAACAGAAGA 165480
GGATTTTAAA ATCAGCTGAA TAAGATGATT CATTCTGACA GCATCAGCTA GTCTCTTTCC 165540
CCAGCCACTG TTGCCAGTG GGCTTACATA TATCATGGCC ATGGGGGCAG GGCTATGTAT 165600
GGACACAGCA ACATGAATTT CCACTCATCA AGGCCAATTT GGCTCCAGCC ATTGCTGAGT 165660
GCTCAGCCTG CCAAGATAGA AATCTACGCC AATATGGCAC CATTCCCTGG GCTAGAAAAC 165720
CACTGGTGG AAGGTTGATT ACATTGGACC ATTTCCATCA TGAAGGGGC AGTGCTTTGT 165780
CTTCCCTGGA ATAGACATTT ACTCTGGATA TGGATGTGCC TTCCCTGACT ACTACAATGC 165840
TCTGCCAAAC CTACCATCCA TGGGCTTAAT TTTATTTGTT ATAAAATTTT AACCACCATT 165900
GCTTCTGACC AAGGAAGTAA TCTTACAGCA AAGGAAGTAC AGATATGAGC TTCTGATCAT 165960
GGGCTTCACT GGCCTCACAG TGAAGCAGGT GGCCAGATTA GAACAGTGGG ATGGATTTTA 166020
AAGGCTCAGT TACAGCACCA GCTGGGTAGC AACACCCTGC TGGCCTGGGG TTATGTCCTG 166080
CAGGATGCTT TAAGTCAGTG ACCAATATAT GATGCTATTT CTCCATTGT CAGGATTCAT 166140

FIG. 6.63

GGGTCCAAGA ATCATGGGGT CAAAATGGGA GTGGCTTTTC TCACTATCAC CCTGGTGTTC 166200
GGGTAGTAAT TTTTCCTTCC CATTCTGTGA ACTTTGGGCT CTGCTATTGC AGAAATCTTA 166260
GCTCCTGTGG GGGGAATGCT TCCATCAGGG AATACAATGG TGGTCCACT AAAGTACAG 166320
CTGAGTTTGC CATCTCCTCG TGCCAGTGAA TACACAAGCA AGGAAGGGGG TTCCTTTCTC 166380
ACCTAGGGTG ACTGATCCTA ATTACCAAGG AGAAATTGGA CTGCCACTTC ACAATGAGGG 166440
TGAGGAGTAT GTACTCTATG TGTCTGTGAT TAATGTCAAT AGAAAGTGAC ACCAACCTAG 166500
TACACAGAGG ACTGATCATG GTCCAGGCCC TTCAGGAATG AAGATTTGAG TCACCAGGCA 166560
AGGAACTTGG ACTCACTGAG GAGGGCATAT TCCAAGGAGA ATATTTTATC TATGTCCATC 166620
TATGTCCATC TATATCCAT CTGTGTTCCC CTGGAATTC CTATTCATGA ACATGGGGAA 166680
TTCCAAGGGG AATATAGAAT GAGTAGTGGA AGGTAGTTAT AAATGTAAGT CAAAAACCAC 166740
ACAACCAATT TGAGAAATGA GGAAGGTAAT AGTGTTGAAT ATGTCTTCTT TATCTTGATA 166800
TAAATGTATT TGTGCATATA TTAACAGTT TATTTATTTA TTATTATTTT TTGAGATGAG 166860
CTCTCGCCAT GTTGCCCAGG CTGGTCTTGA ACTCCTGGGC TCAACTGATT CTACCATTTA 166920
GTCTCCGAG TAGCTGGGAC TACAGGCATG CACCACCATA CCCAGCTGAC CAGTTTTTTC 166980
CTATTCCTCT ACTTAATTTC TCTACTATAC AACATAATAT GTGTTAATGG TAGTTAACTT 167040
TATATCTCAG TATTAAGTCA CAAGATATCA AAAAGGGAAT GCGACTTAGT TACAAGCAGA 167100
ATGAATATCA CTCAAAGATG AATAAAGAGA AGAGGGTTAG TGCATTTTCT GTTGGATGAG 167160
AGAAAGTTTC ATTGTTAGGC AGAAGCATGA TTTTGCCTTT TTTTTTTTTT TCCAAGGTCT 167220
CACTCTGTGG CCCAGGCTGC AGTGCACTGG TGCGATCTTG GCTCACTACA ACCTCTGCCT 167280
CCCGGGTTCA AGTGATTCTC CAGCCTCAGC CTCCAGAGTA GCTGGGATTA TAGGTGCGCC 167340
AGGTTAATTT TTGTATTTT AGTAGAGAAG GTGTTTCTCC ATGTTGGCCA GGCTGGTCTT 167400
GAACTCCTGG CCTCAAGTGA CCCACCTGCT TTGACCTCCC AAAGTGCTAG GATTACAGGT 167460
GTGAGCCACT GTGCACAGTC ACCACGGTCT TTTTGGGAGG CAACTTTAGC ATGGTTAAGA 167520
GGTGCGAATG GATGTTAAGC TAACACCAGG TAAGCCCTGG TAGATGTGTA TTGTGTCACT 167580
GGGCCTACGC TGGAGCCATG TTTCCCCAAA TTCACTTTTC CTATGTACCT CTGGATTAGT 167640
GTGGGCCACT GGAGACATTT CACATGAGAT GAGGAAGGTG GGAGTGAAGG AGCAGCATCT 167700
TTTACACTA AGCAGGTCGG GGAGGGCATG TGGCTCTGTC TCACATTGTT GGAATCTGT 167760
CCATCATCTG GTTGGCTTAG GTCAGTGGGT GAGTTCACAG CTGTTCCAGC TTCTGCTGGA 167820
AACTCCTTCG GTTCTCTGA CTGCTCCGTG ATGAGGGCAT CAGATTCTCC TGCAGAAAGC 167880
CCCAGTGTG AAGTTGGGGC TTCATGTTGG TGAGTGATAG TTACGGGTTT TAGCCCAACC 167940
TGTGGTTTCT TGCAAAATTC AGTGTCACT CAGTCTGCG GGTTTTGGGT TGTCTTGCT 168000
TCCCACACTT CATGCCTTTC TTTCCCTCCT GACAGTCTGC CCTTTAGATT TTAGGATTCA 168060
GCACCAGCCA CAGAAACAGC AACCTCACTG TTAAGGGTTG AATTGTATCT CCCCCAAAGG 168120
TAGGTTGAGG CCCTACCTGC CAGGACTTCA GAATGTAACC TCATCTGGGA ATAGCATCAT 168180
TGCAAAATA ATTAATTAAG ATGAGGGCAT ACTGGCTCAG GATGGGCTCC TAATTCAATA 168240
CAACTAATGT CCTTCTATGA CAGCCACAGG AAGACAGAAA CGCCAAGGGA GAACACCATA 168300
TGCTGATGGA GGCAGTGGCA GCTGCCAGCC AAGGATTATA ACCAGAAGTC AGGAAAAAGC 168360
AAGAAGGAAT CCTCCCTTAG TGATTTTACA GGGAGCATAG CCCTGCTGAC ACCTTGATTT 168420
TGGACTTTTA TTCCCCAAA CTGTAAAACA ATACACTTCT GTTGTTTTAA GCCACTCAGT 168480
TTGTGCTACT TTGTTATGGC AACTCCAGAA AACAAAAATA CACTCAGACT GTTTAATCAA 168540
CCTCCATAAT TGCATAAGGT CTAATCCCTA TAATAAATCC CTAAAAATG TCTGTGTATA 168600
TATATTTAAA AATATAAAAT ATCTTCTAGT GGTTCTGCAT CTCTGGTCAA TCCCTGACTG 168660
ATACAGAATA TGTATTTTCA TTTCTAATGA TGAATACCT GAATGAAATT TCTAGGACAT 168720
ATGGTAAGTG TATGTTTAGC TTTTAAGAAA CTGCCAATT GGGGGAATTG CTTGAGGCCA 168780

FIG. 6.64

GGAGTTCAAA CAGCCTGGGT AACAGTGATA CCCTGTCTGT AAAAAATAAA AAATATTAGC 168840
AGCGTGTGGT GGTGTGTGTC TGTAGTCCCA GCTACTCAGG AGGCTGAGGT GGGAGATTCA 168900
CCTGAGCCCA GATCTTTGAA GTTATAGTGA GCTATGATCA CGCCACTGCA CTCTAGCCTG 168960
GGTGACAGAG TGAGAAAGCT GGTCTCTAAA AAACAAACAA AAAAAAAGA AACTGTCAAA 169020
CTCTTCCCAA CATGTTGCCA TTTTACATT TACCATTTTA CATTCTTACC AGCAATGATT 169080
GATAGTTCCA GTTGCTCCAT ACCCTTGCTG ACCATTCCAA TAGATGTATT GTGTTATCTC 169140
ATTGTAGTTC TAATTTGTAT TTCCCTAGTG ATTAATGATG TTTAACATCT TTTTCATGCAC 169200
CTATTGGCTA TATGTATATC TTCTTTAGCA AAATATATGT TGTATTGGA AGAGCGGAAG 169260
TTTTACATTT TGATGAAGTC TAATTTATTG ATTTTTTTTT TCTTAGATGG CTCATGCTTT 169320
TTGTGTTATC TAAAAAAAT TTGCCTTCTT CATGGTCACA AAGACTTTCT CCTATGTTTT 169380
CTTTTGAAG CTTTATATTT TTAGTTTTTA TGTTTATGTT TAAGACCCAT TTCTAGTTAC 169440
AATTGTGTG ATTTTTTGA AGGGTCAAGG TTCATTTTCT TTTCCATAAG AATGTACAGT 169500
TGTCTAGCA CCCTGTAA AAAGACTTTC CTTTCCCAT TGAAGTACTT TGCAAAAAAT 169560
CAACTGAGCA TATATGGGCA TCATGAATTT TAATCCTGTT AGAACTGAAT GTTCCCAAGG 169620
CAGGCCATGC CCATGACTGA CCTCCTTTCC TTGGATTGCC TACAAAACAG ATAAAGCTAA 169680
GTCTGGAGCA AAGAAATCCA TGTCTAACCT GTATTTTTTT TTTTTTTTTT TTAGATGGGG 169740
TCTCGTCTG TCACCCAGGC TGGAGTGCA TGGCGTGATC CCAGCTCACT GCAATCTCTG 169800
CCTCCTGGGT TCAAGTGATT CTCCTGCCTC AGCCTCCCGA GGGGCTGGGA TTGTAGGCGT 169860
GCACCACTAT GCCCATCTAA TTTTGTATT TTTAGTAGAG ATAGGGTTTT GCCATTTTGG 169920
CCAGACTGTC TTGAACTCCT GACCTCAGGT GATCTGCCTG CCTCGGCCTC CCACAGTTTT 169980
GTGATTATAG GCATGAGCCA CCGTGCCCGG CCTTAACCTT TGTTTCTTA CACAACACAC 170040
TACGTGATGT TTTCCACATG CATGGGTCAT TTGCTTCATT TACGTACAAA TGCATAAGCA 170100
ATATACTGTG TGGTGTGAGT TTGTGATGGG AAAAGGAAGA AGTTTTGCGG ATACTACACT 170160
GGCTCCTGC TATCTGTCTG TGTGAATGGC TATGGACTTT GTCTTCTATT TGTTGCTTA 170220
GCGCAGATAT GATCAGCTTA CAACTTAAGA TTCTAGAGAA AGAGGGTCAT ATCTGTAAAG 170280
CACTCTGAGC ATGTGTGAAG TTTAATCAAT AGCATATGAG GTTACAGCAA ATTCACTATC 170340
TTTGTTCCTT CAGCTATAGA ATGGCATGAG GATTCATCTC AATTTAGTTC AATTCTGTTC 170400
AGAACCATGA GCTAGCTGTT CATGGAAGGA AAGCCACCT GATTGTGGCC AGGGAAGGAG 170460
AAACAACACT TTAACCAGGT TGATTGGTT CTCACAGACA CCATTGGCAT GTGACATCTG 170520
GAACAGACCA TGCCTGGTCT CTGTTCTGAT CACTTACTAT TCAGCTCAAT ATTGGTCTGA 170580
ATATTCTTTA GACTGACTGA AATGAAAAGG AACTGTTGTG TAACCATCCA TAATTCCAGC 170640
CTGTAGACCT GGGCTGTATC TCTATGCCCT GCCTGGCACA GACCCACCT CCTGCTCCTT 170700
CTCCCTCACC ACCAGTCAAT CCTTGTCTA ATGAACAGGG AGGGCAACCC TGAATGGGA 170760
GTGGAGGGAA GAGATGTCAT GAGATGGCAA CGTGCACCCT GAAGTGAGGA TGAAGGCTAT 170820
GTGAATGTTG TAGGCTGACA GCCGGGCATA GTGGCCCCGT TGCCATGGCG ATGGAGGCAT 170880
GTTGATGCGA AGTGTCTGCA CAGCTCCTAG GATTTTAAAC AGCAGCTGGG CAGAGCCTCG 170940
GCGTCCCTGA ATTGTTGCCC CCCTGAGTCA CTGCTTGGCC CCAGCTGTCC TGATCTCTGT 171000
TGACAAATGG TTGTCCTTCA CAGTCAAAC ACTAACAGTA CTCTAATTAA TGAATGTGCT 171060
AATTATTCTT GCCTACTCCC AGCATATTTG TCTAACTAAC CTGTCACACA CAGATCAGTG 171120
CAGCATATGC ATAATTACGG AGAGCGCTGG GAGCAGGGGA TGGGTGGGAG AGGGGTGGGC 171180
TCGACGCCCT GTCGCTGTGG GATATTTCTT GTAAAGTTAC CTTTGCTAAC GGTCAGATGT 171240
CGTGGGGATA TGTTATTTCC CGTGAAGTGT ATATGTCTTC CTTTCTTTCC TTTCTAAGAA 171300
TCTCTTTCA GGGCTGAGGG GCCATTGCTC AGTGCTTTAG CCTGTGAGGG GATTGCCAGG 171360
TACAAATGCA GAAGGACCAG GGAGCCCAGG TTCTGAAGAC GATTCCGGTA GCAGCACGTA 171420

FIG. 6.65

GGGTGATTAA AACTCCAGAC TTAAAGCCA GACCGGCTG GGCTTGAACC CTTGTTCTGC 171480
TCCTTGCTAT GTGGGTCTTT GCCTTGACCA CATTTTTTTT TTTTTTTTAA GACAGGATCT 171540
CCCTCTCTTG CCCAGGCTGT AATGCAGTGT TGCGATCACA GCTCACTGAA GCCTCCATCT 171600
CTACAGCCTC AAGCGATCCT CTGCCTCAG CCCCAGTAG CTGGGACTAC AGGTCTGTGC 171660
CACCACGTCC AGCTAATTTA CTTTTGTAGA GTTGGGGGTC TTGCTATGTT GCCCAGGCTG 171720
TTCTCCAACT CCTGGACTCA AGCCATCCTC TAGCCTCGGC CTTCCAAAGT GCTGGGACTA 171780
TAGGCGTGAG CCACGGTGCC AGGCCCTTGA CCACATTTTT AACCCCTCTG AACCTCAGTT 171840
TCACTTTCTG GGCAATGGGA GGGGGGTAAT TTGTCCCTCA GAGGGTTGCA CTGAGGGGCA 171900
AATGTGAGGC TCTGGGTACA ATGCCAGTA CAGACTAGGT CCCCACGACA CAGCCGCTCA 171960
GCGGCTCCGG ATTCTGGGCT GCTCTGGAAT GCGGCCAGGC GGTCTTCTGC GGGAATCCGG 172020
GCAGGCAGGG CGGGCTGCGC TCCCCTCCCC GGCTCTCCCG GTGCCCCTTG TCTTTTTGTT 172080
CTGTCTCAGC AGCTCTCTAT TAAGATGAAT GGCATTTCCA AAGGCTTCAC CTCTGATAAG 172140
TGTTCTCTG CAGCTGCAGC CAGAATCTTA ATGTGCGCGC TGTAATTTAA TGGCCGTCTC 172200
GGCTATTAAC ACGCTCTTCT CGGGTGAAGT GGACTCCCTC CATCCCCGGG CCTCTGCACG 172260
TGCTCTGCGC GCTGGCTGGG GGTGACTCCA AGGAGCTCAG AGCGGGGTGC CCGGCACCTC 172320
TCGCCAGGCG CCTTTCGACC TTCTAAAGCG CGAATGGCTG GACTTTTCTC CCATGTGTGG 172380
GGCCCCAGAA GGTGTGGGGC CCCAGAAGGT GTGGGGTCCC TCGTTCCAC GGAGCCCGGA 172440
AGGTTTCCAG TGATGGTGGG GGCTGACCAC GTTGGTCCCC GTGGGTGCTG TTTTCATGTG 172500
CCGGCAGATT GGGATGAGTT TAAAGACAG AAGCGTGTAG GATAGAGAAA CTTCTTTAAA 172560
AACTGGAAAT TTTAATCTGG GGATTATAAC TATTGGACAG TCAAGTGCAA GAGTGAATAC 172620
ACTTCTCACT CCCTCCTCCC AATTTTTATT TGCGGGATTA GTCAGTCCCC CTCTGCCACA 172680
TGATAATTGT GAGAACTACC AGGGTCTTCA TTCTCCTGCC ATCTGGTTGA CCTCTCCAAG 172740
AATGGACACC CGGGCAGCCT GGGCCAATGA GGCTGTCTTA AGAGTTTGA TGAGAGAAGT 172800
CAGTCTTTGA CAGGTGATGG AAGCTGTAAA ATGTAAACT CCACAGTTGG TGAAGATGTC 172860
TCCAGGAAAC AGGTCTGCAG AGAGAATACG TTTGACATGC TAAGAGAAGC TGAGAGAGAG 172920
CGAGAGGAGA GATTGGAAGA AAGACAGAGA CAGAGGTAGA GAGAAGGGAA AGAGAGAGAG 172980
AAAGGGACAG AAGAGAGAGA AAAAAGAGGG GCGCGGGCGC GGTGGCTCAC GCCTGTAATC 173040
TCAGCACTTT GGGAGGCCGA GGCGGGCAGA TCACGAGGTC AGGAGATCGA GACCATCCCG 173100
GCTAACACGG TGAAACCCCC GTCTCTACTA AAAAATATAA AAAAATTAG CCAGGCGTGG 173160
TGGTGGGTGC CTGTAGTCCC AGCTACTGAG GAGGCTGAGA CAGGAGAATG GCGTGAACCC 173220
GGGAGGCAGA GCTTGCAGTG AGCTGAGATC GCGCCTGCTC ACTCCAGCCT GGGCAACAGA 173280
GCAAGACTCC GTCTCAAAAA AAAAAAAAAA AAAGAGAGGA AGGGCGGGAG AGAGAGAGAG 173340
AGAAAGCTCT CTAGCTCCAA GGCCTAACCA CATCTCTGTT CTTTCAACT TCAGCTGTCA 173400
GATTTTGA GAATCTTGT GAATAAATC TCCTTTTGC TTAACTAGT TTGAGCTAAG 173460
TTTCTATTGC TTGCAACTGG AATACTTGT AAGAGGACTG GCCTTCATT CTGATGCATT 173520
GTCATAAGA TGTAAGTGT AGAAGAGCTA ACGCTTTATG GGGTTCAAAC TCCTTGCTA 173580
CCAAAACCTA AACATCCCCT GAAACTTACC AAAGTGCAGG TATGAATTGG ATCTCACTAA 173640
GGTGAATATA CAAATCTTGC AAGTGCTGAG CCCTAACCAA TCTTGAATA ACTCTGTGGT 173700
AGTTAATTTT ATGTCAAATT GATTGAGCTA AAAAATGCC AGGTAGCTGG TAAATGTTT 173760
TTTTCTGGGT GTGTTAGGGA GGGTGTTCT GAAAGAGATC AGCACTGGAA TCAGCGGACT 173820
AAGTAAAGAA TTCCACCCCT CACCAATATG GTGGGTGTCA TCAATCCACT GAGGGCCTGA 173880
ATAGAACAAA AAGCGGGCAG AAGGGCAAAT TCCCTCTTCT TCTTGAGCTG GGCCATCCAT 173940
CTTCTCCTGC CTTTGACAC TGGAGCCCCT GTTCTCCAG CTTTGGATT CAGACTGGGT 174000
CTTGACCAT TGCCCTCCAT CTTCTCCTGC CTTTGACAC TGGAGCCCCT GTTCTCCAG 174060

FIG. 6.66

CTTTTGGATT CAGACTGGGT CTTGCACCAT TGCCCTCCTT GATGCTCAGG CCTTTGAATG 174120
CAGACTGGTC TCCACCAGCA GCTTTTCTGA GTCTCCAGCT TGCAGATGGC AAACCATGAA 174180
ACTTCATGGT GTCCATGAGC ATGTGAACCA ATTTCTATTA TAAATCTGCA ATATATATAT 174240
ATGAGGAGAC TTATTTATAT ATTGGTTCAG TTTCTCTGGA GAGCCTTGGC TAATATAAAG 174300
TCTATACTCT ACAAAGTGCC CTAGGTACTC AGGGAGTACC CAAGTGTGTC ATGACCAGCC 174360
CGACAGCCCT GGCTGCTGGC TTCCCCGCAC ACAACTCTGC ACGCTGCCTT CATCAGCCTT 174420
TCTCTCTCAG CTGAACCGAG GGCATTGAAG CGGGCCTCTG GCACTGTACC TATGAGGGAG 174480
CAATATCTTC CCCTACACTG ACCTCTTCCG TGCCGAGATG CAGCCCTCCC TGCTGCCACT 174540
AGTTACAGTG GTCCATGTTT CCTTTCAAAG TGAAGTTTGG ATAAAAGCAC CTCTTAACCA 174600
ATGCCAAATA GCTAAGTCTG GGACAAAGAT TGCAGGTATT TTGCATTTTC CATGTAACCT 174660
CAGAGGGGATT GCCATTACCA CTGATCTGAG CTGCAGAATA CCAGGCAGCC ACCTCACCCA 174720
CCCAGCAGGT CCACTCTTAT ACTTTCTCAG AAAGCACAGC CACTCTACTC TTATTCAGTT 174780
GAAAAGAATT TCCAGGAAGG TGTTTCTGCG ATTGCCTCAG AAAAGTCAGT TCCCTTTGGG 174840
AATTTCCCTT AGGGATCATC TGTAAGTCCA TTTCTGCCTT TTACCTGAAT TCTTTGGTTT 174900
GGTTTGAATT CTTTGGTTTA ATTTATGAAT TCCCTTTATT ACTTTTCTCT GAAGAAATGG 174960
AGATATCAGC TGTCCTCCC CACTGCCATT TATTCCTTCC TTCATTCAAA CCTTATGTGG 175020
CTGCTACTTA CCGTGTGTTA AGTGTTCACT TTTTCTTG GAATTCAAAA AAAGAAGGAC 175080
AGTATTTGGG GCACAGATCT TTTGGTGTTC TATACATTTT TTTAAAGTTT CATTTTACAT 175140
TTGTGTGTGC GTGTGTGTGT GTGTGTGAGA CAGTCTTGCT CTGTTGCCCA GGCTGGAGTG 175200
CAGTGGCATA ATCATTGGCT CACTGTAGCC TCAAAGTCCT GGGCCCAAGC AATCTTCCCA 175260
CCTCAGCCAC CAAAATGCT GGGGTTACAG GTTTATGCCA CTCTGTCTGA CCTGAAAGTT 175320
TTGGGTTTAC TTTCCCTTCT TTCTCTTTCG TGAAGTCAGA GATGATGGCA GCTTCCAGAT 175380
TCTCTGGTGC CTGTGCTGGG CTCGTGCTGG TCATGGTCTT GGGTCCAGGA TTCATTCTGG 175440
AGACTCTCAG GGAAGTTTCC CATGACAAGG AAATGTAGGA GAGTGTGCTG GCTTTGCGTG 175500
CTCCTCTGCC AAGCCCTGCT TCTCCTGGTG GGACACACTG AACCACAGCC AGGGCATTTT 175560
GGTGGTTAGT TAAAAAAAAA AAAAAAAAAA AAAAAAGGAA GAAGAAGGCA CTGTGTAATT 175620
GTGCCGGGGA TCTTCAGAAA TTGTAAATGAT GAAAGAGTGC AAGCTCTCAC TTCCCCTTCC 175680
TGACAGGGC AGGTTGTGCA GCTGGAGGCA GAGCAGTCCT CTCTGGGGAG CCTGAAGCAA 175740
ACATGGATCA AGAACTGTA GGCAATGTTG TCCTGTTGGC CATCGTCACC CTCATCAGCG 175800
TGGTCCAGAA TGGTAAGGAA AGCCCTTCAC TCAGGGAAGA ACAGAAGGGG AGATTTTCTT 175860
TGATGGTTGT TTGGAAGTCA GGCTTAAACA ATTGTGTCTG TGTGTGCGCA TGCACAAACA 175920
CTTTTACCTT ATCTTTATTT TCTTCTTTT ATTTGAATGT ATAGGGTTGT GTGTATTTCT 175980
GTGTAAATTT GGGGTTTTCC TCCTCTTAGT CTTTCACTTT TGTGGTGATT ACCAGTCCCA 176040
TTTTTAGAGC CAGGGCTGCA ACTTGAAGGT TTTGCTAAAA CCCTCACCGA AGTGTCTATG 176100
ATCAGCATTT TAACTATTAA TTAATGTGGC CAGGCAAGGG GTGGAAGGTG AGAAGACTAG 176160
AAAGGGAACA TGATATACAC ATTTACTCAG ATACTGGGCT TTTCTAACAT CTGCAGTGCA 176220
ATTGAAGTTA CCAGTCATCT GCAGTCTAAA AAGAAAGTGA TTTTGGGAGG TCGTAGAAAA 176280
AAATCATCTT ATTATTTTTC CTCTATATTA CTTTTTCTT TTTTCTCCT GAAGAACTT 176340
TTTTTTTGG TGATACCTTC TTTTCTCTA GCACGTATAA TTTTGAAGC ATTTTTCATA 176400
TGCAGTGTAT ACTTCAGAAA GAGAGAGAGA GAGAGGAAAA TTGTCCTGTT CAGCGTTTGC 176460
ATTTCCATTA TTCCTGCTAT TAGTTAAAAA CAACAACAAC AACAAAAAAC AAGCAGGATA 176520
CCTAGATCTG GAAAAGGGAG AATTGTGTAG AGCTGTCTTC CTAAAGTTCT GAGTTAGGGC 176580
TGCCCTCAGAC CACTTTCATA ACTATCTCCA GTGGCTTTGT GTTTTATATT TATTAAGATA 176640
GAGAAAAAAA GAGTAATTAC TAAGGGCAGC TGCTGTAGCT TTATGGTGAT TACTGAACAT 176700

FIG. 6.67

TGACATGCTG TCACGTTTTT GGAACCTTTGA GTATTTAATC ACTTTGGGAT ATTCTATTTT 176760
CCCCCATCTT GAGTGTGGAC AGATGCTGGT GATGTAGCCT TCTGGGCACA GAGCAAGCCT 176820
CCCCCTCAGC CTCTGCACCA GAAAGGCTCA GCTTCACACA CTCCAAGTAT GTTTTCTACA 176880
AGAACTACAC TTTGTGGCTT TCTGACCCAA ACATTTTTAT ACTAAATTAC ACACAACAAA 176940
GTTGTAGCTC AGAGAGGGAA CAAATGGCTT ATTTAGGCCA CCATTTTCTT GAGCCATTAT 177000
GATTTACAC AGGGCTCCCT TGGCCCTGTA AATTGGCAAG GATTCCATTA TTCAACCCGC 177060
ATACATGTAC AGAGACCTCG CTCTGGCCCA GATAGTATTC TGGGTACAGG CGGATAGAGC 177120
AGGAAACAAA ACAGCTACAG TGATGGACAG GTCAGCCTGC AGCAATGCCT GCAGTCTCTG 177180
CAAAGGTAGC TGTATGGGTG GGCAGGTGGC TAGCACTTAT TCAGCTCTGG AAGGATCTCC 177240
CCTCTGGCCT CTCCCCTGAC ACCCATCAAT AAAACTGAGG AGCATCGGTG GACAGGGGAC 177300
CTTGCGCCCC CTCCCCTGCCT GTGCAGTTGG GGCTGAACCC AGCTACGAAG TTTGAGCTCA 177360
CTCTCTCCAG CTCCCTCTCA ATTCAGAGCT GAACTGTGGG AAGCTTCAGA GCTCTCTGTT 177420
TCAAGGACAG GTTCTCCTCA CCTCTCCTAA TGGAGGTGCA CCAGGGAACCT GGCCCTGCTC 177480
TGCCAGGGC TTTCTCCTGG ACTTTGCCAT CATGGTCTAG CAAACCCTGT TCAGATTGAG 177540
GTGAGTGGTG AGATTTGAA TTCTTTTGA CAGATAGGAT TAAGTCTTCT TCTGTGGGAC 177600
AAGTGGGAGG TAGAGGTAAG ATTAAAGATG GCCAAATGTC TGAGTCCTGA CAGCCACAAT 177660
ATGGAGATCT AGACTTTTTA CAGACCACAG GGCACAGGGG CCTCACTAAC AGAGTTCCCG 177720
GAAGTGATGA GTGTGCTGGG GGCTTCCTGG TTGAAGAGAC ACTAGAATGG ACCAGCTGGG 177780
AGCTAATTTT TTGGGCTGGA GTGTGATGGC CTGCACATCA CTGCCTCTGT CCCTCCATTG 177840
TCACAGCTGC CCCTTAGGAG CCAGCTGAGG CAATTTGTGG TCAGAGTGAC TTTGCACAGT 177900
TGTCTGCCT GTGTTAGGA AGGGAGTTTC TGTGGTCCCT TTGAAACCAC AGAAGAGCCC 177960
CTCGTATAGC TCTCAATGGA GGGGGCAAAA CATTCAAATA ACTCAGGAGA TAACACAACCT 178020
ATTTGTTTTT AACTGTGAGT TTTTAGGCAA TCACAAAGAT CCAGATGTAT GTCCAAGCCT 178080
CTCTTTGCAA TTCTAATTAA CCTCAATGTT GCAACCATAG ACCTACCTTA CAGAGTTCAA 178140
AAAAATATGC AAAAACCCTG CCTTTCTTCT TCCTCATACC CCAAATGCC ATTCTGAACA 178200
TTTCTGTTA GTTAAAAAA GATTTCCATG GTGTTACCAG GCACTGTACA CAGTCTGTGT 178260
CCCAAGACAA GGAGGTACAG TTCCACATGC GCCCATGACT GGGTTGGGCT CTGCACTCTC 178320
TCTATACTT GAGAGCCTGA TTTTCTGTGA TTGGGCAGAG CTGGCCACC TGGTGCAATG 178380
TCCTCCTCTG CCTTTCAAAC ATGTTTTAGT CATCAAGATC TTCAAATTTG TAACCCTTTC 178440
CAGCTTGATC CAGCAGAATG CAGATTTGGA AAAACAGAAC GAGTTTAAAA TACATGATTC 178500
TAAGAAACCT GGACCAGAAC TATCAAACT TGGTTTCCCA GAGAATATAG CAAATGGGCT 178560
CATTGGCCAA TACTATGACA TTGGCTTTTG AGAAAAGAAA GGCTTTATTG CAAGGCTGGC 178620
CAGCAAGGAG ACAGGAGTTG GGCTCAAATC TGTCTCCCCA GTTTGGGGCT TAGGGCAAGT 178680
TTTAATTACA CAGACGCATT TCTTATGAGT AGCAGGCAGA GAGCCTCAA CTTCTTCTGC 178740
CTAGGTACCA GCAGCTTAGA CATGATGCAA ACCTGGGAAG CACATACTGT ATTTGGAGAA 178800
AGTGATTGGG AAGAAATGTG AGCTGAGGGG AGGGGCTCAG TGCCCCTGAG CTACACTTAG 178860
TGATGGCAGA GGAAGGATGT CCTCCCGCAG GAGGCTGTTT CACATCTGCT CTGGTTGTAG 178920
GGGGAGCTGG CAGGCATTAG CAGCGCCTC TTTCCCCCAA GAGAGGCAGC CTCCTCCAAG 178980
TTTTGGCGAC ATTATGGCCC TGCAATCATA AGGGTTTGTG AGCATAGTGC TAAGGAGGGA 179040
AATGGAGCTG CTGTTACTAG TTCCACCCCA ACACACACAC ACACACTCAC AAGAAACCTC 179100
ACAAGCACCG TATTGGAAGA CTTTGCCATC CAACCTGGGA TTTGACAGGC TCTAGAAGCA 179160
GAATCATAGA CTCATGAAGT TCCCCCAAAG CAGGAATCTT CCTTACAGTA ACCCCCAACC 179220
ACCCCCCTOC ACCGCCTCCA CCGGCTGCTT CTTCTGAAC ACTGCAGTGT TTGGAAAACCT 179280
CACAACTTC CAAGCTTGCC TTTCTATTG TTGCATGGAT TGAAAGCTTG CGTTGTGTGA 179340

FIG. 6.68

AGAATGGCGC TTCCTGCTGT GCTTAGTTTT ATCTCATATA ATCTTTGCAC CATTTAATCC 179400
TTGCACTCAC CCACTCATGC AACTGCCTTT GCAGAGACTG GAGGGGCCGC TGTAGGCTGA 179460
CCTTTCCTTC ACTGTACCTA TTTTGTTCCC TGCTTTATTC CCCTGCACCC AGGACACTGC 179520
CTGGCACAAA GACAGGTCTT TATAAGTGTA TGCAAGTGAA TAAAGATATA TATATTATTA 179580
TTGTTATTTT TGAGACAGTT TCACTCTGTC ACCCAGGCTG GAGTGCAGTA GCGCAATCTC 179640
AGCTGACTGC AACCTCTGCC TCCCAGGCTC AAGTGATTCT CATGTCTCAG CCTCCTGAGT 179700
AGCTAGGACT ACAAGCATGT GCCACCACGC CCAGCTAATT TTTGTATTTT TAGTAAGGAC 179760
AGGGTTTCAC CATGTTGGCC AGGTTGGCCT CCAACTCCTG ACCTCAAGTC ATCCTCCTGC 179820
CTCGACCTCC CAAAGTGCTG GGATTACAGG CATGAAACCA GCCTAGAAAT ACATACTATT 179880
ATTTATTCTT GTTTTACAGA TAAGCAAAGT GAGTCATGGA GAATTTGGTT GAAAGTCCCA 179940
AGGTCAGGAG TCGTGAAGCT GGGATTAAAA CCTAATCATC TGACTTTAGA GAGTAGACAC 180000
TTGCTCCATG CATATTGCCT CCAATTCATT CATTCAAGCA CTCCCTGCTC AAGAAGTTCT 180060
TTCTTATGTT GAGCTGAAAT CTGCAGCCCT ATGCGTTTTA CCCAGCAGTC CTGGTGCTGT 180120
TCCCTAAAAT CACTTAGACT GTGCCTGCTC TTTCTGTGTT TACAGTGTC A GCTGTAATAT 180180
CCCCCTCTTC GGCCTAACGT TTCTGAAGTC CTTGCCACT GGGTCTCCTC TCCTCTTCCT 180240
GTGTTCTTTC TAAGAACACC TATGCAGATA GGTGTCTTCT GTACAGGGAA GCTGTTCTCG 180300
AGATCCGGGC ATCGACTCTG TTAGAATAAT CTACGTATGA GTTATTTTTT TGAGAACTAT 180360
GTGTCATTGC TGA CT CATAT TAACTCTGTG GTTAACTAAA ATCTCAAGAT CTCTTTATGT 180420
TTGTTGAGAA ACTTATTTAA CTTCTCTGGC CCTCCGTTTC CTTCACTGAG CAGTGGAGTG 180480
ATTGATAACC TCCACCTGTG GTTGCTGAAG GTCTTGCACA AGATGATATA GTTAAAGTAG 180540
CTAGCAGTGC CCACGTACGG CGGATGCCTC ACAACGGTTT GCAGCCATCT CTCTATCTGT 180600
GTCTTTGTCT CTCTCTCACA CTGGTTTTGG CTTACTGTTA GCAGCTAGCC GAGATAAGTG 180660
TGTTTATGGT CTTTGCATGT ATTGTTTCTG TAGCATACTG GAGGATTACA AGAGGTTGGG 180720
GAGTGAGGGG GCGGTGAGGA GTAGACAAAG GCAGCCAACT CTTCCAAGTT TAGCTTAGAA 180780
GGAAGGAGCG GTAAACCCTA GTTGAATGTT GGA CTGAAGC AGGTTTGT TTGTTTTGTT 180840
TAAAGGATAG GGAAGATCTG TGCGTGTTTC CAGGATAAAG AAAAGGAGAG AATATGATAT 180900
TAAAGATTCT GGAAGTGGA GAAGGAGCAA TGAAATACAG ACTTGAAGTC AGTGGCATGG 180960
ACAGGGTCAA GATCACAGTT AGAGGATGCA GCCTTAGAGA AAAGGAAGGG GCTCGGTTCT 181020
CTGAGCAAGG AGGGAAAGAA GAGAGGCAGA TGCAGAGAAG TACGGCACAT CGTGCTGCTG 181080
GTTGTAGAAA TAACCTCTGA CTTTAAATAA AGTCATCCCT CGGTATCCCT GGGGGATTAG 181140
TTCTATGACC TCCCTCGGAT GCCAAAATTC GTGGATGCTC AAGTCCCTGA TATAAAATGG 181200
CATAGTATTT GCATTTAACC TACACACATC CTCCATATCC TTTTTTTTTT TTTTTTTTTT 181260
TTTTTTTTTT TTTTGTGAG ATGGAGTCTT GCTCTGTGC CCTGGCTGGA GTACAGTGGC 181320
TCGATCTTGG CTCACTGCAA GCTCCGCCTC CCGGGTTCAT GCCATTCTCC TGCTCAGCC 181380
TACAGGTGCC TGCCACCACG CCCAGCTAAT TTTTTTTTG TATTTTTTAG TAGAGACAGG 181440
GTTTCACCAT GTTAGCCAGG ATGGTCTCGA CACATCCTCC ATATACTTTA AGTAACCTCT 181500
AGATAATCTC TAGATTACTT GTTTTGTCTT TTTTTTTTTT TTTTCTTTT GAGATGGAGT 181560
TTCACCTCTG TCACCCAGGC TGGAGTGCAA TGGTGCAATC TCAGTTCACT GCAACCTCCG 181620
CCTCCTGGGT TCAAGCAATT CTCCTGTCTC AGCCTCCTGT GTAGCTAGGA TTACAGGCC 181680
CTCCCCACCC CCACCCCCCA ACAACTGGCT AATTTTTGTA TTTTGTAGTAG AGATGGGGTG 181740
TCACCACGTT GGCCTGGCTG GTCTTGA ACT CCTGACCTCA GGTGATCTAC CCGCTTCAGC 181800
CTCCCAAAGT GATGGGATTA TAGGCATGAG CCACTGTGTG TGGCCTAGAT TACTTATAAT 181860
ACCTGATAGA ATGTAAATGC TATGTAAACA GTTGTTATAC TGTATTGTTA AAAGACAGTA 181920
ACAAGAAAAA AAATCTGTAC ATGTT CAGTC CAGACAAATG GTTTTCTGTT TTTTTTTTTT 181980

FIG. 6.69

TTTTTAATA TTTTGGTCA GTGGTTGGTT GACTCCAGGA ATGCAGAACC CGCAGATATA 182040
GAAGGTTGAT TATGCGTTCA GAGGCAGGGA ATACCATCTT GGGTTCCAGA AAGAAAATGA 182100
TCAGCATTTT CTGTCATACT CTGGTAAAAA CAGATCTTTT GAATGGACAG GTGTATTAAA 182160
CCCTGTGGAG CTGGCTGGGC CTGGCGGCTC ACGCCTGTAA TCCCAGCACT TTGGGAGGCT 182220
GAGGCAGGTG GATCACGAGG TCAGGAGTTC GAGACCAGCC TGGCCAATAT GGTGAAACCC 182280
CAACTCTACT AAAAATACAA AAATTAGCCG GGCCTGATGA CGCATGCCCTG TAGTCCCAGC 182340
TACTCGGGAG GCTGAGGCAG AAGAATCGCT TGAACCCTGG AGGTGGAGGT TGCAGTGAGC 182400
CGAGATCACG CCACTGCACT CCAGCCTGGG CAACAGAGTG AACTCCGTA TCTAAAAAA 182460
AAAAACAAA ACCTGTGGAG CTGATGAAAT CCTGCAGGGA GCTTCACGGT GACAGCAAGA 182520
GGAGAAACAC ATCCCCATAT GCCCCGAGA GTTTGAAGTC CCGGCTGCAC CTCTCCCCAG 182580
CAGCAGGTTG ACTCTGAAA GTTGCAGCGT TCTTACCTAC AGAGTGGGAA CAGTACTACC 182640
CATTGCACAG AGTGGGTGCA AAGCTCTGTG ACGGAATACA TGGCAAGTGC CCACCACATT 182700
GCCTGGGATG AGGTGGGCC TCTCTTACG TAAGAGAGCC CTACAGATACT ACTCAAAGTG 182760
GGCACATTCC TACAGAAGGA GTGTTATTTG TGTAGAAAAG AAAACATGA AAGGCTTTTA 182820
TTCCTATACA CAATAAAGCA CCCCTTTAAT GTCTTTTGA GGAGGATAAT ATGAAATTGA 182880
TGAAAAGGAA CCCTGTGGTT GGATCCCTGA CAATCACATG TATCCCTTTT TCACTCTTG 182940
AAAAAGGAGT AAAGGAATAA AATAGAAGGG GAGAGGGGGC AGAGAGACCT TCACCGCCCC 183000
CCCCCACCC CCCATCATCC AATCTATAGT CAAACCCTCC AGACTGTGTC TCCTTGGCAT 183060
CTCTGACACC CCCACCGCCA CCACCCAGT CAATTCCTAT CTTATCCCC TATCCTGGAT 183120
CTGATTCTGC TAAGTTCTG CCACACTAAA GACAGGGTGG CTTTCTGATG ACAACATTCC 183180
TCTGCTTAAA CCTGTCAGTA ATTCCTTGT GCTCTCAGAC GGAACAAAGT TCTGAATTC 183240
TTCACACGGC TCTCAGCAAG GTCACAGTCA CCCTGCTAGG CCCCAGGGGC AAATCTCAAT 183300
GGTCATCTTC TTGAAGACCT GGCTCAGTTA TTTCTTCTC ATTGAGGCTC ACGACCCAC 183360
CTTCTTGCAT GCCTCAAACG GCCCCTTACC ATGCTCTTCT TCGCCCATG GTCAGCACA 183420
CCATATCATT TTAATTTATG TATTTTGCTT AATGTGGATG ATCTGTCTCC TCCTCTGCTG 183480
TCCTCACCAG AGCATCAGTT CCTCAAACCA AGGCTCTTTG TTTTGTCTT GGATGCAAGC 183540
TAAATGTCTG GCATGTGGCA AATGGTCATA GATACATGTC ATTGAAAGAA TGATTTCATCA 183600
CCTCCCTCTT TGGCCTTGTG TGTGGTCTA CCAAATCCCA TTCCCTCCCC AGTGCCCTCC 183660
ATCCCCCTC CTGGCTGAA CATTCTGAAC CACAGACAGT TCTTACCCT GAACCTTTGC 183720
ATATTTTGT CTCTTAGCTT AGAGCGGCC CTCTCCCTCC GTCTGCTTGG CTAATTTCTA 183780
CTTGTCTTC AGATTTTATC TTAGATGTCA TTCCCTCAAG GAATCCTTCT GTGACTCAAC 183840
ATGGAATTAA GTTGCCCTCT TTGACCCTGA AAGCACCATG TACTCAATCT CATCTTGGCA 183900
TGACTCACTT TGCTGTGTGG AATGTCTGCT TTCCTTGTTT GTCTATTCTT TTAGACTGTA 183960
AGATCCTAGA AAGTGGGGGC CGTGCCTTGC TCATGACTGT GTTCTAACA CCAAACACAG 184020
TGTTCACTAG AGAGCAGCTG CTGAGTACGT TTCTGCTAAA TGACAGTTGA TGGAGGACAT 184080
TTAGGGTTGC TTGGAGGTCA AGTCAAGGAG GCATTTAACA TTCTAGTAAA ACAAGGAAGT 184140
AACAGGCTCC TGAACATGCC CACAATGAAC CAGATGCAAA CCTTTCCCT TGGCAGGATT 184200
CTTTGCCCAT AAAGTGGAGC ACGAAAGCAG GACCCAGAAT GGGAGGAGCT TCCAGAGGAC 184260
CGGAACACTT GCCTTTGAGC GGGTCTACAC TGCCAAGTGA GTCTAACCC TGATGTTGCT 184320
AATAAGTGGG GGCATGGGCA GGGGGGCCCTC CTTCTAGGAG TGATGACCAC CCTTAATACC 184380
ACATGTCTGT CTGAGCCAAG TTTCTGAGCG CCAGGGAGGT GAGGAAGGTT GGACTTCACC 184440
AGAGAGGCTT TGTGGACACC CTTTATCATC TTAGTGAGTG CTAGTGTCAA AACAAAGGGA 184500
GTGGGGATAT GGGGCACATT GGTGGAGGGA GGTGTGATCT CTGCAGCTC AGAAAGATCT 184560
GAAAGAGTCA TTTGGTTAGA GAAGTTGACC TATTCCTGT GGGGTTAGAC CAGGGTTGCT 184620

FIG. 6.70

ACTGTGAACA CCAGCCATGA CTCACCAGTC ACCTTCAGAA GCCACAGGCA GGACATGCTG 184680
ACGACAGCCT TCAACTCACC CACCCCTTGC TCCCTGCGG GTGGAAGTCT GGAGGTGACA 184740
CCACTGCATT TTCTAACACG GGGGCTCCTT GAGCAACTAG AACAGAACA GAAAGAATGG 184800
GGACATTAGC AGGTGCTTTC CCCCTCTCTC ATTCTTTTCT TTGAATAAAA AGGTTGTTTG 184860
AAAACACCTG AGCGGCTCCT AAAGATGGGT GCAATCTATT CGGGATGCAA ATCCGAATGA 184920
ATGTTATTCA AATGCTCCTC TCTTCTTTAT GCAGAGTGTA TTTCAAGGCT CAGCCAGTGG 184980
CAGGCATGCT GGGGACTATG GACTACGGAC TAGGGGCTG TCACAGAGGA AGGCCTCATG 185040
CTAGAGAGCT AAGGGAGGAG CTGGCCTTCA GTTCCATCCC AGGAGCAACT TTGATGTTCC 185100
CAGAGATCCT TCCAAAGGGG GAGTCATGGT CACCCAAGAA AAATGTATTC AGAATGCCAA 185160
GAATGGTGCA AACTCAGGAC AAAGATTCAC ACTGCAGGGT TGGAGTCCCT GGGCTTGCTG 185220
CTGGCACCAT GGGAGGGAGG GTCCCTTCA GGGGTAACCGT TGGTTTCCTG TGAATTAAAC 185280
TGGCTTCAAG GGATCTCGAC TGAACAGGCC TATATCACAC TCACTGATAT ACTCTCTCTT 185340
CAGTCCTTCT CCTCATCTAG GTATTTTAA TTGTTTCAGT GAGGTGTAGG CATGAGGGGA 185400
TTGGAGGGGG CATCTCCTCC ATTGCAGTTT TTCATTGGCT GCTTTGCTCC CTCAGCTCCG 185460
AAATCGCTGG GCCACTCTCG AACGCATTAG TACGGTAGTC ACAGGTTGAT TGCTTGCCCC 185520
CTTGCCCTCT GTGGGCATTT TCCCTTTCAG ACAGCCCCTG AGTACTCACA GTGCTGCTAC 185580
AGTGGGCCAC CTAGATCTCC CTCTTTCTCC ATGCTCCAC GTGCTCTGGG CTCCACTCCC 185640
TTCTCCCAAG CACTTCTGTC CAGGGCTATT CCAGCAGTCT GACCTCAAGG AAATCCTTTG 185700
CTAAACTGAT TATAGAGAGG TTTCTATTTT AACATTTAGG TCTTCCATGT ATTAATTCTC 185760
AGAATCAATT TAAGATGTTT AAAGGTGTGA TTTAAGACAT TTTAAACCA TTTGGAGGAG 185820
AGTACAGAAA TTATGTCAC TGTGTGCAGC CTCTTTGCAC CATCTGCAGA GAAAGATACT 185880
AGAGTCCCGC CTTGGACACA TCCACATGCA AGAGGTGCAA AGAAGGTGTC TTTGATGAGG 185940
CAAGGTCAAA ACTTCTCCCC AGACGAAATC CAAAGAAAGC ATTCCTACTA TGCTATATCA 186000
GTTTGAAAG AAAAATTCT GCCAGGTGAC TGCATTCTCA CTGGTCACAT TGTGTTCTTA 186060
TGGACTCCTC AGCTCAACCA ATTTGGAGAA GTTATGGTGC AATTTCACCA TATCTGGTTA 186120
GAAGTTAAGT TTCCAATTG CTGGCAATGA AGAAGAAATG GAGCAGGCCA GGCTGTGTAG 186180
TTTCTGCCAC GTGCCCCCGG GAGTGAACAG CTCTGTTTGT AAGAAGCCAT GGTGCTTAGA 186240
CCTGGGCTCG CTAGTTGCCA GCCTCCAAAT TGCAGAAGTG CCCTTTGGTT GGTGGCTATG 186300
CTGTGTCACT TGGGAAGGTC GTTTGGAAGT TCCACAGTCG TTGTGGGGTG CCAGAGATTA 186360
AAAAGCGTAA GAGGAGAGTG GAAAGTGATT GTTGCTGCTT GGGCATCCCC ACCGTGTGGG 186420
TGCTGCAGCC CAGCTCTCAA AACCCATGGG TCTGTACACT CAACCTCCAT GAGAGGGAAG 186480
GAGAAGGATG AGGGAGGGGA GAGATAGCCA TGGAAAGGTA GGAAC TAAGC AGGCAGGGTG 186540
GAGAGTTTTC TGTAAGACAA AAAGTGTCTG GACACTGCTG CGGTTCTGTT ACAAAGACCA 186600
CTTCTCCCT GGGCCAGCAA CATATCTGTG TGCCTGTCTG GGTTGTAAAA AGGGTCAAAG 186660
ATCAATGCAG CAGGCAGCTA CATGCTGGCA AAAGCCAGAG GCAGCTGGTC TGTTCCTG 186720
TGCCAGGAAA CCACTGGGAA TGGGGTTGTG TGTTATTCTA GGAGAAAGTC GTCCCAGCAG 186780
CAGCTTCTCC AGGGGCATCC AAGAGCACTG AAAAGGGTTG CAAGATGACC CATGAGGCTG 186840
CAGGAAGAAA AGAACATGCA TTTAATCTTG CTATCTGAAA AGTAAGACAT GAAGCTTTCC 186900
TCATTTTAA TATACACATG GACAGTAGTA TGTGTATATA GTTTATATGC AAATATACTT 186960
GTTATAAGGT TGCATGCTCA AAATTTTGG TTCATGGGGT GTGGGATCAT AAATGTTTAG 187020
GGACCATGGC TATCAAGGAA AACAGCATG AAGGATAAAT GATACTGGTG GATTAAAAAG 187080
ACAGATGCAT GTATTTT TAG CATAAAACAC AACTGCTGAC TGATACAGAT AGCTCAAGAT 187140
TCTGGGGCAG CTGCTGAACA GATACACTAG CCAGTGTGGC TCATCGGCTC AGACTTGGCC 187200
TTAATTAATG GGCTGTCCCT CCACCCATCT CCCATGAGGG CAGAGCTGAG CCAGGGTTTG 187260

FIG. 6.71

AGAGCTAAAA GGAATTGGAC CTGGACTCTG TTCACGTGTA TATTTTAATT CTAATTAATT 187320
CATTCTTTTG AAAGACAGAG TCACACTCTG TTGCCTAGGC TGGAGTGCAG TGGCACGATC 187380
TTGGCTCACT GCAACCTCGG CCTCCCAGGT TCAAGTTATT CTCCTGCTTC AGCCTCCTGA 187440
GTAGCTGGGA TTATAGGCAC ATGCCCCCAT GCCTGACTAA TTTTGTATT TTTAGTAGAG 187500
ACGGGGTTTC ACCATGTCAG GCTGGTCTTG AACTCCTGAC CTCAGGTTAT CCACCCGCCT 187560
TGGCCCCCTCA AAGTGTGGA ATTACAGGTG TGAGCCACCG TGCCTGGCCT GTTCACATGT 187620
ATAAACACA GTTTAATGTC CTATTCCCAG CCAATGAGCA TGGCTAGAGC AGCCTTGGTC 187680
AAAGTTTGGT TTTTGGAGAA AAATCCTTGT TAGCTGACCT AAGATTCCTC TTTGTGAGTG 187740
TAAGTAAGCA CAGGTTGCAG AGAGGAGAAG GGTCTCTGGA GAGGTGTAAT TTTCTAAATG 187800
GATTACAAGT TCATGGACTT TTAACAGGTG TTACAGGGGA TAACAAGTTC TTTATAGACA 187860
GACTTTTGAG GACGTTTAAG GGTATTCTGA TTCTTGGTTT TCTAAGAGGG GAATGTATTA 187920
TTTAACTACA GACACCCCTA CCGCCCACTT TTTGCAGAGT GTATCAAAAC ATGTTTTTGG 187980
AATACCACCC TCATGTCGCT TCTCCCTGCA TCTCTTATCT CTGGGTGTCC ATTCTAGACT 188040
CACTTTCTTT CTGTTTTTTA TTTTATTTT TTTTGTAGAT GGAGCTTCAC TCTGTCACCA 188100
GGCTGGAGTG CAGTGGTGCA ATCTTGGCTG ACTGCAACCT CTGCCTTCCG GGCTTAAGCA 188160
ATTTTGTGC CTCAGCCTCC TGAGTAGCTG GGATTACAGC ATGCACCACC ATGTCCGGCT 188220
AATTTTGTGA TCTTTAGTAG AGACAGGGT TCACTATGCT GGCCAGCCTG GTCTCAAAC 188280
CCTTACCTCA GGTGATCTGC CCGCCTCGGC CTCCCAGAGT GCTCAGATTA CAGACGTGAG 188340
CCACTGGTGC CTGGCCTAGA CTCACCTTCA AGTGGCATAG ACTTGTAATA TATTATAAAG 188400
GTGATAGGTC TACAATGATC CTGTCAATTA GTATTGACAC TATTATTAAT AAAGTGTAT 188460
TAATTATATT TACTTACTTT AAATTAATCC AAATAATTA ACGGAACACT AAAGAGTTTC 188520
TATGTTTTAT TCCCAGAGGT GGAGAAAAAT GAAAGGGAAT ATAGCAACGA ATTCTTTTCT 188580
CCATAAAAC ATGAATAGTG CAGCACATCA AGTTGAACAT ACCACAGCAA ATTGTTGCAA 188640
GATCTGCTGA GTAGCTCCTA TTTAGACCTC AAGGAATGAG ACTCAAAATG GGTTTCATCAG 188700
TTCTGTTTTG CAGAAAAAAT AGCGCAAAAT TTCTCAAAAG AAAATCCAGA ATAATAATA 188760
TTTGTCATA GGAAAGACAT TTCCACTGGG GGTTAAGAAG GAAGACATTG GAACAATGAT 188820
AGCCACCACT TATTGAATGC TTAGTGAG CCAGGTGGCA CTTCACCTTG TTTCACTCTC 188880
ACAACAGTCT AGGGAAGTAA TTAGTAATGT CTCCATCCAC CTCTTGTAAG TGAGCAAACT 188940
GAGGCTCATT GAGGCTAGGA AATGCACCCA CACTCACATA GCCCATAAGA GGCAGCCATG 189000
GCATTGGGCC CAGACCATGT GAACTTCAAA GACTACACGA GCAGCCACTG GGCAGCTGTC 189060
ATGGCTAAAG CCACTTGAAT TCAGCCCAGC AGCAACCCCTC TCTCCAGGAG GGGCACATAA 189120
GCTTGACAGT TTGGGTAGAA GCTGCACTTG AAGTCCTGGA TGGCGAGAGG GACTGGCTTG 189180
AGCCAGAGCC AGGAACAAGG CTCTGAGAAT ATTCTGGAAA TCCACAGGAG GAACCCATTT 189240
TCTTACAGCT GGGAGAATTT CATTCAACTC CAGGCTGACC ATGTTTTATT AGGAACGAAG 189300
GTGACTTGAA CTAATAGTCA GGAATGGTTG AATACGGACC CAATGTCAA TCACTAGGCA 189360
GTTACATTT CTAATGAGCA AATCCCTTAG ACAATTAAGA ATTTTTTCC TTTTGCATAA 189420
CCCAGACAAA ATCGCTACTT AAAACAAAC CAAAGACCCG AAACATGAGA AAGAGAAGGA 189480
AGCAGGGGAA ATCTTTGGTA CTAATAAGTT TTTAAACAAT AAGAGCACCA GATATTTTAC 189540
CCCATCAGAC ACAGAATGTT ATTGGAATAA CCAAAAAAGG AATTTTTTCT CTAAGTTTCT 189600
TGAAGTGGAA AATGAATCAT ATTTTCTCAG TCCTGAGGCT GCAATTTTGT GCCTCTAGTA 189660
ACATATAAGA ATAGATGTGA TGCCAGTGCC CAGTAGCTGC TGCAATTGTT ACTTGGGGAC 189720
CTGTTTATTC ACTAAGCACT TCACCCCACT GATAAATTTG TAGGGGCCCTC CTGCCCTTTG 189780
GAGCTCCTAC CGTGTCCATT AGATCAGTGG AAATCTGGG ATTGAGAGCA CTTTGCAAGG 189840
TCAGCAGGGG TCTGCTCTTT CTGTCCTGTT CCTGGTTTTT GGTTGTGCCT GGATTCCAGG 189900

FIG. 6.72

GTAGGTTTCT CATCTGTTAC CTTTCATAGAC TTCTCCAGAA AAGGATCTTT TGACCATCAG 189960
AGGACCACGA AGATTCCATT GGTGAGGCGC AGATAACCTG ATCTCTCTGG GTTCTCTGCA 190020
GGGCACAGAT GAAGGGCTGG CCATTCCCAA GTTCTCAGTG GTACCACTGA GGCATGAGAC 190080
CCTAATGGTT TGCATGAGCA GTTTGAAAAT TGCATCTTTG TTTTACCTA TATAATCACA 190140
TGAAACCCGT GGTTCTCAAA CGTCAGCAGG CATCAGCATC ACATGGAGGG CTGTGTTAAAA 190200
CAGATTTCTG GGCCCCAACA CAGAGTTTTA AATTCTGAAG GCCTGAGGTG GGTGTGAACA 190260
TTTGCATTTT TAACATGTTT TCGATGCTGC TGCCGCCTCT GGTCCCGAGA GCATGCCTGG 190320
AGAACTGCCA CCTTCGACCA TGGACTGTGA GAATTCACAT GGACCTCAGA ATTATAATCA 190380
GTCTCTCAGT TTTACAGATA AGGAACTAA ATCCAGAGAG ATTGTTTTGC CAATGGTGAA 190440
CAGCTGGTTA AAGTCAGGAT GGAGACTTTA ATCCTAGTCA AGTGACCTTT CCTCTGTATT 190500
TATTTCCCTC CCTTTTATG CCTCTCAAGT CTAGTTACAC TGTTTTTCAT GGATGGGCAT 190560
ATTTATTGTC CTGATCTGGA CTGCAGACTT CTCAGGAGGA CACCTATGAT TTAATTTAGT 190620
ATAGTTGAAG AGTTAAACAGA CATGGCTTTG GAGACAGACT GATTATGGTG TGAATCCCGG 190680
CTTTGCCACT CCCTAGCTGG ATGACCCTGA GCAAGTTATT CAGCTTCTCC AAGCCTGAGT 190740
TCCTTATTGG AAACATGAGA GCAATTGTGA TAGGCAGAAT AATGGCCCCC TCACCAATCA 190800
TGCCACATC CTAATCCTAG GAACCTGTGA ATATGTTATG TTACATGGCA AGGGGAAATT 190860
CAGGCAGCTA GCCAGTTGGC CTTAAAATAA AGAGATTATC CTGGATGATC TGGGTAGGAC 190920
CTGATGTAAC CACAAGGGTC TTTTAAATGT GGAAGAAGGA GGCATAAGAG TAGATGTCAG 190980
AGTCATTCAA AATAAGAAAG ATTTGATGGG CCATCCCTGA CTTTCAGGTT GGAAGGAGGT 191040
TCTGAGTCAA GGAATACAGG TGACCTCTAG AAGCTGGAGA AGGCAAGGAA ATGGTTTCTC 191100
CCCTAGAAGT TCCAGAAGGA TTGCAGCCCT GCTAATATCT TGACTTTATA GCCCTTGAG 191160
ATTTATTTTG GATTTCTGAC ATCCTGAACC ATAGTAAAAG GGTGTTTTT GTTTTTTTGA 191220
GACAGAGTCT TGCTCTGTTG CCTGGGCTGG AGTGCACTGG TGTGATCTTG GCTCGCTGCA 191280
ACCTCCGCCT CCCAGGTTCA AGTGATTCTC CTGCCTCAGC CTCCTGAGTA GCTGGGATTA 191340
CAGGTGCTTG CCACCACACC TGGCTATTTT TTGTGTTTT AGTAGAGACA GGGTTTCACC 191400
ATGTTGGCCA GGCTGGTCTT GAACTCCTGA CTTGTGATC TGCCTGCCTC AGCCTCCCAA 191460
ATTGCTGGGA TTACAAGGCG TGTGTTTTTA AGCCACTCAG TTTGTGGCCA CTGTGTACAG 191520
CAGCAAGAGG AAACATACAT AGTTATCATG TGAACCTACA GGAATATGGT GAGTTAAAAA 191580
GAGAGGAAGG GTGCAAAACA TCCACGGTAG AGTGAGAACT CTCCAGGGAG TGAGGACTGT 191640
GCCCAGCATA CAGTGATCAC CCTCTTAGTA AGCTAAGTTT CTGAGCACCA GCTTTTTTGA 191700
GTTGACTTTG TTGTCTTTAA CATTTGAAGA TCACCCTTCT TTGCTCAGCC TGGCTTGCA 191760
ACCTGGGCTG ATTTGTGGAT CTGATAGAAA AGTTTCCTTA GTTGGGCTCT TCTCCCGAC 191820
CACCCCATG CCAGTGTGGC CACATCCTCT GTCTGCATTG CTCACTCTT AATTCCAAGA 191880
AGCGCAGGGG CACCGCCAGG AACAGGAACC CTGCCAGAGG AATACATCAA GAAACCAAGT 191940
CTCCCTTACG CATCACCGTA GGAACAGAGT TAATGGATTA TGAACATGTG TTTGCTTTAT 192000
ACCATGTTT GTTTCCAGG TGGCAGCTGG CTGCCCATC TTATTGGGTA GATGTAAGTG 192060
GAATTACGAA TGGGATTTAT GTTTCATGCA CGATGGTGAT TATTAACCTC AACTTTCAGG 192120
TAATTTTCAG ACCACATTGC ACTAAGTTGG TCTCTGATTG TTTTCTCCT TGTTTGTTTA 192180
TTCTGCAGCC AGAACTGTGT AGATGCGTAC CCCACTTCC TCGCTGTGCT CTGGTCTGCG 192240
GGGCTACTTT GCAGCCAAGG TAACTCAGAC TTCCCTTTGT TCATTCTCCT TCTATAAAGT 192300
GCATCTCAAG GAGGTTCAAA GGGCAGGCTT TTTGTTGAAA GGACTTTGCC TGACCTCTGG 192360
CTCCCATCTG TGAAGCCCTG GAGAGGTGAG AGCCCTCGGG AGGCCGTGTT TCAGGCATGC 192420
TCTGCACCCG TGCAGAGCGC GTGTGATAAT GCATTGCTAA TGCTTGCTCC CTGGTGGCTG 192480
GCTGAGAGCT GCTGTGCTGA CAAGGGTGGT TTAAGGCTAA ATGTGACTCA GAATCCTTAA 192540

FIG. 6.73

GCAGTGTTAG TTCAGATACA AGGGCATTAT AAATGAGAGT GCCTGAGGGA TCTATTTTGG 192600
GACCGCTGTC ACTTGGCTCT TCTGCTAATA AGCTTCCAGT GTGGTGGCCC TCCTTCAGGC 192660
ATGTTTCCAC TGAGCCACGG GCTGGATGCC ACATCCCCGG CCTTCCCACA GTTATCAGCA 192720
GCCCACAGGC TTGACTTGAG CAAGTTGGAA AGACAAATCA ACTTCCAGAG TTGATTAAAC 192780
ATTGAGTGGA AATCAGTCAT ACTTTTGGTC CCCTTTCGGG GCCACGCCTG GCACTGTGCC 192840
TGGTGGCAGA TCGGCATGAA CTGGCCAGCT TCTGTGGCCC TGGAGGGCAC AGGCAGAAAAG 192900
GCCACACTCA GTCCCATGAT GAAGTGTTTA AGACTTATTG TTGTCTCCCC GCTCTGTAAA 192960
GTAGATAGAG TGGATTTTAT GTCCCTTATT ACCTTTCAGG ATACTTTGAC TCAGGGAGAT 193020
AAAGTAACTT GGGTACAGCT ACTCAGCTGG TGAAGAACAC AGGCAGAATG AGTGCCTGGG 193080
TCTTTTGAAT TAAAATTCTG GATTTTTCAC AAAGATCCTC TTAATTTTATT CATTACATA 193140
ATAAATATAT ATTGAAGAGC TACTCTGTGC CAAGCCCTGT GCCTAGATAT ACAGTGATAA 193200
ATAAAGAGTA GCTTCTAGAG GTCACCTGGC GGTGAGGCAC AGGCCAGCTG GCAAGATGGA 193260
CCACAGAAAT CAGTGAATGA AGACAATGAC AAGGGTGGGA AGCGCCATAT GGGAAGAGAA 193320
CCAAGTTCAG TGATAGAGAG CAGAGGTGAG GCGGCAGCAG AAACCACTTA AGGGACACCA 193380
CGTGGCACTC CTTCTGTGCT GAGAAGGCTG TCAGTAAGCT CACCATTAT TCCCTATTTT 193440
CTCTCCTGAG TTAATAGGA AACATGTCTC GCATTACTTG AAAAATCAAG TCAAACTATG 193500
CTCTTACTAG GAGTTATGGT TCTTTTATG TCTTAGATGA TGCTTGATCT AGATGAATGC 193560
GGACTTGCTG TAGCTAGATA AATACAATGG GAGTTTGAAG GTGTTTCGTA GCCCTGGAAA 193620
TAGGTATTTT CTGTCAAAAC AAGCTTTGTC ATTGCCAGCA GACAAAAGCA TCAGTAACCT 193680
TGTTTGATAA TCGTCATTTT TTAGGAATAA AGTAGACTGT AGAATTTTTT TTAGCAGAAA 193740
GGAAACCCAA AGATAATTCT AGTGCAAATC CCTCACTTTA TAGAGCAGAA GCTCAAGTCC 193800
CAGAGGAACA AGTGGCTTGA ACGAACATCA GAATTTTAGG GGCTGGATT GTACCCTCCT 193860
GGTGCCAGCA GCCCACTTCC CTGCAGGAGG CACTCACCTT CCTTGCACAG GGGTATGAGT 193920
GTGGCCATTT TCCACCCATA ATCTCTGTGA GCTCATGTTT AATTGGGTTT CCATTGAAAG 193980
AAAAATGGAC CAGTAAGTTG GAGCAGAATC ATTCAGATGG TATAACATAA GGAAAACTT 194040
TGCCCAAGGC AAATCGTGAT TGTGACAGCT TTGTGATTTT TAGAGAATAG CATGGGCCAG 194100
GCACAGTGGC TCATGCCTGT AATCCCAGCA CTTTGGGAGG CCGAGGCAGG CAGGTCATTT 194160
GAGGTTGGGA GTTCGACAAC AGCCTGACCA ACATGGAGAA ACCCTGTCTC TACTAAAAAT 194220
ACAAAATTAG CTGGGCGTGG TGGTGCATGC CTGTAATGCC AGCTACTCGG GAGGCTGAGG 194280
CAGGAGAATC ACTTAAACCT GGGAGGCGGA GGTGCGGTG AACCAAGATA GCACCATTGC 194340
ACTCCAGCCT GGGCAACAAG AGTGAAACTC CGTCTCAAAA AGAGTTCACA GTTTCTCTTT 194400
TGCTTTGATT TTCTTATCTG CCGGATAACA ATAGTATTTT GGAAGGCAGG AGGAATTGTG 194460
GAAAGAAATG GGTTTTGGG AGTGGCTGAT TGGAGGCAAA TCCAAGGACA CTCATTGCTG 194520
GTGTGTGACT CCAGGCAGTT ACTCAGCTTT TCCAAGCCTC AGTTTCCTTA TTGTAAACA 194580
GGACCATGGT CTAGCTAGTA GCAATCCTAT GGTGAGTGAA ATAATATGTA TAAAGCTCCT 194640
GACACAGTGC TTGGCATATA TCAGATTGAG CCATGTAAAA CTGCCAATAT CTGGCTATTT 194700
ATGACCTACA AAAATAGCAT TTCATATGAT TCCACCTAAC ATCTGAAGCG CAATAAATGT 194760
TATTATTGAT AATGCAGGTG GTGGTGATAA AGTTTTGAAA TCAGAAAGAC CTGGCTTCAA 194820
ATTCCACGCC TTCCTGGCC TGACTTATTT TCATTATTT GACAAATATT ATTTTGAACA 194880
CCCCATGTG CCAGGCACTA TGCCAGGCTC AGAGATGATC TAGGAAAAAG ACAGATGTCC 194940
TCATCTGTCT TAGGCTCTTG TGGCCTAAGC CTAAATTTCC TCGTCTGTCA AATGGTGACA 195000
GTAACACACT CTTTACCAGA GAGCTGGGAG GATTGGAGAC TCAAGTTCCC AAAACGCCAG 195060
GAGCACTGCG GCAGGTGAAA AGTATTCCCT CAATGGCGGA AGTGTTTAAA TTGCTTTTAT 195120
ATCTGTAGCT CTAGATAACA CTAGTTCAG CTTAGTTAAC TCCAGCTCC AAGCCTTCAG 195180

FIG. 6.74

GACTTCATAG AGTTATTGGG GTGCTGCTCT TGGCAGTTTC CCAAAAAGCT AGAATGCAGA 195240
GGGAATCTCC TTCCCAAAAA GCTAGAATGC AGAGGGAATC TCCTTCCCAA AAGGCTAGAA 195300
CGCAGAGGGA ATCTCCTTCC CAAAAGGCTA GAACGCAGAG GGAATCTCCT TCCCAAAAGG 195360
CTAGAATGCA GAGGGAATGT CTTTCTCTTC TAAATGGTAG CTGTAGTTTC AAGAAAGGTT 195420
AAACATTGTG CTGTGGGGAG GCTCAGGGGT GAAGGGTGTA CTTTAAAGAG AACCAGTTTC 195480
AGAGCTGGGT TTGGGGTTTA AGCCCTACCC TCTGCCCCCT TTTACGAGCT GACAGCCTTA 195540
TGCAAGCCTG GTTGACCACC TGAACCCACG TTTCCACATC TGGAAATAGA AATGTGGGTA 195600
CTAGTTATGT TGAAAGGACT CAGGTTAGAT GATAGATATG CAAATACCTT GGAAACCAGG 195660
AGTGTCAGT CTTTTGGGTT CCCTGAGCCA CACTGGAAGA AGAGTTGTCT TGGGCCACAC 195720
ATAGAATACA CTAACCCTAT CAATAGCTGA TGAGCTAAAG AAAAAACGTT GCAAAAAAAA 195780
TCTCATATTT TTAAGAAAGT TTATGAATTT GTGTTGGGCT GTATTCAAAG CCATCCTGGG 195840
CCACGTGCGA CCCGCAGGCT CCGGGTTGGA CAAGTTTGTT GTAAACAATG CCATGATGCC 195900
GGCATAAGGT CGTTACCAGT ATTAGGAAGG TTCTCAGGTT TCCTCTAGCC CTTGGGCTCT 195960
TTTCTGAAG TGCGTGTGTC TTCTGCTAGA TTTTGTGACC AATGTTGATT GCCTAATTGG 196020
GCTAACAGCA TGTTTTGGTG GCTACGAAAC TGACACAGGT GTTTTCATTT CTCCACTTAG 196080
TTCTGCTGC GTTTGCTGGA CTGATGTA CTGTTGTGAG GCAAAAGTAC TTTGTGCGTT 196140
ACCTAGGAGA GAGAACGCAG AGGTAGGTAA CTGGGACTAC TAAAGAACTG TGGAGCGATT 196200
CCTGATTTTT GAGCAGGAAG AGTGACAATT CAAAACAGTA TTTGACTAGA TTCACGGCTC 196260
CGTAGCATCC CTTGGGTGG GAGGGGGAAG GCTGACTAGG ACCTCTGATT CTTCTTTCCC 196320
TGAGCTTTGA AGGCTCTGAA AATACAGCTG GGGGGACTTG CCCAGTTTTC TTATTAAGCA 196380
ATTCTCCGC ATGGTGCTGG CTTTCAAAGG GTGCTTCAGT GCTGTTTGCT GCACGTGCCT 196440
TGCAGCCCCA CACCCTGCAC TCCCGCCCTG CAGAGTCTGG CGCTGGAATG ACATTTTAGG 196500
TCTGGGTTCC CAGGCCTCCT GAGAGTGAAA TGTTTCATTG TTTGTCTAGA GAAATGAGAA 196560
CTAAAGCTTG CACCTTGTA TAAGTTGTCC TGAGGAACAT ATCTTTCAGG GACCAGAAGA 196620
AAGAATGTTG GGAAAATAAG ATGCAGTAAG ATGCAGACAT GACAGCAGGG TGCAGCGGCT 196680
CACGCCTATA ATCCCAGCAC TTTGGGAGGC TGAGGTGGGT GGATCACCTG AGGTCAGGAG 196740
TTTGAGACCA GCCTGGCCAA CATGGTGAAA CCCCCTCTCT ACTAAAAAT ATACAAAACA 196800
TTAGCCAGGC ATGGTGGTGG GCGCCTGTAA TCCAGCTAC TCCATAGGCT GAGGCTGGAG 196860
AATCGCTTGA ACCCAGGAGG CAGAGGTTGC AGTGAGCCGA GATTGCGCCA CTGCACTCCA 196920
GCCTGGGCAA CAAAAGCAAA ACTCCATCTC AAAAAAAAAA AAAAAAAAAA AAAAAAGAT 196980
GCAGACACGA GACTGTGAAA CTGACTAGCA TCACCATTGC ATTGTTTATA GATGTTGCCA 197040
GACAGAAAGC CCCAAAGCAG CACAGTACCT TCCTGACATC TGGACTAGGA AATCTAGATT 197100
TTAGTAAAT ACATGCTAAT ACTTACAGAA GAAATGTGCG CGTTAGAGTA TGCCGTCAGT 197160
TCCTTAGAGA TTGCAATTCC TAATGCACTA GATGTTTTC AGGTGCCAGG AACACGTTCT 197220
GTGAGGCTGC TGCCCCAGGT GCTGACCCCA GCCTTCCACA CCATTTTCTT TCCTTGTTGT 197280
CACAGCCGCT CTGTCTTTTA CAATAGCACC CCTCTCTAGT GGCTAATGGG CTCTATGATT 197340
AGATAGCATC CTTAGTAGT GATAAAGGCA GTGACATCCT AGGGAGGTCA GCGGGTGAAA 197400
GCGCTATATC TGAAAAACCT GAGAGCCTGT GAAGCTCAAG GACTTGACGG GGTTAGACCG 197460
TGAGCCGGGC TGCAGCTGGA AAAAGAATGA CTGTTCTTTC AGCAGATCCT TCCCTGTGCC 197520
ATCTCTTCT TCATTCCTCT CTAGTGGCAT TCTTATTTAT CCTCTAAAC CACAATTCCA 197580
TTATCTCTCC TATTCTTATC AACACTGCCC TAAATGATAT TCTTTATTCT CTTTGGCCCT 197640
GGAAAACCTC TATCATGCCT TTTCCCATGT GATTACCTCG TTAAGAGTGG GGGTGGAAATG 197700
TCTAGCAATG AAATAAGAGG GTCTTCTCTT TTGCCTGGCT CCCTATGCAG CCCTATCTTA 197760
CCCCCTGCAA AGTCCCAGGG ATGTGGCTCA GTCAGTGCTC CTCTCTTCAT CTGTACCAC 197820

FIG. 6.75

TTGCTTGAGA TCCTACAGCT GCTTTAATTC CGAGACCATC TGCAGAACAT GACAAAATTT 197880
GTCCACCTAC CCACATGTCC TTTAACTTT AAAGGCTTTA CTAAGTATT CCTATTAGGG 197940
AATGAACAGA GGTGGCAAAA ATAAACAATA GGAGATTGAT TTACAAGAAA TCTTTAAAAT 198000
AGTAGATTTC TTCGGACCTC ATTGAAATAT AAATGGCCTG CCTTCTTG TG TCCCTCCCTG 198060
GTCTCCCTCT TTAGGTGATA AGAAGAAGAT CCTGCCAGCC CCATAACCCG CCATCTGCGC 198120
GGGTTCTAGA CCCCCTTCTC CTCCCCTCTG GCCGTGGTAG GCATTACTGA TGAATCATGG 198180
TGCTCTTTCT TCCAGAGACC AAACCTGGCC TCGGAATCCT TCTTAACACA GATACTGCTT 198240
AACACAACCA CTCTGAGCAG CTGTCATAAG TAGAAGTAAT AGATACTAGA AGAAATGTCT 198300
AAGCCTAATC TAGACCAAAA TACGGCCTGA TATAGATGCA AGCCAGAGGG GCTTTATGGT 198360
TAAATGCAAG GAGATTTTCA ACCCTGCCGT CTAGAAGCTA CTTGCTGAGA TCTTCTTCAG 198420
TTGGGCCCCAT CTCCTCCCCA GGCCCTCTCT CTGTTCCCTGG GCTATGTCAC ACTTGGACTC 198480
TGCAGACACC TAATGCTCTT GGGACCTGCT TTAGTCTTG ACCTCACCAA CCGAGGAGGA 198540
ATTGCTAGAT GAGATCCTTC CCCCAGGAATT TCTCTCTTGA ACCCCAGATG GTCCGTTGCC 198600
CCTTTCCAGA AGTTGCTCCA GCCCTGTCCG CTTAGGAAGT TCAGTGTCAT CCTTGATCCA 198660
GTGGGTAGGG AAGACATTCC ATAATGAATG CCCCAGTCTG AGCTTCTTCC TTCAGGCTTC 198720
AGGCTGCCCT GCGAGGATTT TGCAGCTCCC TTTTAAATGC CCTCTAGAAG TTTCTGGCTC 198780
TTATTTTCAG CCCTTCATCC TACTCTCTCT GACCCCTTCC TCTATCCTGT TTAGTTCACC 198840
TGAGCAGTT ACTACCCAGC AGTGAAGGAT GAATCTTGGT TTCGTTTCTT TTCTCTTCTT 198900
TTCTTTTTTC TCTTCTCTT TCCCCTTCCC TTCCCTTCCC TCCCTTCACA TCACCTCATC 198960
TCACCTCACC TTACATAGTC TTGCTCTGTC ACCCAAAGT GAGTGCAGTG GCCTGATCTT 199020
GGCTCACTGC AACCTCCACC TCTTCCCAGG TTCAAGTGAT TCTTATACCT CAGCCTCTTG 199080
AGTAGCTGAG ACTACAGGTG TGCACCTACA CACCCAGCTA ATTTTTTGTA TTTTATAGTAG 199140
AGATAGGGTT TAGCTATGTT GGCCAGGCTG GTCTCGAACT GCTGAACTCA AGCAATCTGC 199200
CATCCCCGGC CTCCCAAAGT ACTGGGAGTA TAGGCATAAG CCACCCATGA TGCCAGCCT 199260
GAATCTTGGT TTCTTCCCCA TTCATTTAAG CTATTACCTG GGCCTGAACT CAATGGCACC 199320
TGGCACCAAC TGGCAACTGA CTCTTGGTCT TTTATTACCT ACCTTCCCTA GCAGGCACTG 199380
GGTTGCTCCC TCTTCTATC CCATGGAGTC CTGTCCTCTG TTGGGGCTCC TACTGATCCT 199440
CTTGGAATA TGAAGTTCTC AGCTCAATGG TGGGTGGGCA ATGACTGCCA ACTCTTGAGG 199500
CCAATGAACT CAGGTTACCC CACTCCTCCT CCTCCTGAGT TGCTCACTCA CTCCTCATTC 199560
ACTCAACATT GATTCACTAG ATATTGCTA CCTGCTCTGT GCCAGGTACC AGGTCAGTTG 199620
CTGAAGGAGT AACAGTGAAC ATGACGGAGT CTTTGTCCCC AAGGAGACCC AAGGTGTCTC 199680
CTAGAGCCAG GGGCACATTG CAAGACCAAA TATATTCAAC TTACCAAAT AATCATAGAC 199740
CTAGTTCTCA AAAAGCAAGA AGACTGATTC CTCGTTGTCA TTTCTCCTCC TCAGCATCAA 199800
TGTTTTAGAG TCTGTGGGCC CCTCCAAGTG TGGAGTATGG TGTTACTTCA CCAGAGTTTG 199860
AGGAGAAACA TTCTTCTTTT GGAAGGCCGG GGAGCATAGA TGGATATCAA GGCTGCTGTT 199920
TCTAAAAGCG AAACCCACCA AACAACAGTA TTAGAATCAT CTGTGGTGCT TATTAAAGAT 199980
ACAGATTCTT GGGCCCCATC CCAGACTTAT GAATCAGAAT CTCTGCCAGA GGAAGCCTGA 200040
GAATTTGCAT TCTCAGATGA TTCTGCATTC TCAGATAACA CATTCTTTAG GTGATTCTTA 200100
CACACACTGG AGTTTGGGAA TCGCTGAAGG CTGTTCACTT CTCTTTTCTG AGAAATGATT 200160
CATTCATTTT AGAAATATTT GCAGAGGTCC TTATTTATTG GAGATTTGTG GGTGGGCAGA 200220
GGAGAAATAT CTTGTCCTCA CAGAGCTTAC AATTTTTATT TTCTTTAGAG GTCACCAGGC 200280
TTAAATGAC ACTTCCCTAA ATTCTGAAAA GAACAGATTT TTAACAAG AAGGGACTGT 200340
AATGTTTTCT GTTCTACCT CGTATTTTGT TCACATTAAG AACCTGGGGT GGAAGTGGA 200400
GGAGGGGGGG TGACTGGCGG GGGGCCACAG AGAGCTGAGC TGGGGTGGTC TCGAACTCCT 200460

FIG. 6.76

GAACTCAAGC AATCTGCCAG CCTCAGTCTC CCAAAGTGCT GGGATTATAG GCATGAGCCA 200520
CCCACGATGC CTGGGTGGAA CTCAGGGCTC TGGATGCCTG GCGCCCCCA TCTCCCACAC 200580
TACGGCGCCT CATCCTAGAA GTGGTTAGCA CCTTTGAGAT GGGAAATTATT TAGCAGGATG 200640
CTTTTGTTT TTCATGTAAG TTTTATGCTG CCTGTGGAGG GCACAGCTGT TTCAAAATA 200700
ATAACCAAAT CCTGGTCTCC GAAGTCTGAA GGCATCCTTT GCCCTGCAGT GCAAAGCACG 200760
GGATTCTGGC CTCACACAGG CAGGTCTGAA CTCCTGTGTT GCCTCTTGCT GGCTGTGGGA 200820
CCTGAGGCAA ATCATGCAAC CTCTCTTTTC TGTTGCTA GATGGAAAAT AGGTTTACAA 200880
TAGCCCCCA TAGGATGGCT GTGAGAATTA AAGGAAGTCA TGGGTGTACA ATACCTGGCC 200940
CCGAAAGATG CTTAATAATT TAATTCTGAC CTTCTCACT CATTTAGGAT TATGTACCA 201000
CTTTTAGAAA CAATGAAAGA TTAGTGAGTC TTCTGTGGTT GGTATAAAAA AAAAATAGAA 201060
ACATGAAAGA GATGTCCTCC TTGTCAAGG GCTAATGACC CTGGTGTGCG CTGTCTAGGC 201120
CCCCAAGGTC TTCCTCCCT GCTCACAGCA TTTCAGGTC TCCGCAGCTT TGCTGAGCCT 201180
GGGTCAGGTT CGGTATCTGC CCACCATGCT CACTTGCCAC AGCTGTGGCC CCATTTCCAA 201240
ACTTCAGAGA CTTAAAGGTG CAGCTAATGA TGTGCCCGGC CTGGGGTCAC ATTCCCTGAG 201300
CCCTGCAGAC AAGGGAGCAG GAGGCTGAGC TCTTATCTTC CACACCCTGT GCACAGCCTG 201360
GGAAGAGTTA AAGCACCTA GTCCTATGCT GCGAGGGCCA CATGCCCTGA GACCTTGGA 201420
AAAATCCTAC CTGAATTGAA GAGCATCACT ATTTATCAG GAGGCGCTGC CATTTCAATT 201480
TTCACTTCGG TTTTATCTTG AGTGTAAC AGCTTCGCA ATCACTTTT CTGTTTCTG 201540
TAATGAGCAT ATGGTGGCCT CATTCTGTG ATAAATCTGA GCCACCACGA TATTGACTT 201600
TTCACAATT AATTTATCTG AACCTCTAT TCTCTGGCTA AAAAATATCC CTTACTTGGA 201660
CTTCTTTATT TTATTTTCAA TTCCCTTACC AGCACTAGCA GGGGACTCTG TACTCATCTG 201720
CTGGCGCTGC CATAACAAAG CACTGCAGCC TGGGGGGCTC AAACCACAGA ATTTATTCTC 201780
TCACAGTCT AGAGGCTAGA AGTCCAAGAT CAAAGTGTGG GCAGGGTCGG TTTCTCCTGC 201840
AGCCTCTCTC CTTGGCTTAT AGAGTGCCAC CTTCTACCTG TGTCTTCACA TCATCACCTC 201900
ACTGAGCATG TCTGTGTCCA AATCTCCCCT TCTTATAAGA CCCAGTCAT ACTGGATGAG 201960
GATCCACCCA TATGAGTTCA TTTTACCTTA ATTATCTCT TAAACACCCT GTCTCCAAAT 202020
ACAGTCCCAT TCTGAGGAAC TGAGAGTAA GATTCAACAT ATGAATTTT GAAGGGACCT 202080
AATTCAGCCC ACAACACCCT CTTTGGGAT GTTTATTTT CCCCTTAAGG AGCTAGTTAG 202140
GATGCTTAT CTCATGAACA TGAAGTGAA CAGGAAAACA GGGAGAGAAT GAAGCTGGCC 202200
AAGGAACAGG GCTGGTGTCA GCTAGCAGTG CTTTCTGAT GTGAGTGGGT CCCACAGGGA 202260
GCTTGTTAAA ATGCAGATTC TGATTCATTA GGTTCAGAG GGACCTGAGA TTTCCCATTT 202320
CTGACAAGTT TCCAGTGTGG GGGCTGATGC TGCTGGTCCA CGGACCATAC TTTGAGTAGC 202380
AAGGAGCTTG ATACATAATG GCTGAGTGAC TTTCAGACTC CTGCTGTAGA AAAATTATGA 202440
GTTGGCTGGG CGTGGTGGCT CACGCCTGTA ATCCAGCAC TTTGGGAGGC CGAGGTGGGC 202500
AGATCACCTG AGGTCAGGAG TTCGAGACCA GCCTGGCCAA CATGGTGAAA CACCATCTCT 202560
ACCAAAAATA CAAAATTAG CCAGGTGTGG TGGCAGGTGC CTGTAATCCC AGCTACTCAG 202620
GAGGCTGAGG CAGGAGAATC GCTTGAACCC GGGAGGCAGA GGTGTCAGTG ATCTGAGATC 202680
GTGCCACTGC ACTCCAGCTG GGCAATAGAG CTTGACTCAG TCTCAAAAAA AAAAAAGAA 202740
AAGAAAAAGA AAAATTATGA GTTATATTAT CAGCATATGG GGTGCCTTTC AAATTGATA 202800
AATTTCTAAT ATTAACCTG TGGATGCCAA ATGCTGCTCT CTGATTATGG CAGGAAACGG 202860
CACTTGGCAG TACGAAGTTA GCTGTTGGGC TGAGCTGGCT CATCTTGTG TGCGGTCTCTG 202920
ATTGCCATAA GATGCCCTCC CAGGATCTTT ACTAACAATC CTCCTGAGTC ATTTGACTT 202980
TCCCAACCTG TTATCACCTC TCAGATGGGC CAGCCATGGA GGCAGTCAGA GGAGGGCTCT 203040
GCAGAGGGAG GGCAGAAACA GGGTGGCTC TGCATGCCAT TAGGAGGTCA CATCTCACTG 203100

FIG. 6.77

GGGGATGCAG TTTAGGATTT AGTGCCTTGG AGAGAAGGAT AGAGTATATT AAAACATGTC 203160
TCCGCTAGGC ATGGTGGTTT ACGCCTATAA TCCCAGCACT TTGGGAGGCC GAGGTGAGTG 203220
GATTGCCTGA GCTCAGGAGT TCAAGACCAG CCTGGCTAAC ATGACGAAAC CTCATCTCTA 203280
CTAAAATACA AAAAGTTAGC TGGGAGTGGT GCGTGCGCC TGTAGTTGCA GCTACTTGGG 203340
AGGCTGAGGC ATGAGAATCA CTTAAGCCCA GAAGACTGAG GTTGCAGTGA GCCGAGATTG 203400
CACCCTGCA CTCCAGCTTG GGCTACAGAG TGAGACTCTA TCTCAAAAAC AAAGAAACAA 203460
ACAACAACAA TAACAACAAA AACCAAGTCT CTCCCTCCAC TCAAAAATGC AAGGGCCTGT 203520
CTCCCATTCG TGGGTGCCCA GGTCTCATGA ATGTAGATAT GAATTATTCC AGTCAGCCTC 203580
AGGAGAATAG AATGAGCCCT CAGATGCCGA AGCACCTTC AGATTCCACC GGTTTTATCG 203640
GCTCATTTAA ACTTCACTC TAACACAGTC CTGCATTACA CACGTGTCTG TCGTTATGGG 203700
CAGCTGCAGA GAGGGTCTTA ATGGTCCTAA TGCTCAGTGA GGATGCCCAA TGGTCAACAG 203760
AACCTGCCAT CTTGAGGCCA TCAAGGAGCT CTGGAGTTAA GGAAATCATG AGAGCACAGA 203820
GGGGCGGGTA CAGCAGAGCC CTCGTGGTAA TGGGTTTGA GGTCTAGGCT CTCTTCACTT 203880
GGGTTTGAAT TAAGTTCAAT GACTAGTAAT AGCTGAGACA CTTCTACCCT TCAAATGAAG 203940
TAAATGGGAA AATGGAGCAT TGTGAGTCC AGGGAGCTAT AATTAAACC CCATATATCT 204000
AAAAGGGGTA ACATTTTTGT GTGTGTGAAA TTGGTGTCT TCGCACTGCA TCTACAGTTT 204060
TCTTTTCTCT TCTCTCCAG CACCCCTGGC TACATATTG GGAAACGCAT CATACTCTTC 204120
CTGTTCTCTA TGTCCGTTGC TGGCATATTC AACTATTACC TCATCTTCTT TTTGGAAGT 204180
GACTTTGAAA ACTACATAAA GACGATCTCC ACCACCATCT CCCCTCTACT TCTATTCCC 204240
TAACTCTCTG CTGAATATGG GGTGTTGTT CTCATCTAAT CAATACCTAC AAGTCATCAT 204300
AATTCAGCTC TTGAGAGCAT TCTGCTCTC TTTAGATGGC TGTAATCTA TTGGCCATCT 204360
GGGCTTCACA GCTTGAGTTA ACCTTGCTTT TCCGGGAACA AAATGATGTC ATGTCAGCTC 204420
CGCCCCTTGA ACATGACCGT GGCCCCAAAT TTGCTATTCC CATGCATTTT GTTTGTTTCT 204480
TCACTTATCC TGTTCTCTGA AGATGTTTTG TGACCAGGTT TGTGTTTCT TAAATAAAA 204540
TGCAGAGACA TGTTTAAAGC TGATAGTTGA GGGGTTTTGT TAATGGCTTT TGGGGGATTT 204600
ATCTCTATAC CCACAAACGA CTAGTTTGT TTCTCAAAC TAAATGATAA TATTAATAA 204660
ACACATCCTG GCCAGGTGTG GTGGCTCATA CCTGTAATCC CAGCACTTG GGAGGCCGAG 204720
GCAGGTGGAT CACTTGAGGT CAGGAATTAA GACCAGCCTG GCCAATATGG TGAAAGCCTG 204780
TCTGTACTAA AAATACAAAA ATTAGCCAGG TATGCTGGTG GATGCTTATA ATCCCAGCTA 204840
CTTGGGAGGT TGAGGCAGGA GAATTGCTTG AACCCGGGAG GTAGAGGTTG CAGTGAGCCA 204900
AGATCATGCC ACTGCACTCC AGCTTGGGCA ACAGAGTGAG ACTCCATCTC AAATTAATAA 204960
AAATACACAT CTGGCTTCTG GAAAAATTAC TTGAAGATCT TTTATGACAT CCATCCCTCT 205020
TCACACAGCC ATGTGAATTA GGTGTTATC TTCATATACT AGCATCGTGC CCAGCACTTC 205080
CATGTTATAC AGTTTAAAT GTTCTGTAAT TCCCTGTGGG AACCTAAGAT AATGCGAGGA 205140
CCGTCATACG TGCCCCAAA TATTGGCAAA CCAATGAATA AATGAATGAA TGAGTTTATG 205200
AATCGCTAAC TGGCTGTATT TAATGAAGTA TGTGTGTTGA GCCATTTCC ACAGTGTTGA 205260
CAGATTTGTC CCACAATATG GGCTCTTCC CAAAGGCCCT ACCACCTAAT GCCATCACAC 205320
TGGGGATTG ATTTCAACAT GTGAATTTGG GGAGAGTGCA AACACTCAGA CCATAGCACC 205380
ATCTCAGTAA ATGTCCCACT GGTCCTCAG TTCATAGTGA CAGTGATCCA GCCACTGTCA 205440
TGACAGGTGC CACTTGGCAG AAACAGCACA GCTTGAAGA TGGCGGGGTG TAGTCAAGAT 205500
TCCAGGATCC CCAACAGAGA AGCCAGCTCT TATAGGGGAG CCATTCATCA GGATTGAACT 205560
CTCAATCGAG CTGGACAGTA ATAGGTGGGT CTGTGTTATT CCCCAGATGA GTATCATGAC 205620
AGTCACAATC CTAGGAAGGA TGTGAAGCCT CCCCAGCTC TCCTCCAGTT GCCTGCTTGG 205680
GCAGCAGAGA TGATGGAATG TGGAGTCTGG CGTGGTCTGA GGCCTGAATC CATGTGCCTC 205740

FIG. 6.78

ATGTATGATG CTCAGGCAAG AGGATCTCTC AATTCAAGGG AGAGGGCCTG AATGAGCCTT 205800
GCTTTCCAGG CCTGTCTGAT GGTCCAGGCT GAAGCCCTC CTGGCTTGCA CTGCCAGACC 205860
TCATCCAGCA GGAGCTCCTT GGCATTGACT GCTTCAGGAT AGTTGCTTCT GCTCTGAGTG 205920
CTCTCTAAAG AGCAGTGCTC TACCATCCAA GCTGGGCTTT TCTTTCTTC TTGCTGATAG 205980
GGAAGGCATG GGACATTGCA GGATGGAAGT GGCCCCCAGG CCTTCTCATG CCTGGGCTTG 206040
GTTTGGAAGG TGGTCAGGTG ATCAATAATC CTGATTGGCC TGGCATTGAG GAGTTTTCCT 206100
GGGATGTGGT CCTTTCGGTT TTTTAAAAAT TATTTTATT GATACACATA TTTGTAGGTA 206160
TTTGTGGGGT GCATGTGATA CTTTATTATG TGTGTGGATT GTGTAATGAT GAAGTCAGGG 206220
CATTTAGGGT CTTTCATCACC TTGATTATCA TTTCTATGTG TTGAGAACAT TTCAAGTTCT 206280
CAGTTCCAGC TATTTTGAAA TAGACAGTCC ATTTTGTTAG CTACAGTCAC CCAACCCGGC 206340
TGTCAGACAT TGGAACTTAC TCCTATTGAA CTGTGTATTT GTACCCATT CCAAACCTCT 206400
CTTTGGGCTT TCAGTTTAC AACTGGGATG ATCCTGGGAA AACTAAAGTA AATCAGACAC 206460
CCGACGTGTG AGCTAGGTTA TAATATGCCC AGTGGACCCT GGGGACATCT TAGCTTTCAG 206520
AGGTCATGCT GTCCAAGCTG ACTGTGGGGC TTCCAGAAGG TGGGGAGAGG AAATGATGCA 206580
ATGGCCCATC AGAGGCACTA CTTGGGGCCT GGGGCCAGAG TGCATGTCTA AGGCATTAAG 206640
GGGAGGGGAG AGCAGCCTTC ATAATTATGA AGAGGAGTCT CAGGTGCACA GCTTCTGATG 206700
AGGGACAGCT TCTAATTGAA GACAGCATTG TGTAATGCTC AACTCCCTG TCTTCAGAGT 206760
GCCTGCTGTA TCCCACCATC AGTTCTGTGA CTCTCCCTA AGCCTCAATT TTGCATGTGT 206820
TACATTGGGA TAATAATAGT GCCAAACTCA TGGGGTTGTG AGGAATAATG AGGTAAAGCA 206880
ATTGAAAAGG TTTAGCACAA TATAAGTGCT CAATAAAAGC CATTATTATT ATTTTATTAC 206940
ACTAGTTTTC AATTCCTGCA TAGCAAATTC TTGCAAATGT AGGGACTCAA AACAATATAA 207000
ATTTATTATC TGACAGTTTT TCTGGGTGAG AGGTCTTACT AGGCTGTAAT CAGAGGGCAA 207060
CCAAAGCTGT GATCTCAGCT GAAGCTCAGG ATTCTCTTCC AAGCTCACTG GTTGTGCGCA 207120
GAATTCAGTT CTTTCCAGTT GGAAGACTAA AGCCTACAGT CTTCACTCTC TAGAAGCCTT 207180
TTCTCTGGCA CAGGTTTCTC TACAACATGG CCATTTATGT CTTTAAGGCC AATAGGAGAA 207240
CATGATTAGC ATATTTTTTT TAAGTGAAGT TTAGACCCTT TTTAAAGGC CTATCTGATT 207300
AGGCCAGGCC CAAGTGAGCT TTAAGTCAAC TGATTAGAGA TCTTAATTAC ATCTGCAAAG 207360
TCCCTTCATG TTTACCGTAT AACATAACTT AGTGAAAGGA GTGAAATTGC AACCAGGTTT 207420
TGCTGCACT CCACGGAAGG GGATTCTGCA GAAGTGTTGGG TCACGGGGGG GTTATTTTGG 207480
GATTCTGCCT ACGTCACTGA GTCAAAAGAA GCTGAATGGT TGTGATGCTG AGGTTTTTGG 207540
GCAGCAGCAG TGTGTGTGTG TGAGTGAATT CATACGTATG ACCACCTGGG AAGAAAGGAG 207600
GCTGTGGTTT CCTCCACCTC CTGGCAGACA GAGAAATTTT TTTTTTTTTT TGAGACAGGG 207660
TCTGGCTCTG TTACCCAGGC TGGAGTGCAG TGGCTTGATC TCTGCTCACT GGCTCACTGC 207720
AGCCTCTGCC TCCCAGGTTT AAGTAATTCT TGTGCCTCAA CTCCAAGTAG CTGGGATTAC 207780
AGACACACAC TGCCACGCCT GGCTAATTTT TGATTTTTTA GTAGAGACGA GGTTTTGCCA 207840
TGTTGGCCAG GCTGGTCTTG AACTCCTGAC CTCAAGTGAT CCGCCACCT CAGCCTCCCA 207900
AAGTGCTGGG ATTACAGACG TGAGCCACCA TTAACCATTT TTCTATCTCC TGTGGGAAAG 207960
GGCACAGTGA AAGAACAGAT GAAGCTGAGA CATACAAGTG AACTCCTCCC TCCTCTCCAT 208020
TTAGACTAAA ATAGGATTAT TCATACTGAG ATTCTCCCTG GTTGCAAAGA GATAATCTGT 208080
GCAACTGGGT TTTTACAATT ATCCCTACCC TATGCTTTCC TCATCTGTCT TCCTCGTAGT 208140
CAGCTCAGGC TGCTATAACA AAACACCATA ACTGGGGGCT TTTGAACAAC AAACTTTTAC 208200
TTCTCACAGT TCTAGAGGCT GGAAATCCAA GATCAAGTTT CTGGCAGATT CGGTGTCTAA 208260
TGAGGTCTTG CTTTCCAGTT TATAGACAGT GCCTTATCGC TACCGCCTTA CACAGTGGAA 208320
GGAGAGGACG AGAAGCTCCT TGGGCTTTTT TTTGTTTCTT TCTTCTCTC TCTCTCTCT 208380

FIG. 6.79

TTTTTTTTTT TTAATAAGGT CACTATCTTA GTCCATTTTG TGTGCTAAA AGGAACATCT 208440
GAGGTTGAGT AATTATTTTT ATTTTAAAAA GTGGCCAGGC ATGGAGGCTT ATCCTGTAAC 208500
CCTAATCCTT TAGGAGGCCA AAACAGCAGG ATTGTTTGAG GCCAGGAGTT CAAGACCAGC 208560
CTAGGCAAGA TAGTGAGACC CCATCTACCC CATCTCTACT AAAATTTTAA AAAATTAGCT 208620
GTGTGTTGTA AAGTGTGCTT GTAGTCCCGG CCACTTGAGA GGCTGAGGTG GGTGGAGTTC 208680
AAGGCTGCAG TGAGTTATGA TTGAGCCACT GCACTCCAAC CCGGGTAACG GGGCAAGACC 208740
TTGTCTCTAT TTAATAAAAA AAAATCTTTA TGTGGCTCAC TATTCTGGGT GGCTGGAAAG 208800
TTCAAGATTG GGCATCTGCA TCTGGTGACA GCCTCATGTC GCTTCCAGTC ATGGGGGAAG 208860
ACGAAGGAGA GCTGGCACGT GCAGATATCA CGTGTGAGG GCAGAAGCGA GAGAGAGAGG 208920
GGAGAGATGC CAGGCTCTTT TTAACAACCA GCACTGGGGA AACTAATAGA GTGAGAGCTC 208980
ACTGACTCCT GAGGGAGGAC ATTAATCTAT TGATGAGCGA CCTGCCTCCA TGACCCAAAC 209040
ACCTCCAACG ATACCCACCC TCCAACACTG CCACACTAGG GATTAACCTT CAACTTGAGA 209100
TTTAGAGGGG GGAACTTAC AAACATCGC AGGCACTAAT ACCACTCATG AGGGCTCCAC 209160
CTTCATGACC TAATCACTTC CTAAAGGCCT TACCTCTTAA TCTCATCACA TTGAGGATTC 209220
GATTTCAACT TGAATTTTGG GGGGACACCA ACATTCAGGC CATAGCATCA TCTCAATAAC 209280
TGTCCTATTG GTGGTCACTC AGGCCCCAAA CAAAGGAACC TTCCTCCATT CCTTCCGCC 209340
CTCCACCCCA CAGTCAATCA TCCCAAGCT CCATCAGTC CACCTTTAAC GGCCAACCCA 209400
CCTCTGCCAC ATCTCACCAT CTCCACTGCT ATCCCTGTCA CCTGGGCCCA CCATTCTCTC 209460
TCCTGGACAG TCTCCATAGC CACCTCTGTC AGATTTATTT TATTTTTTTA TTTTTTTTTT 209520
TGAGACAGGT TCCTGCTCTG TTGCCCAGAC TGGAGTGCCA TGGCATGATC ACATCTCACT 209580
GCGGCCTCCA TCACCTGGGC TCAAGCAATC CTCCCATCTC AGCCTCCAA GTAGCTGGGA 209640
CTACTGGCAC CACCATACCT GGCTAATTTT TTGTTGTTGT TGTTTAATTT TTAATACAGA 209700
TGAAGCCTCA CTATGTTGCC CAGGCTGCTC TTGAACTCCT GGGCTCAAGT GATCCTCCGG 209760
CCTTGGCCTC CCAAAGTGCT GGGATTACAG GCATGAGCCA CCGTGCCAG CCCATCAGAT 209820
GTTAATGCTA CACGCACTTG CTAAAATCC CCCAGATAAT TCTCGCTGCT CTTGGAATAA 209880
TTCCACACA CCTTGGCGTG GCCATGCAGG CTCTGTGCCA TCGGATATGT CCCTGCCCCC 209940
TCTCCCAACT CCTCCTTTCTG CTTGCTCGTT CACTCAGTTC CAGCCACATT GCCCTGGGAG 210000
CTGCTCCAC CATGGGGCTT CCTAATGCAC TGGTCTCTCT CATGCAGTGG GGCCTCTCCC 210060
TCCTTTTACT CAGTGTCTCC CAGCACCCAC CTCCTCCAGA GCCTTCCCTG ACCACCACAC 210120
CTACACCTAG GCCCTTCTC CTCCACGCTC CTCCTCCAC CCCGGCCTCC TACCCACGTG 210180
TCACTTCTTT ATACTCGCTG CCACCTGAAA TTAGATCATT TATTTACCCC TTTATTTGTT 210240
CAGTTTGCCT TGTCCGTTAG AATATAAGCT TCAAAGGGC AGGAGCTTTG CCTATATTGT 210300
TAGGCCGGGC ATACAATGAG CACTCAAAAA AATATTGAT GAGTGTATGA AAGAACAGAC 210360
TGGGTATGT AATTGTGCCT ACTTACCTAT ATGACCGTGT GGTGGGGTTT ATGGTGGGTG 210420
TGGTGGTGAT GGCTATAGGG CTATAAGCAA ATTTGGGACA GGGAGTCTAA GAAATGTTCT 210480
TAAATTTTAG TAAGCAAAGC ATCCTCTACA GAACCTGTCT TAAAACATGA AAGTTCCTTA 210540
GTGCTACCCC CAGAGGTATG ATTTGGTAGG TCAAGGATAG GGCCTGGAAA TTCACATTCT 210600
TGTTAAGATG TTCTTCATCC GGGGTTTGT GACCACCTTT TCAGAAGATT TTTGCTCTGT 210660
AGCTGTACTA CCCAATGCAG TAGTTCGTAG TCAGTGTGGC TCCTGAGCCC TTGAAGTGTA 210720
GCTCCTCTGA ACTGAGACGT GCTGTAAATG TAAATTGCAC ACCGGAGTTT GAAGAGTTAA 210780
TACAAAGAAA AAGGAATGCA AAACATCTCA TTAATAATGC TTTACACTGA TTACATATTG 210840
AAATGGTAAT CTTGTAGATA TAGTGCGTTA AATAAAATAT ACTGTTAGGC TTAATTTTAC 210900
GTCTTTATAC TTTAATGTG GCTACTAGAA AAATTTAAAT AACATATTCA GCTCACATTA 210960
TACTCCTATT GAACAGAGCT GATCTATAAG TTCCATGGAA GATGGCAAGT CTTGCGAGCT 211020

FIG. 6.80

GAAATAAAGG CTGGATCCCA TTCTACGGGC TCATCTTTAG CAATGATTTC TTGCAGACGA 211080
TATTGAAAAA TGTGGCAATG AAAGTTACCA CAAGCATCAA ACCAGTCCTG CCTAAATCTG 211140
GAAAATAGTT ATCTGAGGCT GTTAGCATAT GATCATGAGA GCGTTTCACC ATGGATTCT 211200
GATCACAGAT GTGGCACATT ATTTAAATAT CACTTTTACA GTCACCCTAG AGGCTAGGGT 211260
TATCTGAATA TGGAGAAAGA AACAGCTTGT GGAGCTGTTG TATAAATGAA ATTACTAGAA 211320
AGTAATGCAC TCAATTGCAT ATTGGCTCGG GGGGTTATTC TTATTAAAT GTTTAGAGAG 211380
GACTTTCTGT TCATTTCTGC AGAATTGCTC TTCAAATTAA GAATTTGCTT GACACGCTAA 211440
TAGACCACAG TCCCAAGAGA AGTTTATCCT TTTTCTTCT TATCCTTGCT AAGCACTTAG 211500
ATGCTCTGCT GATAGGTAGC ATATATTGTC TATATGAAGC TTTTGTGTTA ACATTGACTA 211560
GTCCTGCAAG TTGGCACACT CTTACTTGGC CTAAAAGAAA TCAGCACCAG GCTTTAAGAA 211620
AATCAGATGA TCTACCTAAA GGAACACAAC TCTGTCTCTC TTTTGACAAT TGTTGTAAAC 211680
AAATTTTAAT GGAAATTTGC CTTAATTGTG AAGAAGTTGC TGCTAAATG GACTTGCCAT 211740
TAATGGACTG GAACCCATTG CATAAGCAGA ATGAAATATA AGCCTTCTCA GGATTCACAC 211800
TTATAAAAAA CCATTGAGCC AATCAACAAG AGGGCAAAAG AACAAACATT TGATGTGTAA 211860
TTACTTAATT TAGTGCATAT GCATTTGGGT CCTCAATGTC AGCACTATGG CAACCAGAAC 211920
ATGGCCACAA TAACTGTCTG GAAATGTCTA TTCTTACCTG GACCCAGCAG GCCATGCCCC 211980
ACTGATTATA TAATCTCCCT CTCTCCTTGT TACGGTCTGA ATGCTTGCAT CCCTCAAAAA 212040
TTCATGTGTT GAAATCCTAA CCCCCAAGGT GATGATATTA GGAGGTCGGC CTTTGTAGAG 212100
GTAATTAGGT CATGAAGACA GCATCCTCAT GAATGGGATT AGTGTCTTA TAAATAGGC 212160
CCAAGGGAGC TCATTCACCT TGTCACCAT GTGAGAACAC AGCGAGAGGG CACCATTAT 212220
GCACCAGGAA ATGGGCCTTT TCCAGACAAT CTGTGGTGC CTGGATCTTG GACTTCACAG 212280
CCTCTAGAAC TGTGAGAAAT TAATTTGTTT TTTATAAGCC ACCAAATCTA TGGTTTTTTT 212340
TATAGAAACC GTAATGGACT AAAACACTCC CTAATTATAT TAAACTTAT CAGTGCACCTG 212400
GGCAGTGACA TATTAAGA ATGCTGGCCA ACGTAATTGA CACCATAAGG CTGGATGATT 212460
CTTGTAATTT TCAGCCTCAG AAAAAGGCTG GGGAGAGGAG TCAGGGGAAA GGAGGTGGTG 212520
TGTGTGTGTG TGTGTGTGTG TGTGTGTGTG TGTGTGTGTG GGTGGATGCC TGCTGAGAGA 212580
GAAAGAGCTA TAATAACATT CTGTGGTTCA GCTGACACAT CCTTCTGCA TCCCCTCCAA 212640
TCACCTGGGT TAATGGGGAC CTCGCTAATG TCTGAACCTC ATCTCATTTT AACCTTTTGT 212700
TTCAAAGCCT CTCTTTTCAT GACTTCCCCG CCTTCATTTT TCCCATATGG TGGGGTTATT 212760
ATTAAGACAT TAAATGAGAG TGGACAGGTA GGCAAAGGAG GTGGGTTGCA GGGGAGTTGA 212820
GGGTGCGCTG TGTACTTTTC TAGACTGTTT CACTTCACAT CAGTGAAATA TTCCCAATTG 212880
ATACTATCAT GAAACAAAGC AAATGAAATG CTGAGCACGG AGCTTCGTCT TGATGAAATG 212940
CTGAAAGAAA AGAAAGGAAA AATAAAGTAG CCATTATTTT TGCCCTTCCT CCCACCCCCA 213000
TGTTTACTAC TCTTATTCT CTTTGTATT GTTGTGTTGG AAGCACAGCA TCAGAAAAAC 213060
TCCCAGTTTT GAGAGATAAC TCAGTGTTTA GTTCACTTAA ACCTGAGAAA GGAGAAGAGG 213120
ATGCCACCGT GAGGTCCAGG ACGTAAAGAG GAAAAAACA GACAAAAAAA TCCATATGAA 213180
ATGAAAATGT GAAAGAGGCG CTTTCGAGCA GATGAGTGT GTAGATTACA GTGTTGAGAG 213240
CTGTTTGTGT CCAGAGCTGC TTGCTGCACC TGGCGGGATA AACACTGGTC TAACAGAGGA 213300
TCCTTGTTTC AAGGAGGCTG CTTTATTTT GGGGGGACAA AATTGTTCTT GAAAGCTGCT 213360
CAGTGGTTCA AGCTACAGCA TGGTGGACTA GCAGAATGGA CTCCAGGGCC TCCGAGGAGA 213420
CAGTGAAGTGC TGCCAGAAAT AGTCAAGGAT AGAAAGGAAG GACTTCACTG AGGCCTGGGA 213480
GAAGATTATG GAATGGGACT GACAGCAGTG ACGGGGAGTA AAAGGGGGTG TCTGGGGGAA 213540
TTGTGCCCCA TGGTGAGAGC TAGAGGGTTC ACAAAGACTT AACCCGACGC ATCTCTCTCA 213600
CCCTGGAGAT TGGGCCCGTT CAATCTAACT GGATGGCTAT AATTTAAAAG GTTTAGGTAT 213660

FIG. 6.81

TATGACAAAC ATGGATATAT TAGGTGATAG CAATGCAAAA TGCATATGGC TTCTTGATAT 213720
AAAACACAAG ACTTGAAAGC AGCATCTTTG GCTGGGTACT ACAGCCACCC TCCTCTGTCA 213780
CTAAGGGAGG CTTTGGTGGA AAGGGCTGAG AGCCTCTAGA CTGTGAACAA AAGTAGGCAC 213840
AGAAGAACAG TTGGAGATAA TAAGTAAACC ATCTTGACAG GAATGAAGAA TTTCTGAAA 213900
GGAAGGTCCC TGAGTTAGGT TGTGGATGC TTTCAGTAGT GAGTTATTGA AAGGTTTGG 213960
GGGGTGTGTG TGTGTGTGTG TATGTGCAGT ATGTGTGTGT 214000

//

FIG. 6.82

Amino acid sequence of FLAP (>alox5ap_protein translation NM_01629)
MDQETVGNVLLAIVTLISVVQNGFFAHKVEHESRTQN
GRSFQRTGTLAFERVYTANQNCVDA YPTFLAVLWSAGL
LCSQVPAAFAGLMYLFVRQKYFVGYLGERTQSTPGYIFGK
RIILFLFLMSVAGIFNYYLIFFFGSDFENYIKTISTTISPLLLIP
(SEQ ID NO: 2)

MRNA of FLAP (NM_001629_mRNA)

Acttccccctctgtacagggcaggttgtagcagctggaggcagagcagtcctctctggggagcctgaagcaaacatgga
tcaagaaactgtaggcaatgttgctctgtggccatcgtcaccctcatcagcgtggtccagaatggattcttggccataaag
tggagcacgaaagcaggaccagaatgggaggagcttcagaggaccggaacacttgcctttgagcgggtctacactg
ccaaccagaactgttagatgcgtacccacttctcgtgtgtctctggtctgcggggctactttgcagccaagttcctgct
gcgtttgctggactgatgtactgtttgtgaggcaaaagtactttgtcggttacctaggagagagaacgcagagcaccctg
gctacatatttggaaacgcatactcttctcgttctcatgtccgttgcgtgcatattcaactattacctcatcttcttttcgg
aagtgactttgaaaactacataaagacgatctccaccacctctccctctacttctcattccctaactctctgctgaatatgg
ggttggtgttctcatctaatcaatacctacaagtcataatcagctcttgagagcattctgctctctttagatggctgtaaat
ctattggccatctgggcttcacagcttgagttaacctgtcttccgggaacaaaatgatgtcatgtcagctccgccccttgaa
catgaccgtggcccaaatgtgctattcccatgcattttgttgtttcttacttatcctgttctctgaagatgtttgtgaccaagg
ttgtgtttcttaaaataaaatgcagagacatgtttt (SEQ ID NO: 3)

FIG. 7

SNP name SNP amplimers

SG13S421

GATTATATCCCACCTACCACTGCAGCTCCAGGATCCAGCTTCACAA
ACATTTGTTGAATGAATGAATAAGAAAAGAGGACACCCCCAAAGAGGCT
GCAAGGGAAAAAGCTACAAAGACAGAAGCACCAGGAAAAAGTAGGGTC
ATGTAAGTCAAAGCAGGAAAAAAGTTCCATGGTGGGGTGGTCAGCAGTGT
CTAAT[A/G]CCACGAAGGCACAAAGTAGGATAAAGGTTAAAAATCAGCCT
TTGGTTTTGGCAAATATGAAGCTTATCGGTAGCCTTAGCGAGAACAATTCC
ATCAGGGAGCAGAAGCTAACTGCAGTGGGTTGAGTCATCAAGCAGGCAT
AAGGAAGTAGGGATACCCATTATAAGCTACTCTTTCAAGAAGCTCAAAAT
CTGAAG

SG13S417

ACAAAAATTACCATCATATGCTGTCATGCATGTCTGCCAGTCTATTT
ATCATATTATTTAAGAAACAAACATTTATTGAAGATTTATCATGTGCTCAG
CACTGCCAAAGAGGAAATAAAGAGCATAATATCTATTCTTAGAAAAATAAC
ATTAACACAAATAGAAAACAAGAAACCATAATGTAAAAAATATTACATAG
[C/T]AACACAGAAAGACAATGTATAATTATACATACGCACTAAAGCAAAG
ATAACATAATTTATAAATTATGAGGTACAGAATAGTTAGATTCTGAAAAAT
TAAATAATCAGGAAAAACTTCATGAAGATGAGATCTGGGCTGGATCCCA
AAGGATAGGCAGGTGGATCATGTAGAACAGGGGAAAGGAGTTCCTGATC
GG

SG13S418

AACTAAAGAAAGCCACAAAAGTTCACCTCAATGCCAAGACATTTCT
TGATTTTTGAAAACCCAGTTGTGCGAACCACCCATCTATAGAACTTGAAA
GACTAAAAACTATCTTACTCTAAACATTTTCTAGGAAGTTGATTCTACAAC
ACATTTTGGTTTTTCCAATTTGGCTTCTAATAATTATTTCAAAGTTTCTGTG[
A/G]CCTAAATTTTGTTTTACATTGATCCTTTGAATGGACTACTGTTTCCACA
TTTTAGAACATTTAAAAAGATATCTACAACCCGAGTCTAATCATAAAAAA
AATCAGACAGATCCAAAATGTGGAACATTCCACTAAAAAAGGAGTGGGG
AGAGGTCTTTATTCTTCCAAAAATATCAATGCCATAAAAGACAAAGACG
SG13S44

ACCCTTCAACCCCAGCCCAGCTGCTAACTGACTACAGCCACATGAA
CAGAACCAGGTGAGACCAGAGGAACTTCCAGTCACCTACCAGATCATGA
CAAATAATAAACGATGTTTTTTAAACCACAAAGATTTGGAGCAGCATTG
TTACACAAAATTAGACAACCTATTACAGTTCGACTAAAAACATGTTCAATTA
C[A/G]ATACTAAATTAGAAGTGTAAGAATGGGAGAAAAAAGTTCATACTTTA
AAAGTCATTTTTTCTTCCAAAAAAGTTCCTTGAATAAAGTTCATTTTAT
AATGCATAAAAAATTAATAAACCTTAGAATTTATATGAGTAGCATAGCCA
GCTGGCTTTATTATCTGTTGTACTCAACACTTCAATAATCACTGATGTTT
SG13S45

ATGACCTTACCTCGTTTTGTTTTCTTGTCTGAGAGAAACACATTAG
CAGTCTCCCATCTTGTTTTTCTTTTCTTGTACCCAGGACAGAGGGCAGT
GGTGTGATCACAGCTCTGCAGCAGGACTTCCCCAGGTTTCAAGGTGATCCTCC
CACCTCAGCCTCCCAAGGAGCTGGGACCACAGGCACATGCCACCACGTC[
C/G]AGCTTAATTTTGTATTTTTTTGGTAGAGATCAGGTTTTGCCTTATTGCC
CCAAGCTGATCTTGAATTCCTGGGCTGAAGCAATCTGCCTGCCCTGGCCTC
TCCAAGTGTTAGGATTACAGGTATAAGCCACCGTGCAGCCTTATATTTTGT
TTAAATTTTCTCTGTATTTTCTCTGCGCAAATTGTTTAGGGA

FIG. 8.1

SG13S46

TTTTTTGGTAGAGATCAGGTTTTGCCTTATTGCCCCAAGCTGATCTT
GAATTCCTGGGCTGAAGCAATCTGCCTGCCCTGGCCTCTCCAAGTGTTAGG
ATTACAGGTATAAGCCACCGTGCAGCCTTATATTTTGTTTTAAATTTTCCTC
TGTATTTTTCTCTCTGGCAAATTGTTTAGGGAGTTTCTTTAGTTTATC[A/G]
GACTAAATTTCAAGGCTTTCCTTCCAATTTTGACATGTAAACAGTCCCTCA
TTTCTGCTTATCTAGTGATTATCCCAAATCTGTGTTTACAGTCTAGCTGTC
TCTCCTGAGATTAAGACTTGTTTCTCTAACTACCTGACGGCAGAATCTCCT
CTTGGAAGTATCAAGGAGGCAGTTCAAACTGAACTGGGCATT

SG13S50

GCTGATCTTGAATTCCTGGGCTGAAGCAATCTGCCTGCCCTGGCCT
CTCCAAGTGTTAGGATTACAGGTATAAGCCACCGTGCAGCCTTATATTTTG
TTTTAAATTTTCCTCTGTATTTTCTCTCTGGCAAATTGTTTAGGGAGTTTC
TTTAGTTTATCAGACTAAATTTCAAGGCTTTCCTTCCAATTTTGACATG[C/T
]AAACAGTCCCTCATTTCTGCTTATCTAGTGATTATCCCAAATCTGTGTTT
ACAGTCTAGCTGTCTCTCCTGAGATTAAGACTTGTTTCTCTAACTACCTGA
CGGCAGAATCTCCTCTTGGAAGTATCAAGGAGGCAGTTCAAACTGAACT
GGGCATTGGCTCCACTCCTTCTCCTTCTCTTTACTATTAATACCC

SG13S52

TAAGTCTTATTTAGGCATCGTTTCTTCTGGGAGACCTTTGTAGAATC
TCTGAGGTTATGTAAACATGCTAAGGTTTTCTTGACATTCTCAGATTGGGT
TAGGTGAACTTTGTAGCAACTTATCTTTTACTAAAAAGTCATCCCTCAGTA
TCTGTGGGGAATTGGTTCTAGGACTCCCTAAGGATATCAAAATCTGCAT[A/
G]AGCAGCCCAGGTGAGACCAGCAGAAGCACTTTACAGTCACCTACAGGA
TCATGACAAATAATAAATCATGTTTAAAGCCACAAAGTCCTTTACATAAAA
TGGTATAGTATTTGCATATAACCTACACATCTTCCTGTATCCTTTAAATCAT
CTCTAGTTTATAATACCTCATACGATGAAAATACTACGTAAATAGTT

SG13S53

AAGCAGTTCCTAATTACTGGACATTCTCAGATCTGCTAGAGCTACA
TGTCCAATTACGAGAATATACTGGAAAAAGCCCTGGATTAGAAATGAGAG
GATGTAGGTTTTAGTACCAGGTCAGCCACCTTGTTAATGCAAATTTGAGTA
AATTGTTACTTCTTTTAGGCCTTGTTTTTGCTGTTTTGTTTTCTGACAGT[A/
C]TGGTCTCTGTGGTCCAGGCTGGAGTGCAGAGGCACAATATCAGGTCCCT
GCAGTCTCTACCTCCCAGGATCAAGCCATTTTCATGCCTCATCCTCCTGAG
TAGCTGGGATTACAGGCATGTGCCACCACACCCTCGAACTCCTGACCTCA
AGTGATCTGCTTGCTCAGCCTCCCAAAGTGCTGGGATTAGAGGTGT

SG13S55

GAATATACTGGAAAAAGCCCTGGATTAGAAATGAGAGGATGTAGG
TTTTAGTACCAGGTCAGCCACCTTGTTAATGCAAATTTGAGTAAATTGTTA
CTTCTTTTAGGCCTTGTTTTTGCTGTTTTGTTTTCTGACAGTATGGTCTCTG
TGGTCCAGGCTGGAGTGCAGAGGCACAATATCAGGTCCCTGCAGTCTCT[A/
G]CCTCCCAGGATCAAGCCATTTTCATGCCTCATCCTCCTGAGTAGCTGGG
ATTACAGGCATGTGCCACCACACCCTCGAACTCCTGACCTCAAGTGATCT
GCTTGCTCAGCCTCCCAAAGTGCTGGGATTAGAGGTGTGAGCCACTGTG
CCTAGCCTTACACATTGTTTTCTTACTGGTAAAGTGGAATATCTAGA

SG13S56

GTTTTGTTTTCTGACAGTATGGTCTCTGTGGTCCAGGCTGGAGTGC
AGAGGCACAATATCAGGTCCCTGCAGTCTCTACCTCCCAGGATCAAGCCA
TTTTCATGCCTCATCCTCCTGAGTAGCTGGGATTACAGGCATGTGCCACCA
CACCTCGAACTCCTGACCTCAAGTGATCTGCTTGCTCAGCCTCCCAA[

FIG. 8.2

G/T]TGCTGGGATTAGAGGTGTGAGCCACTGTGCCTAGCCTTACACATTGTT
TTCTTACTGGTAAAGTGGGAATATCTAGAAGTTGCATGCTACATAAATTCA
ACCATATATTATTGGCAAAAAATTTTAAAGAAAAACATCAGCTTAAGAGT
ACTAATTGAGTACATGCCTTGGAATGAGCATGAGCTGGAAAGAACAAA
SG13S57

GGCAAAAAATTTTAAAGAAAAACATCAGCTTAAGAGTACTAATTG
AGTACATGCCTTGGAATGAGCATGAGCTGGAAAGAACAAACCTGTTGTTA
CATCACTCATTGCTGTTTTTCATATGCTGCTCATTGTAAATCTTGCTCAGTGG
CATGATTTTAGTGTTTAAAGATTTATTTGTTTGTGTTTAGGACAAAGTC[
C/T]CTACACATAATCTACTTGCTTCATATATACATACTTATGCATATTATGT
ATGTACATACATGCTCTCAGGGCTCACATGAAAAAACAGCCATTCAGGTG
ATGTGATTTATCTCATATGCTTACTTTAGAGTCAACAGGGTGTGACTCCA
CTATACAATACTGGCATGGAGAACACATAAGTCAAAGTAGACAGGAC
SG13S58

TTTATTTGTTTGTGTTTGTGTTTAGGACAAAGTCTCTACACATAATCTACT
TGCTTCATATATACATACTTATGCATATTATGTATGTACATACATGCTCTC
AGGGCTCACATGAAAAAACAGCCATTCAGGTGATGTGATTTATCTCATAT
GCTTACTTTAGAGTCAACAGGGTGTGACTCCACTATACAATACTGGCAT[
A/G]GAGAACACATAAGTCAAAGTAGACAGGACCCAGCCGTACCATTGGCT
AGGGCACAAATATATTCACATATGTGGAGAATGATGTACGTAGAAAGGTC
TTCATTGCACAATGCTCTTTAATAAAGATCTGGAAAAAAAAAACACCTAA
ATGTTCAAAGGATAGGGTAGATGAAATAATGGTACATTATAAAATGGAA
SG13S59

TCTGTCACCCAGGCTGGAGTGCAGTGGCATGATCATGTCTCCTTGC
AGCCTTGACTTCCCTGGCTCAGGTGGGCCTCCCACCTCAGTCTCCCAAGTA
GCTGGAACCTACAGTCGTGCACCACCATAGCCAGCTAAGATAGTGAGATGG
TGGCCCCACTGTCTTGCCCAGGCTGGACTCGATTTCCTGGGTGCAAGCACC
[C/G]TTCCCGCCTCAGCCTCCCAAAGTGCTGGGATTACAGGCATGAGTCAC
CATTCCAGCCTACTTGTCTTTAATTCTTAAAAATATTAATGTTGAGTTTTGT
CTCCCAGCATGTGGGAAAGATGTCATCCATTGCTTCTGTTTCTTGAGGCC
TGGGAGCAAGGAGCCAGGAACAGTATCACGAAGCTTGAGATAATAC
SG13S60

ATCATTGATGGGCATTTGGGTGGTTCCAAGTCTTTGCTATTGTGAT
TTTTTTTTTTTTTTTTTTTTTTTAAAGACAGAGCCTCACTCTGTTGCCCAGGC
TGGAGTGCGATGGCATGATCTCAGCTCACTGCAACCTCCGCCTCTCAGGTT
CAAGCAATTCTTCTGCCTCAGCCTCCCAAGTAGCTGGGACTACAGGC[A/G]
CCCACCACCAGGCCAGCTAATTTTTGTATTTTATAGTAGAGACAGGGTTTC
ACCATGTTGGTCAGGCTGGTCTTGAACCTCAGACCTCATGATCTGCCTGCC
TTGGCCTCCCAAAGTGCTGAAATTACAGGTGTGAGCCACCATACTGGCC
TAGGCAGTCTTTTTCAAACCTCTAAGACTGTGCTTGTGTCTCAGG
SG13S419

TGGTATGAGGTAAGGATCCATTTTTTTTCCCATTTGCATAGCCAGTTT
TTGTAGCTCCACTTTATTTTCTCACTTGATCTGCCATGCCACCTCTAGCATG
TATCAACATATCATGTATGTGTGCAGCTGTTTCTTAACCTCTCAATTTTATTC
TCTTGGTTACTTTGTCTAACCCAGCACTCATACTTTTTAAATTATTA[C/T]G
GCTACCTTGTAGGGCAAGAATCCTCACTTTTATTCAACTTCTTTTGAAGTG
TCTTGATGCATATTTTTTCTGATCTTACTTGGCCATATATATTTTGGGGACA
GATGTGACATCATACCAAGCTTTCTTTGCTTGACATTGTAGATATTTTCTTA
TTCATTAATGTGCTAAAAATTTGAGTTTGGTCATACAGTC

FIG. 8.3

SG13S61

GTTTCTAACATTATAGACACTAGTTTTAGGCTCTTGGAGGCTAGCA
GCAATTCTCAGAGGTAATGCAAGCTTCCCCATTTCTTCCCGTAGTCCTGTG
AAAGACCAGCCACCTCCAGAAGCCTACACATGAGTCTTCTCAGCCATACT
TTCTGCTTTTCTAATGCCTCTCAGCAGCGTATTAGAAAGGCCATGATCGA
[C/T]GTACCTGTTACCTTCAGGCTTTGCATAAGGTGTATATGAAACATAAT
GAATTTTCGTGTTTAGGCTCAGGTCCCATCCCCAGGTTACCTCTTTATCTTG
GAGACACTTCTGGTCCCATAACATTTAGATAAGAGATATTCAACCTGTACC
CACCACGTAAGGAGAGGAATAGGTTTTAGAAAGAGGAGTCAGGGAGGCA

SG13S62

GCATCTATTAAAAGTGATGGTTTTAGTATCCTGTCTCATTTTTTCT
TTCCTTACATCATGTATTATAGGTAACACATGCGCATGTGTGTATTTCTC
TTTTAGACAAAGGATGAGATTACTACTGTTAGCTCAGTTTTTTTTTCCCTAC
TTAACATCTTTGCTTTTTATTTTTTAGACATATTTCTAAGACTATTAAA[C/T]A
TTAGACTTACGTAGCCCTTCTGTCATTGTGAAATACATAGTTTACTAACAG
CTACCATCAAGATAAAGCCTTTATTTAAATAATTAACTTCTTAGTGGA
GCTAAGTAAGCACAGTTTATGGATTTTGGGAATTTTGCCTTGCATTGTG
TGATATGGTAAAATATTGAGTTTGTTTTTCTCATAATGTTTAC

SG13S63

GATAACTCAATCCCCTTAAAGGGTGTATCAAGCCATTGATAAGGG
CTCACTTTGATATAACCATTTTCTGTTATTTAGACACTCTTTCACACTTCCT
ATTTTCCTCCTGGGGATGGTTTGAATGGATGACACAATACCATATTATAAA
AGCACTTTACAACTGTAACCTATGTTATAAATGTAAATTATTACCTTAA[A/
G]GTTTTACCCTGTTTCAGATTTGAGTGGAAGTAGTTCTTTACAATACAAA
ACAACTTATTTTAACTTTTTTGCATTTCAAAGAATGATCAATCCACTTCA
GGTGCAGCATGGTTTCCAACCCTGACAGCATGGAAGAATCATTATTTAG
CTTCTAAAAATGTGCAGGCTGTACCCTAGACCAGCCTTGGGGATTAG

SG13S64

TCCTCTCTCTCATTCTCTCTCTCTCTCTCTTTCTCTCTCTCCTTCTTTG
CTCCTTCATTCTCTCTCTCTCTCTTTTTTTTTTGGAGACAGCATCTCACTAT
ATTGCCAGGCTGTTCTCAAACCTCTGGGCTCAAGTGATCCTCCTGCCTCA
GCTTCCTGAGTAGCTAGGACTACAGGCACATGCTATGGCAATACT[A/G]TT
TTAAACATTGTTTTCAAGGCTCCCCAGGTGATTCCAGTGTGGGTCATGTGG
TAGAGAACCACTGACACAGGCAAACAAAGGATACATAAAGTTGTCTATTT
AATGGGTAGGTGCAGGTAGTAGATAAGAGTGTAGCCACATAAACCACAT
GCTTAGTGAACGGTTTTGTTTTGTGTGTATGTGAGGGATTAGCAT

SG13S65

TTCAGGTTCCATTTAGCACGACAGCAGGGAAGGGACTGTTGGCAG
AAAAAACTGGGGCAGTGGGATTAAAGACAGACCACACATTCCAAAAGG
CACCGTGGGAGGGTCAGGGGGCGAGGTAGGTCTAGGCTTCAGTGTCTG
GGAGACTCAGTCTTCACAGGGTGACAGCGATCAAGAGTGCAGCTTAGGCT
GGGT[A/G]CAGTGGCTCATGCCTGTAGTCCCAGCACTTTGGGAGGCCGAGA
CGGGAGGATTGCTTGAAGCCAGGAGTTTGAAGACCAGTCTGACCAACATGG
CAAAACCCCATCTCTACTAAAAATACAAAAATCAACTGGGCATGGTGGCG
TGTGCTGTAGTCCCAGCTACTTGAGAGGCTGAGGCAAGAGAATCACTTG
AACC

SG13S420

TAAATGATCATTATGTTTCATATTCACACATACAATAATGTACTCAA
GTTTATTGCTAAGGTAATTCAGAACTCCTTATTTTGAAGTGTGCATTTGA
TATACCTGTTTGGGAATAACTAGTTTCTTATCTTTGACAGAAAATAATTTT

FIG. 8.4

GTGTTTTGTTTTTACTAAAAAAGCATGGTGAAAAATGGCTCCATTTCTA[A
/T]GAGAGGTAACATAAATATCGCAATTTGCTGGGTGTCATTAAAGTAACT
CACAAGGGAAAAAATGCAAATTGGTATCTGCTGATGGAGTAAATCTCCGC
AGAAGTGATGACCCTGAAAGGATCAATATATTAAAGCCCCTCCCAGCTGG
TCATTCCAGATTGCAACAATAAAGCATTAAGTGTTAAAACCTCAAGGCA
SG13S66

CTCATCAAGCCCACCTTTATACTTCATTTCTCCAGACTTCATGTCCA
GACTGTGGGATGAACAAGTGTTATAAGGTTTTAGAGGCTCCTGTAGGAC
TAGATGGAAGGCAAAAAAAGGAAATAACCTTTAAGCATGCTCTCGATTCC
TTAAATCCCATCTGAAAGTCTTAAGGATGTCTTCTCAGTCATACTTATTTG[
A/G]CAATATTACCTAATTTTCTCCATTAGCCCAAGCTCAGGGGTCTTTCTT
CTTCCATATTACATGGGTGCAATGGTTTTCTGAAAGGAAAAACAGCATT
CTAGGGCAGTAACATTTAATTAATCACAGGTACTTATCAAACCTACAAAAC
AGGCATTCCAGGAAGTGGGTGTTTCTGTTTGTAATAATTACACTCTCGTG
SG13S67

TAGGACTAGATGGAAGGCAAAAAAAGGAAATAACCTTTAAGCATG
CTCTCGATTCTTAAATCCCATCTGAAAGTCTTAAGGATGTCTTCTCAGTC
ATACTTATTTGACAATATTACCTAATTTTCTCCATTAGCCCAAGCTCAGGG
GTCTTTCTTCTTCCATATTCACATGGGTGCAATGGTTTTCTGAAAGGAAAA[
C/T]AGCATTACTAGGGCAGTAACATTTAATTAATCACAGGTACTTATCAA
CTACAAAACAGGCATTCCAGGAAGTGGGTGTTTCTGTTTGTAATAATTACA
CTCTCGTGACATGCTCCCACTAAAATGTAAGTTCGCTGAGGATGGAGGTT
TTGGTCTCTTTGCTCTGTGCTGTAACCCCAACACTGCAGCAGGGCCTG
SG13S69

GCTGCATAGTCTCACTTAGGTGTGGAATCTAAAAAAGTCAAATTAA
AAAAAATGTCAAGCAGAGAATAGAATGGTAGTTGCCAGGGACTCTGGG
AAGTAGCAGGGGTGGGGGTGGAGGGGAGGGGATGGGCAGAAGTTGGTCA
AAAGGTACAAAGTTTCAGGTAGACAGGTGTAAGTTCTGGGGATCTATTGT
ACAG[A/C]GTGGTGACTGTAGTTAATACTGTATTGTGTACTTAAAAATTGC
TCACCAAAAAATGTTCTCACCAAAAAAATGATGTTTGATATGTAAACAG
TTTGATTTAATCATTTTGACGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
GTATACATCAAACATCACATTATATACCATATACAATTAATATATACAAT
T
SG13S70

GGGGTAAATGCTGACTGCCTGTTCTCTGGACAGGAATGGAGAAGA
TGGTGCTAGCAGGGTTGCTGTTTCATATGTAGACATTCATGCAGTCACTCTC
TTTTCAGCACACTTCTTACTTCTGCCCTGGGTTTCAAGTTGCTGACTCTGAGCC
CAGAAACCTTCTAGGGTTCTGTTAGGTAGATTGGCTTCCACCGTCTTTGC[
A/G]ACAACCACAGAAAAATTCTAGACTGTTTTCTCTTCGGGGCTTCATTAGTC
AACTTGCTTCAGTCTGTCTTGCATCTTCTAAATATTTATAGATCTCTCTCTT
TTGTTGGAGTGGCAGAAAAATGCTAGTTGACCACCCAATATTCAAATTATC
CTGCCTCCTTAATAACAGAATATCATTGGATGTGGTGGGTAAATAAT
SG13S71

ATGGAGAAGATGGTGCTAGCAGGGTTGCTGTTTCATATGTAGACATT
CATGCAGTCACTCTCTTTTCAGCACACTTCTTACTTCTGCCCTGGGTTTCAAGT
TGCTGACTCTGAGCCCAGAAACCTTCTAGGGTTCTGTTAGGTAGATTGGCT
TCCACCGTCTTTGCGACAACCACAGAAAAATTCTAGACTGTTTTCTCTTC[A/
G]GGCTTCATTAGTCAACTTGCTTCAGTCTGTCTTGCATCTTCTAAATATTT
ATAGATCTCTCTCTTTTGTGGAGTGGCAGAAAAATGCTAGTTGACCACCCA

FIG. 8.5

ATATTCAAATTATCCTGCCTCCTTAATAACAGAATATCATTGGATGTGGTG
GGTAAATAATATACCCTAACTTTCCTTGCAGAGAGGGGTGGCCAA
SG13S72

CAGGGTTGCTGTTTCATATGTAGACATTCATGCAGTCACTCTCTTTTC
AGCACACTTCTTACTTCTGCCCTGGGTTTCAGTTGCTGACTCTGAGCCCAGA
AACCTTCTAGGGTTCTGTTAGGTAGATTGGCTTCCACCGTCTTTGCGACAA
CCACAGAAAATTCTAGACTGTTTTCTCTTCGGGCTTCATTAGTCAACTT[G/
T]CTTCAGTCTGTCTTGCATCTTCTAAATATTTATAGATCTCTCTCTTTTGT
GGAGTGGCAGAAAATGCTAGTTGACCACCCAATATTCAAATTATCCTGCC
TCCTTAATAACAGAATATCATTGGATGTGGTGGGTAAATAATATACCCTA
ACTTTCCTTGCAGAGAGGGGTGGCCAATGAGATGGAAATGAAAGTC
SG13S73

TGGGATTGAGTTCTTGATTGATTTTGAGCTTGGCCATCATTGGTGT
ATAGCAGTGCTAGTGATTTGTGTACATTGATTTTGTAACCTAACACTACTA
AATTCATTATCAAATCTGGGAGATTTTTGAGGATTCCTTAGGATTTTCTA
GGTATGAGATCATATCATTGGTAGAGGTAGTTTGAGTTTCTCTTTTCCA[A/
G]TTTGGATGCCCTTTATTTCTTTCTCTTGCTGATTGCTCTGACTAGGGCTT
CTAGTACTATGTTGAATAGAAATGGTGAAAAGTGGGCATCCTTGTCTCATT
CTAATTTTTAGGGGGAAATGCTTTCAACTTTTCCCATTCATTTTGATGTTG
GCTGTGAGTTTGTTCATAGATGATTCTTACTATTTTGAGATATA
SG13S99

TCTTTTGCCCTGCCTTTCTGCCTTTCTGTCCTTTTAATTTGCGGGCTT
TTGGCAACCACAGCACGGGTCTGGTTTCCTAGGAGTTTCTTTGTAGGATC
AAACCGCTAGTTGGCTCTTGGCCCTGTGATAGGGCCCTGGGCTAACTTATT
GGGAAAATGTTGCTGTAACCCCTGCCCAGAGGTGCCTGTGACATGGGC[C/
T]GCCATCTTCTCCTCTTCCCTTGGCTTCAGCCCCACCTAGAAACCTGAACA
AACATTTTCTTGTACATTTTATAAAGTGTGAGTGGCTCCTCATTAGCAAA
ATACATCCCAGGGAAGTTCAAAAGTGAAAAAAGGCCGTAACTTCTTCTC
TTCTCAGGGACCTACAGAAAATATGTGGCACCTCGGCAGCCTGGCC
SG13S382

CATGGATTTTGTTTTCCAAGTGGCAAGATGGCGCCTCCACCTTTGGT
ATCCTATTTTAGTTTCTGGCAGAAAGAAAGGAACAGGCTAATGGCCCTGA
TGAGTCTACCCCTTTTAACAGGAGAAAATTTAAAAAACAAAAACCATGA
AACCTTTTCCCAGAGGCAACAACCAGAATTCCATTTATCTTTATTGACCA
[A/G]AACAGACCACATGGTCACTGGTGGTGGCAATGGAGACTGGGGAGAT
GAATATTTTAAAGGTGGCATATTCCAGAAGAACAAGTGTGCACTGATTGCAT
TAATGAACCCATTAATGTGCCAAGGGGAGGTTTACCTATGAGCATGGGCA
AATTAGAACCCACTCTTGGAGCTGCAGGTGAGCCAATCCACCTAAACAG
SG13S383

TGGTGGTGGCAATGGAGACTGGGGAGATGAATATTTTAAAGGTGGC
ATATTCCAGAAGAACAAGTGTGCACTGATTGCATTAATGAACCCATTAATG
TGCCAAGGGGAGGTTTACCTATGAGCATGGGCAAATTAGAACCCACTCTT
GGAGCTGCAGGTGAGCCAATCCACCTAAACAGTGTGGATGCTACAAGAT
GG[A/G]GAAGTAAATTGATTCTATTCCATACCCTAACCTCTCTCCAAGATG
TATTCTTAAATAGAAAGAGGGAAGACAGAAGAAAACATCCAGAATATATT
TTTATTGTCTTTTACTTCTTCAGTGCATTTTAGATCAGTGCTTCTCAATCTG
GCAAGGGGCATGCAGGAGGATGTGAGTTTTATCAGGAAAACCTACACAAC
C
SG13S384

TGAGCCAATCCACCTAAACAGTGTGGATGCTACAAGATGGGGAA

FIG. 8.6

GTAAATTGATTCTATTCCATACCCTAACCTCTCTCCAAGATGTATTCTTAA
AATAGAAGAGGGAAGACAGAAGAAAACATCCAGAATATATTTTATTGTC
TTTTACTTCTTCAGTGCATTTTAGATCAGTGCTTCTCAATCTGGCAAGGGG
C[A/G]TGCAGGAGGATGTGAGTTTTATCAGGAAAACCTACACAACCCCCCA
ACCACAATGCTACCCCCACTCCTGTGGACCTTCTTTAAGAGAGACTCACTA
TTATAGATGGAGTTGATACGATTTTAAGAGAGGGCCATATATTATTGCTTT
CTGTCTTGAAAACTTGTGATTTTTCTGTATTGTGCTACTGCCAAAGAGA
SG13S381

GGGTTGCAGTGAGCAGAGATCACACCATTGCACTCCAGCCTGGGTG
GCAGAGCGAGATTCTGTCTAAAAACAACACCGTATTTGGGGCATGCTGA
TACTAAAAAATTATTCAATTGTTTGTCTGAAATTAATAATTGAGGGG
CCTGTATTTTACTGGGCAACCCATTTGCAATATCAGCAACAATCTCTTATT[
C/G]AGACCACTGATTAAGTGTGCAAAATTTGAATCTCTGAACAGTACCTA
TGTCCTTGATATCTTAAATTAATGAGTGTCTTAGACACTCAAAGCAGGAGG
AAGCATTATGGCAGATGTTTGAGCCCCAGAGATGTCCATGAGCACAGCAT
AGAGCTCAGAGCCTTCTTTATTATTGCTTCACGACAGAGCAAAGGACT
SG13S366

CATTTGCAATATCAGCAACAATCTCTTATTCAGACCACTGATTAAG
TGTGCAAAATTTGAATCTCTGAACAGTACCTATGTCCTTGATATCTTAAAT
TAATGAGTGTCTTAGACACTCAAAGCAGGAGGAAGCATTATGGCAGATGT
TTGAGCCCCAGAGATGTCCATGAGCACAGCATAGAGCTCAGAGCCTTCTT
T[A/G]TTATTTGCTTCACGACAGAGCAAAGGACTGCAGCAGGTTGACTGAT
ATAAAAGTTTTACCATGTCTCACAGCAGGCCTTTGCTCAAGTTTCCAGTAA
GGATATTGTATCATTTCTTGCTGCAGTACTTGTAATCCACTTACACTGC
CTGCTGTTGAGTCATTTGTTTCGTCTTGAGTAGCATGTCATCCTTGTTT
SG13S385

TTGCAGTTCTCATTGCTGGGGAGTCTAAACTGGAATAAAACACCCA
CTATCTCCATCAGGCTTGCACTAGAGCCCAGCTCTAGCTGGAGAGAAAGA
AGCTAACCCGCACAGACACAGGACTGTAGGCAGGGAGCATCCGGGGGTA
TTTGGGTCCTGGCTCTGATGTGCCTAAGGCCAACTTCTCTCTGGCCATGCT
GG[C/T]GTGCATGAGCTCACTAATCTTCCCTTTTGCCTTCCATTTTCTCAA
TCCTGACTTAGCAAAGGTTGGGCAAAAGAGACTCTGTGTGAGTTCGAGCA
AAGCCTGAGATGCTGGATTTTCCAAGATACGAGAAGGGGCTGGGGGCTGG
GTGAACTGGTGGTGGAGGAGGGAAGGATTAATTTCCCAAGGAGGGGAAG
GG
SG13S386

GAGAAAGAAGCTAACCCGCACAGACACAGGACTGTAGGCAGGGA
GCATCCGGGGGTATTTGGGTCCTGGCTCTGATGTGCCTAAGGCCAACTTCT
CTCTGGCCATGCTGGCGTGATGAGCTCACTAATCTTCCCTTTTGCCTTCC
ATTTTCTCCAATCCTGACTTAGCAAAGGTTGGGCAAAAGAGACTCTGTGT
GA[A/G]TTCGAGCAAAGCCTGAGATGCTGGATTTTCCAAGATACGAGAAG
GGGCTGGGGGCTGGGTGAACTGGTGGTGGAGGAGGGAAGGATTAATTTCC
CAAGGAGGGGAAGGGGCCAGGACATCAGGCCCCGGGGACTTTGAAGAGA
GGGTCTGTTGGTAGGAGGTAGATCAAGTGGAGTGACACAAAGGTCAGGAA
AGAGG
SG13S1

CATGCCTCCTACAAATTTGACCTGGGCCAGGGCCATGTTTCGGTGG
TTTTTAAGAACCGAGGCTCCAGAAAGCAGTATTGGGCAGCTAGAGTGGCC
CCAGGATCTATATCAAACCTCTACCTGTTTCTGAACCAAATTTCTTCTAGAA
TTTTATTCCATAAATCTGAATTATGGTGTGCACTCCTAGCATACTAA[A]

FIG. 8.7

G/T]GAACTCTCTGCCTTGCATTAAATAACAGGAGTTACCCCTGGAGGTAA
CTCCTAGCCCTGGCTCTTTAGAGAACAGATGCCGAATAGGCATTAGGGGA
TGTGATGGATGTGCTAACTTTCAAAAAAAAAAAAAAAAAAAGGCCTGAG
CTGAGTGCTCAGAGATTCACAAAAGCTGACAGCATCTCTCTGTTCCATTG
SG13S2

CTTTGGAGCCTGGCAGCCTGGCTTTGAGAACCGGGCTTTAACTTGT
CACATGACTATGGCCAAGTTCCTGGGGCTCTCCAAGCTTCACTTCCTCTGT
AAAAAGGGCAATAATATAATACCTGTCTTATTGGGTTTTGTCCATGTTAGA
TGAGACATTGGGTACAAAGCACTTGGTCCCGTGCCTGGCACATTTACTGC[
A/G]CTTAATGTATGATAGTTTTCTTATTATTCTAATAAACAATATGGCTTTG
GGAGTATAGTTCTGCCACATTGCAGTGGCCAGAGTGAAGGTGGTGAAGTGC
CTTCTGGGGCCCTGGGAGTCAAGGTTATCCGCATGCCCTTTCTTGCTTGCT
CCTCAGTGTGGCTGCCTCTATGTCCACACCATGCAGATGCAACAGGT
SG13S367

ACATGATCATCCCCTTGGGCTTCTGGTTTTTTTTCTTTTCAGGACCTT
ATTTTCAGGCAAGTGGCCTTTGACCTCTAAGGCTGTCTTTCTAGCTACC
GAATCCAGCATTCAAAGTGATGGAAATATGTATATATAGTAATAGTAAAA
TATCAGCACTTAATGGCCTGATAAGAATGTCAGTCAATGCTGAGTTTGG[
A/G]CCAACATTTGCCTGCTCCTGCCATTGAGCCCGGGCTCCCCTCCAGAGC
TGAGCTGCTGCAAGGGATCTGAGTAACTAGGGCTGTGTCAGAGTGGCGAT
GACAGCCACCACATGCTAAGGAAGAGATCCCCAAGGACAAGGAGAATCC
CACGTGGAGCTACTTGCTTCTTTGTCAGTCTTGTTTTCTTATTTCAAA
SG13S388

CCGAATCCAGCATTCAAAGTGATGGAAATATGTATATATAGTAATA
GTAAAATATCAGCACTTAATGGCCTGATAAGAATGTCAGTCAATGCTGA
GTTTGGACCAACATTTGCCTGCTCCTGCCATTGAGCCCGGGCTCCCCTCCA
GAGCTGAGCTGCTGCAAGGGATCTGAGTAACTAGGGCTGTGTCAGAGTGG
C[A/G]ATGACAGCCACCACATGCTAAGGAAGAGATCCCCAAGGACAAGGA
GAATCCACGTGGAGCTACTTGCTTCTTTGTCAGTCTTGTTTTCTTATTTT
ACAACCTTCTAAAACACAATCTCTCAACCTCTATTGTTAGCTTGCATTTT
CAATCATGAGCACAGCTTTACCTGGCTCCATGCTTTGATTGACTCTACC
SG13S10

TCTTATTTCAACAACCTTCTAAAACACAATCTCTCAACCTCTATTGTT
AGCTTGCATTTTTCAATCATGAGCACAGCTTTACCTGGCTCCATGCTTTGA
TTGACTCTACCTGCCAACACTGCAACAACAGGGAAAGGGACACCGGCCTC
ATACCATTAGATGGTGTGTAGCCTGGGCATGAGGATAATTAAAAACTCCC[
A/T]AGGGGATTTTAACATGTAACACAGTTTGGAACCATTGATGTAAGAT
CTTCTTACTCAACATGTGCTCCAAGGAGCTGTTGTATCAGCTTATCAGAAA
TGTAGATCAGGCCGCACTTGGACCTGTAGAATCAGAATCTGCATTTTATCA
GATTCCGACATTATTTGTATGAACATTAGCTTTTGAGAAGTGTTGCTT
SG13S3

CTTTTGACACCAACTACAAGTCAAGGGGTTCCCCAAACCACCCTGA
GTTGTGATAATTCGCTGGGAGATCTGACAGAACTCACTGAAGGTTGTTAT
ACTCATGGTTGTGATCTCTTATAGGGAGGGAATACAGATTAAAATCAGCC
AAAGGAAGAAGCACACAGCACAGAGTCCAGGACAGTGCCTGACATGGAG
CCC[C/T]TACGGTCCTCTCCCGTGGAGTCACGGACAGCGCCACTCTCCTGG
CATTGATGTGTGACAACACACAGGGAGTGTTCCCCACCAGGGAAGCCTTG
GTGTCCAGGGTCTTTACTGTGGCTCTGTACATGAGCACAGCTGACTGCCC
ATGCGGCCGATCTGTTCCAGACTCTCCACCGCTACACATCACTCACAGTC
C

FIG. 8.8

SG13S368

GTGGCTCACAGAACTCAGGGAAACACAGCTACCAGTTTATTGCGA
AGGACATTTTAAAGGATAAAAGTAGGCAGATAAAGAGATGCATAGGGCG
AGGTGTGGAAAGGTCCCTAGTGCAGGAGCTTCTGTCCATGTGGAGCGGGG
GTGCACCACCCTCTCAGTACATGAATGAGTTCTCCTTCACCTGCCTATCAG
CCT[C/T]TACATGTTTACAGCTCCCCAACCCAGTCCTCTTGGGTTTTATGGAA
GCTTCAAGACACCCACATTCTTTCCCCAGAGTATAGGGCAAGACCTTCTCT
GGGGAGGGTTTTAAGACCCACAGTCAGAAAGGTGGGGTGGGGTCAAGAT
TAGAGTCCTGCCTTGACGGGCAGGTGAAAGGGGTAGGGGGAGTAGGTGA
GAA

SG13S369

CGGGGGTGCACCACCCTCTCAGTACATGAATGAGTTCTCCTTCACC
TGCCTATCAGCCTCTACATGTTTACAGCTCCCCAACCCAGTCCTCTTGGGTTT
TTATGGAAGCTTCAAGACACCCACATTCTTTCCCCAGAGTATAGGGCAAG
ACCTTCTCTGGGGAGGGTTTTAAGACCCACAGTCAGAAAGGTGGGGTGGG
G[G/T]CAAGATTAGAGTCCTGCCTTGACGGGCAGGTGAAAGGGGTAGGGG
GAGTAGGTGAGAAAAATTCTGTTTATTTTTCTTTTTTTTTTGAGACGGAG
TTTCACTCTTGTTGCCAGGGTGGAGTGCAATGGCACAATCTCAGCTCACT
GCAACCTCCGCCTCCCAGGTTTAAGCGATTCTCCTGCCTCAGCCTCCCG
SG13S370

ATGAGTTCTCCTTCACCTGCCTATCAGCCTCTACATGTTTACAGTCCC
CAACCCAGTCCTCTTGGGTTTTTATGGAAGCTTCAAGACACCCACATTCTT
TCCCCAGAGTATAGGGCAAGACCTTCTCTGGGGAGGGTTTTAAGACCCAC
AGTCAGAAAGGTGGGGTGGGGTCAAGATTAGAGTCCTGCCTTGACGGGCA
[A/G]GTGAAAGGGGTAGGGGGAGTAGGTGAGAAAAATTCTGTTTATTTTT
CTTTTTTTTTTTGAGACGGAGTTTCACTCTTGTTGCCAGGGTGGAGTGCA
ATGGCACAATCTCAGCTCACTGCAACCTCCGCCTCCCAGGTTTAAGCGATT
CTCCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCGTGTGCCACC
SG13S4

TCTTCATTCCACAAAGCTCAGTGTCAAAACATGGGGTTTACACTGG
AAGCTGAGGTCACATCAGTAGCCGGGATCAGGGTCGCCCTAGCTGCCCAA
TGCAGCTCCCAGGCCTCCTGTAAAACCTTGACCTTTGAGGTCATGACAGCC
CTCTCCTGCTATGCTCATAGCTGACCACTGAACTCCTGGACACTCCCTCCC[
G/C]CAAGTTTACAGAGAATGTGGGCACATGCCTTACAGTCTTCCCTTGATC
CAAACACTGCCTTCATCTTGAGTGACAGCAGCATCTTTTGGATGTCTTGG
CCTGTCTAGCTTTATTTTTTTGTGTTCTGCCATCAAGTTGCTACTTCTGTTG
CCATCGTGCCTGTCAGCGCAGTGCAGGCTGTGGTGAAATCCCACGA
SG13S5

TATTTTTTTGTGTTCTGCCATCAAGTTGCTACTTCTGTTGCCATCGTG
CCTGTCAGCGCAGTGCAGGCTGTGGTGAAATCCCACGAACCTCAGGCATCA
CACTGACCGGGTCTGAGTCCTGTCTCAGTTGTCAGCTAGTTGTGCAATGAA
GGGAAAGGGACCTACACTTTCCAAGCCTCAATTCATCTATGGCAT[G
/T]GTGACAATAATGGAGGTTGATTTAAAGTCCTTTGTAAGAATTAAGAGTT
ATAATAGACATAAAGTGCTGTATCTGGTATACCTAGAAAACATTCCATAA
AAGTTAGTAATTGTTGGTCATGTAATGATGACTCTCTAGGCTAGGATTTC
GCTTCATTGCATGCACATGGTGCACCTCACAGGGCGTGACCTCTCTCT
SG13S389

GGTATACCTAGAAAACATTCCATAAAAGTTAGTAATTGTTGGTCAT
GTAATGATGACTCTCTAGGCTAGGATTTACAGCTTCATTGCATGCACATGGT
GCACTCACAGGGCGTGACCTCTCTGTCTCAGTAACCTCATCTGAGGACC

FIG. 8.9

GGGATAATCATACCGCTTCAAAGGGATGTCATAAAGATTAAATAATATGT[
A/G]TAAGGCTGCTTGCATTTAGCTGCATTCAACAAATATTTCTGTATCTTT
CTCCTCATTTCTCCTTACTTTCTTGCTTATTATCTGCTCTAGGTATAGATTTC
AGAGAACTAAGCTTGTTACAATCCTTCATAAAATAACCAGGTTGGTTAGG
GCATTTCCAAGAGTCAATACTGTTTAGTGACTATTCTCTGTTTAAT
SG13S90

AAGGCTGCTTGCATTTAGCTGCATTCAACAAATATTTCTGTATCTTT
CTCCTCATTTCTCCTTACTTTCTTGCTTATTATCTGCTCTAGGTATAGATTTC
AGAGAACTAAGCTTGTTACAATCCTTCATAAAATAACCAGGTTGGTTAGG
GCATTTCCAAGAGTCAATACTGTTTAGTGACTATTCTCTGTTTAATCT[A/C]
TTTTGATTGTCCAGGGTCATCTTTTGCTATGTCATAGGTTGTTGGCTTCTTC
TAGAGAAGTGAGACGATGGACAAGTTCCAAGTGAGTGAGGCGACTGGTC
AGGATATTCCGCTGAAAACTCATGTCAGTTCTAATTCGTGATTGTAATTC
AATCACAGCCTGAGAACAGTAGGACTGTAGTTCAAATGCTCTGTT
SG13S390

CCTGGGTTCAAGCAATTCTCCTGCCTCAGCCTCCCAAGTAGCTGGG
ACTACAGGCACATGCCACCACGCCAGATAATTTTCGTATTTTLAGTAGAG
ACGGGGTTTCCCTTGTTGGCCAGGGTGGTCTTGATCTCTTGACCTCATGA
TCCGCCCACCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACC[
A/G]CGCCCGGCCTCTAGAGGATAATTTTAAATGTGCTTTTGCATTTGGAA
AATGTGATTGGCATTTTTTTCTAATTTTCTAATATGATACGCTGTCGGATGC
TATGGATTACTTAAACCCTCTGGCTACCTAGAAAGATCTTTAAGTGGTTCT
CAACAAGCTTCATACGCAATGTAAATTGTATTATCTCTCAGGATGT
SG13S6

TGTGATTGGCATTTTTTTCTAATTTTCTAATATGATACGCTGTCCGA
TGCTATGGATTACTTAAACCCTCTGGCTACCTAGAAAGATCTTTAAGTGGT
TCTCAACAAGCTTCATACGCAATGTAAATTGTATTATCTCTCAGGATGTGT
GAGAACATCTGTTTTTCTTCTAATGCAGTAAACATATAAGGGTCTCTTG[A/
G]GATATCTTTTAAATAGACTTAATACAACATTCAGGAATGATAACAAAAT
ATAATCACAGTTGTAAGGGAATGTGAGCATTTTCATATTAATAACATTGGA
ACCTTATGTTAATACAGTGTTAAAAGTTGACAAACATGTAGGAGTCAGA
AAATTCAATTAAATATATCACAGTAATATGAATTTAGCCACATCCTGT
SG13S391

ACTTAAACCCTCTGGCTACCTAGAAAGATCTTTAAGTGGTTCTCAA
CAAGCTTCATACGCAATGTAAAATTGTATTATCTCTCAGGATGTGTGAGAAC
ATCTGTTTTTCTTCTAATGCAGTAAACATATAAGGGTCTCTTGGGATATCT
TTTAAATAGACTTAATACAACATTCAGGAATGATAACAAAATATAATCAC[
A/G]GTTGTAAGGGAATGTGAGCATTTTCATATTAATAACATTGGAACCTTAT
GTTAATACAGTGTTAAAAGTTGACAAACATGTAGGAGTCAGAAAATTCA
ATTAAAATTATCACAGTAATATGAATTTAGCCACATCCTGTGTTAGTTATG
AAATCCATTTAACACCACAAACAGTAATATTTTATAGCCAGTTTATTCA
SG13S392

CATTTAACACCACAAACAGTAATATTTTATAGCCAGTTTATTCAAAA
GGAAAACAGGAACTAAACCACTTTCATGCAATATATACTCTGTAAATGTG
GTCAGGCTAATTTTGCTGGGGGAAGGAACTTAACTTTTGAATATTTGAATG
CCCAGTCATTTAATCTGAATATCCTATTTTCTTGCATGTTGCAAAAATTTTT[
G/T]TCAATAAAAGGCAGAAAAAGAAATCTCTTCTCCATGCTCATCCCTAA
GAGAATGGGTTGTCTGTACCCTGAGAGCATTTTATGGAGGGGACAACCAC
TTTTCTAATTTTCTTCCCACTTCTCTGTGGGCACAAATGCTCTTTGGTTGA
AAGAGTTGTAATTCAGTCCCAAGATGAGGTGTGGTTACTGCATCCCTA

FIG. 8.10

SG13S371

TCAATCCATGCTCCACACTGCAGCCAGAGTGCTCTACAATGCAAAT
CCATTTGTGAGACTCCTCCTCTTAAATCCTCAAGTGGCTTCTCTTTGCCCC
CAGGATCATTTTGAACTCCTTAATGGAAGAGGCATGGCCCTTTGGGATG
TGGTTCCCCAACCCCTCCCACATCATCTTTCAATCAGATTTCCCACTAA[A
/G]TGGAAATTTTTTCAGGTCCTCAACTTTATGGTGACTTTCTCTTGCTCAGG
ATCTTTGAACATACTGTTTCTTCTTTCTTTGTATTTGCCAAGACAACACT
TCCTCTGGTAAGATTTTCCTGACATCCTCTATAAAAAAAGATTGAGATAGT
TGACTACCCAAAATGTTTCCCATTCATTCCAAGCTCTATTCAAG

SG13S372

AACACTTCCTCTGGTAAGATTTTCCTGACATCCTCTATAAAAAAAG
ATTGAGATAGTTGACTACCCAAAATGTTTCCCATTCATTCCAAGCTCTATT
CAAGGCAGTAAAGTGGCCGGCTGACAGATTGCATTCTCATCTTTTCTGAA
GCTAGCAATGGCCATGCAACAGCATTCTGGCCAATAAGATAGAAGTCGAA
[A/G]TTGAAGGGTGGGATTTCCAAGAAAGCTCGTTGAAGACATAATTCCTC
ATTTCACTTCTTACTCTTTCTCTTTCTGCTTCCTAAAAATGCGGTGCAGATG
GCAGACACTTCAAAGCTGTCTCAGGCAATCAGGTGATGTTAAGGCAGAAA
CCAGCTTTATGATGGGTAGAACAGGAAGAAAGAAGGCACCTATGTICT

SG13S393

CCTACAAATCTCATGTTGACATTTTATCCCTAATATTGGAGGCAGG
GCCTAGTAGGAGGTGTTTTGGTTCATAGTGATAAATGGCTTGGTGCCGTTCT
CACAGTAACGAGTGAGTTTTTATTCTAGTGGTTCCTGCAAGAACTGATTGT
TAAAGAGCTTGGATCCTTCCACCCCTCTCTCACTCTTGCTTCCTCTCTC[A/
T]CACCTTGTAATCTCTACAAGCTCTTCACCTCCCCTTCTCCTTTTGCCATA
AGTGGAAGATTTCTGAGGCCTCACCAGAAGCAGATGTTGGTTCCATGCTT
CTTGACAGCCTGCAGAACCATGAGCCAAATCAACTTCTTTTCTTTATAAT
TATCCAGTCTCAGGTATTCCTTTATAGCAACACAAATGGACTAAGA

SG13S373

GTTGTTTCCAGCTTTGAACTATTTTGAATCCTAAAAGACTGCCAGTT
TTGAATGAGACCCCAACAATGAATGTAGGCTCTGTATACAAGTTCAGG
CTGCTGGGCAACTTAGGCCTTAAGACACAACCTCTGCCACTTAGGCCTTAA
GACACAACCTGACATGATGGTGCTTAAAGTGGCTGTGATGGAAAAGGAGG
CT[A/G]TTTGGAGCCTTTGGAGTGCCTTTATAGGTGAACCCCAAGCATAGCA
CCTAATGATTTGGAGCAAAGCTGTGTCAATCCCCAAAGATAACTATTCGCC
TTTTGAGAAACATCTTCTAGCTACTATCAATAATAAACACAGAATGCATC
ACCATGGGCCACCGTGTGTCTTTTGACCTGAGTTTCCATTGTGAACAAGA

SG13S374

AACTCTGCCACTTAGGCCTTAAGACACAACCTGACATGATGGTGCTT
AAAGTGGCTGTGATGGAAAAGGAGGCTGTTTGGAGCCTTTGGAGTGCCTT
TATAGGTGAACCCCAAGCATAGCACCTAATGATTTGGAGCAAAGCTGTGTC
ATTCCCCAAAGATAACTATTCGCCTTTTGAGAAACATCTTCTAGCTACTAT
C[A/G]ATAATAAACACAGAATGCATCACCATGGGCCACCGTGTGTCTTTT
GACCTGAGTTTCCATTGTGAACAAGAGTCATTTGATCCAAGGCAGAAAGT
TGGGTGCACACAGCAGTGTTCATCATCAATGGAATATGAGATTGGGCC
CAAGTAGGTCCTGCAGACACAAATAAGTTGCAAGAGCAAGTAGTACAGG
CG

SG13S375

GAAAAGGAGGCTGTTTGGAGCCTTTGGAGTGCCTTTATAGGTGAAC
CCCAGCATAGCACCTAATGATTTGGAGCAAAGCTGTGTCAATCCCCAAAG
ATAACTATTCGCCTTTTGAGAAACATCTTCTAGCTACTATCAATAATAAAC

ACAGAATGCATCACCATGGGCCACCGTGTGTCTTTTGACCTGAGTTTCCA
[C/T]TGTGAACAAGAGTCATTTGATCCAAGGCAGAAAGTTGGGTGCACAC
AGCAGTGTTCATCATCAAATGGAATATGAGATTGGGCCAAGTAGGTCC
TGCAGACACAAATAAGTTGCAAGAGCAAGTAGTACAGGCGCTTGGCCTGG
CCAGTACTGTTGCCAAGTTGACTGCTTCCCCTCAGTCTGCATCTGTGGCTT
SG13S376

CCCCAAAGATAACTATTCGCCTTTTGAGAAACATCTTCTAGCTACT
ATCAATAATAAACACAGAATGCATCACCATGGGCCACCGTGTGTCTTT
GACCTGAGTTTCCATTGTGAACAAGAGTCATTTGATCCAAGGCAGAAAGT
TGGGTGCACACAGCAGTGTTCATCATCAAATGGAATATGAGATTGGGCC
CA[A/G]GTAGGTCTTGCAGACACAAATAAGTTGCAAGAGCAAGTAGTACA
GGCGCTTGGCCTGGCCAGTACTGTTGCCAAGTTGACTGCTTCCCCTCAGTC
TGCATCTGTGGCTTCATGGGGAGTTTCTATGACCACTTGATGGAGGAAA
AAACAAATTGGAGCATAGTTTATAGTGCTGGTACTACCCAAAGTGGCTAG
CT
SG13S394

GTCCGTGAGTTACAGATCTACACAAAATCACAGAGAGTGGTTAATC
GTTTAGTCTGATGGTCAGGGACTTCCAAGAGACATGATTAGAAAACCTGGT
GACAAGGAGTCCTGGGGAAGAGGCATATGGATACCTCTGAACACACACA
AAACATGAGAATATGTATCCCATATGAATGTAAACCAAGAGCAGCCACA
ACA[C/G]AAGAGGATTTTAAAATCAGCTGAATAAGATGATTCAATTCTGACA
GCATCAGCTAGTCTCTTTCCCCAGCCACTGTTGCCAGTGGGCTTACATAT
ATCATGGCCATGGGGGCAGGGCTATGTATGGACACAGCAACATGAATTT
CACTCATCAAGGCCAATTTGGCTCCAGCCATTGCTGAGTGCTCAGCCTGCC
A
SG13S25

ACATGATTAGAAAACCTGGTGACAAGGAGTCCTGGGGAAGAGGCAT
ATGGATACCTCTGAACACACACAAAACATGAGAATATGTATCCCATATGA
ATGTTAACCAAGAGCAGCCACAACAGAAGAGGATTTTAAAATCAGCTG
AATAAGATGATTCAATTCTGACAGCATCAGCTAGTCTCTTTCCCCAGCCACT
GTT[A/G]CCCAGTGGGCTTACATATATCATGGCCATGGGGGCAGGGCTATG
TATGGACACAGCAACATGAATTTCCACTCATCAAGGCCAATTTGGCTCCA
GCCATTGCTGAGTGCTCAGCCTGCCAAGATAGAAATCTACGCCAATATGG
CACCATTCCCTGGGCTAGAAAACCAACTGGTGGAAGGTTGATTACATTGG
ACC
SG13S395

GGGAATACAATGGTGGTTCCACTAAACTGACAGCTGAGTTTGCCAT
CTCCTCGTGCCAGTGAATACACAAGCAAGGAAGGGGGTTCTTTCTCACC
TAGGGTGACTGATCCTAATTACCAAGGAGAAATTGGACTGCCACTTCACA
ATGAGGGTGAGGAGTATGTACTCTATGTGTCTGTGATTAATGTCAATAGA
AA[A/G]TGACACCAACCTAGTACACAGAGGACTGATCATGGTCCAGGCCC
TTCAGGAATGAAGATTTGAGTCACCAGGCAAGGAACTTGGACTCACTGAG
GAGGGCATATTCCAAGGAGAATATTTTATCTATGTCCATCTATGTCCATCT
ATATTCCATCTGTGTTCCCCTTGAATTCCTATTCATGAACATGGGGAATT
C
SG13S396

TATAGAATGAGTAGTGGAAGGTAGTTATAAATGTAAGTCAAAAAC
CACACAACCAATTTGAGAAATGAGGAAGGTAATAGTGTTGAATATGTCTT
CTTTATCTTGATATAAATGTATTTGTGCATATATTAACCAGTTTATTTATTT
ATTATTATTTTTTGAGATGAGCTCTCGCCATGTTGCCAGGCTGGTCTTGA[

FIG. 8.12

A/C]CTCCTGGGCTCAACTGATTCTACCATTTAGTCCTCCGAGTAGCTGGGA
CTACAGGCATGCACCACCATACCCAGCTGACCAGTTTTTTCCTATTCCTCT
ACTTAATTTCTCTACTATAACAATAATATGTGTTAATGGTAGTTAACTTT
ATATCTCAGTATTAAGTCACAAGATATCAAAAAGGGAATGCGACTTA
SG13S397

ATGTCTTCTTTATCTTGATATAAATGTATTTGTGCATATATTAACCA
GTTTATTTATTTATTATTATTTTTTGAGATGAGCTCTCGCCATGTTGCCAG
GCTGGTCTTGAACCTCTGGGCTCAACTGATTCTACCATTTAGTCCTCCGAG
TAGCTGGGACTACAGGCATGCACCACCATACCCAGCTGACCAGTTTTT[C/T
]CCTATTCCTCTACTTAATTTCTCTACTATAACAATAATATGTGTTAATGG
TAGTTAACTTTATATCTCAGTATTAAGTCACAAGATATCAAAAAGGGAAT
GCGACTTAGTTACAAGCAGAATGAATATCACTCAAAGATGAATAAAGAG
AAGAGGGTTAGTGCATTTTCTGTTGGATGAGAGAAAGTTTCATTGTT
SG13S377

GCAGTGGCGTGATCCCAGCTCACTGCAATCTCTGCCTCCTGGGTTG
AAGTGATTCTCCTGCCTCAGCCTCCCGAGGGGCTGGGATTGTAGGCGTGC
ACCACTATGCCCATCTAATTTTTGTATTTTAGTAGAGATAGGGTTTTGCC
ATTTTGGCCAGACTGTCTTGAACCTCTGACCTCAGGTGATCTGCCTGCCTC[
A/G]GCCTCCACAGTTTTGTGATTATAGGCATGAGCCACCGTGCCCGGCCT
TAACCTTTGTTTTCTTACACAACACACTACGTGATGTTTTCCACATGCATG
GGTCATTTGCTTCATTTACGTACAAATGCATAAGCAATATACTGTGTGGTG
TGAGTTTGTGATGGGAAAAGGAAGAAGTTTTGCGGATACTACACTGG
SG13S189

GCCAGGCTGTTCTCCAACCTCTGGACTCAAGCCATCCTCTAGCCT
CGGCCTTCCAAAGTGCTGGGACTATAGGCGTGAGCCACGGTGCCAGGCCC
TTGACCACATTTTAAACCCCTCTGAACCTCAGTTTCACTTTCTGGGCAATG
GGAGGGGGGTAATTTGTCCCTCAGAGGGTTGCACTGAGGGGCAAATGTGA
G[C/G]CTCTGGGTACAATGCCCAGTACAGACTAGGTCCCCACGACACAGCC
GCTCAGCGGCTCCGGATTCTGGGCTGCTCTGGAAGTGCAGGCGGCGGTCT
TCTGCGGGAATCCGGGCAGGCAGGGCGGGCTGCGCTCCCTCCCGGCTC
TCCCGGTGCCCTTGTCTTTTTGTTCTGTCTCAGCAGCTCTCTATTAAGAT
SG13S100

TTTTGTTCTGTCTCAGCAGCTCTCTATTAAGATGAATGGCATTTCC
AAAGGCTTCACCTCTGATAAGTGTTCTCTGCAGCTGCAGCCAGAATCTTA
ATGTGCGCGCTGTAAATTAATGGCCGTCTCGGCTATTAACACGCTCTTCTC
GGGTGAAGTGGAAGTCCCTCCATCCCCGGGCCTCTGCACGTGCTCTGCGC[A/
G]CTGGCTGGGGGTGACTCCAAGGAGCTCAGAGCGGGGTGCCCGGCACCT
CTCGCCAGGCGCCTTTCGACCTTCTAAAGCGCGAATGGCTGGACTTTTCTC
CCATGTGTGGGGCCCCAGAAGGTGTGGGGCCCCAGAAGGTGTGGGGTCCC
TGCGTTCCACGGAGCCCGGAAGGTTTCCAGTGATGGTGGGGGCTGACC
SG13S398

GGAGCCCGGAAGGTTTCCAGTGATGGTGGGGGCTGACCACGTTGG
TCCCCGTGGGTGCTGTTTTTCATGTGCCGGCAGATTGGGATGAGTTTAAAAG
ACAGAAGCGTGATAGGATAGAGAACTTCTTTAAAAACTGGAAATTTTAAT
CTGGGGATTATAACTATTGGACAGTCAAGTGCAAGAGTGAATACACTTCT
CA[C/G]TCCCTCCTCCCAATTTTTATTTGCGGGATTAGTCAGTCCCCCTCTG
CCACATGATAATTGTGAGAACTACCAGGGTCTTCATTCTCCTGCCATCTGG
TTGACCTCTCCAAGAATGGACACCCGGGCAGCCTGGGCCAATGAGGCTGT
CCTAAGAGTTTAGATGAGAGAAGTCAGTCTTTGACAGGTGATGGAAGCTG

FIG. 8.13

SG13S94

CAGTGATGGTGGGGGCTGACCACGTTGGTCCCCGTGGGTGCTGTTT
TCATGTGCCGGCAGATTGGGATGAGTTTAAAAGACAGAAGCGTGTAGGAT
AGAGAACTTCTTTAAAACTGGAAATTTAATCTGGGGATTATAACTATT
GGACAGTCAAGTGCAAGAGTGAATACACTTCTCACTCCCTCCTCCCAATTT
[C/T]TATTTGCGGGATTAGTCAGTCCCCCTCTGCCACATGATAATTGTGAG
AACTACCAGGGTCTTCATTCTCCTGCCATCTGGTTGACCTCTCCAAGAATG
GACACCCGGGCAGCCTGGGCCAATGAGGCTGTCCTAAGAGTTTAGATGAG
AGAAGTCAGTCTTTGACAGGTGATGGAAGCTGTAAAATGTAAAACCTCCA
SG13S101

TAAGAGAAGCTGAGAGAGAGCGAGAGGAGAGATTGGAAGAAAGA
CAGAGACAGAGGTAGAGAGAAGGGAAAGAGAGAGAGAAAGGGACAGAA
GAGAGAGAAAAAAGAGGGGGCCGGGCGCGGTGGCTCACGCCTGTAATCT
CAGCACTTTGGGAGGCCGAGGCGGGCAGATCACGAGGTCAGGAGATCGA
GACCATCC[C/T]GGCTAACACGGTGAAACCCCCGTCTCTACTAAAAAATAT
AAAAAAAATTAGCCAGGCGTGGTGGTGGGTGCCTGTAGTCCCAGCTACTG
AGGAGGCTGAGACAGGAGAATGGCGTGAACCCGGGAGGCAGAGCTTGCA
GTGAGCTGAGATCGCGCCACTGCACTCCAGCCTGGGCAACAGAGCAAGAC
TCCGTCTCA

SG13S95

TCCACCAGCAGCTTTTCTGAGTCTCCAGCTTGCAGATGGCAAACCA
TGAAACTTCATGGTGTCCATGAGCATGTGAACCAATTTCTATTATAAATCT
GCAATATATATATATGAGGAGACTTATTTATATATTGGTTCAGTTTCTCTG
GAGAGCCTTGGCTAATATAAAGTCTATACTCTACAAAGTGCCCTAGGTAC[
G/T]CAGGGAGTACCCAAGTGTGTATGACCAGCCCGACAGCCCTGGCTGC
TGGCTTCCCCGCACACAACTCTGCACGCTGCCTTCATCAGCCTTTCTCTCT
CAGCTGAACCGAGGGCATTGAAGCGGGCCTCTGGCACTGTACCTATGAGG
GAGCAATATCTTCCCCTACACTGACCTCTTCCGTGCCGAGATGCAGCCC

SG13S102

GCCTCTGGCACTGTACCTATGAGGGAGCAATATCTTCCCCTACACT
GACCTCTTCCGTGCCGAGATGCAGCCCTCCCTGCTGCCACTAGTTACAGTG
GTCCATGTTCCCTTTCAAAGTGAAGTTTTGATAAAAGCACCTCTTAACCAA
TGCCAAATAGCTAAGTCTGGGACAAAGATTGCAGGTATTTTGCATTTTCC[
A/T]TGTAACCTCAGAGGGATTGCCATTACACTGATCTGAGCTGCAGAAT
ACCAGGCAGCCACCTCACCCACCCAGCAGGTCCACTCTTATACTTTCTCAG
AAAGCACAGCCACTCTACTCTTATTCAGTTGAAAAGAATTTCCAGGAAGG
TGTTTCTGCGATTGCCTCAGAAAAGTCAGTTCCCTTTGGGAATTTCCCT

SG13S103

TACTTTTCTCTGAAGAAATGGAGATATCAGCTGTCCCTCCCCACTG
CCATTTATTCCCTTCCTTCATTCAAACCTTATGTGGCTGCTACTTACCGTGTG
TTAAGTGTTCACTTTTTTTCTTGGAATTCAAAAAAAGAAGGACAGTATTTG
GGGCACAGATCTTTTGGTGTTCTATACATTTTTTTAAAGTTTCATTTTA[C/T]
ATTTGTGTGTGCGTGTGTGTGTGTGTGTGAGACAGTCTTGCTCTGTTGCC
AGGCTGGAGTGCAGTGGCATAATCATTGGCTCACTGTAGCCTCAAAGTCC
TGGGCCCAAGCAATCTTCCCACCTCAGCCACCCAAAATGCTGGGGTTACA
GGTTTATGCCACTCTGTCTGACCTGAAAGTTTGGGTTTACTTTCC

SG13S104

GCATAATCATTGGCTCACTGTAGCCTCAAAGTCCTGGGCCCAAGCA
ATCTTCCCACCTCAGCCACCCAAAATGCTGGGGTTACAGGTTTATGCCACT
CTGTCTGACCTGAAAGTTTTGGGTTTACTTTCCCTTCTTTCTTTGCTGAA

FIG. 8.14

GTCAGAGATGATGGCAGCTTCCAGATTCTCTGGTGCCTGTGCTGGGCTC[A/
G]TGCTGGTCATGGTCTTGGGTCCAGGATTCATTCTGGAGACTCTCAGGGA
AGTTTCCCATGACAAGGAAATGTAGGAGAGTGTGCTGGCTTTGCGTGCTC
CTCTGCCAAGCCCTGCTTCTCCTGGTGGGACACACTGAACCACAGCCAGG
GCATTTTGGTGGTTAGTTAAAAAAAAAAAAAAAAAAAAAAAAAAGGAAG
SG13S191

CTTCAGAAATTGTAATGATGAAAGAGTGCAAGCTCTCACTTCCCCT
TCCTGTACAGGGCAGGTTGTGCAGCTGGAGGCAGAGCAGTCCTCTCTGGG
GAGCCTGAAGCAAACATGGATCAAGAACTGTAGGCAATGTTGTCTGT
GGCCATCGTCACCCTCATCAGCGTGGTCCAGAATGGTAAGGAAAGCCCTT
CA[A/C]TCAGGGAAGAACAGAAGGGGAGATTTTCTTTGATGGTTGTTTGA
AGTCAGGCTTAAACAATTGTGTCTGTGTGTGCGCATGCACAAACACTTTTA
CCTTATCTTTATTTTCTTCTTTTATTTGAATGTATAGGGTTGTGTGATTTT
TGTGTAAATTTGGGGTTTTCTCTCTTAGTCTTTCACTTTTGTGGTG
SG13S105

TTTTCTAACATCTGCAGTGCAATTGAAGTTACCAGTCATCTGCAGTC
TAAAAAGAAAGTGATTTTGGGAGGTGCGTAGAAAAAATCATCTTATTATT
TTTCTCTATATTACTTTTTTCTTTTTTCTCCTGAAGAACTTTTTTTTTTG
GTGATACCTTCTTTTTCTCTAGCACGTATAATTTTGGAAGCATTTTTC[A/G]
TATGCAGTGTATACTTCAGAAAGAGAGAGAGAGAGAGAGGAAAATTGTCCTG
TTCAGCGTTTGCATTTCCATTATTCCTGCTATTAGTTAAAAACAACAACA
CAACAAAAACAAGCAGGATACCTAGATCTGGAAAAGGGAGAATTGTGT
AGAGCTGTCTTCCTAAAGTTCTGAGTTAGGGCTGCCTCAGACCACTT
SG13S106

TTTTGGAAGCATTTTTTCATATGCAGTGTATACTTCAGAAAGAGAGA
GAGAGAGAGGAAAATTGTCCTGTTGAGCGTTTGCATTTCCATTATTCCTGC
TATTAGTTAAAAACAACAACAACAACAAAAACAAGCAGGATACCTAGA
TCTGGAAAAGGGAGAATTGTGTAGAGCTGTCTTCCTAAAGTTCTGAGTTA
GG[A/G]CTGCCTCAGACCACTTTCATAACTATCTCCAGTGGCTTTGTGTTTT
ATATTTATTAAGATAGAGAAAAAAGAGTAATTACTAAGGGCAGCTGCTG
TAGCTTTATGGTGATTACTGAACATTGACATGCTGTACGTTTTTGAACT
TTGAGTATTTAATCACTTTGGGATATTCTATTTTCCCCCATCTTGAGTGT
SG13S107

GGAACCTTGAGTATTTAATCACTTTGGGATATTCTATTTTCCCCCAT
CTTGAGTGTGGACAGATGCTGGTGATGTAGCCTTCTGGGCACAGAGCAAG
CCTCCCCCTCAGCCTCTGCACCAGAAAGGCTCAGCTTCACACACTCCAAGT
ATGTTTTCTACAAGAACTACACTTTGTGGCTTTCTGACCCAAACATTTTT[A/
G]TACTAAATTACACACAACAAGTTGTAGCTCAGAGAGGGAACAAATGG
CTTATTTAGGCCACCATTTTCTTGAGCCATTATGATTTACACAGGGCTCC
CTTGGCCCTGTAAATTGGCAAGGATTCCATTATTCAACCCGCATACATGTA
CAGAGACCCTGCTCTGGCCCAGATAGTATTCTGGGTACAGGCGGATA
SG13S108

TGTGGACAGATGCTGGTGATGTAGCCTTCTGGGCACAGAGCAAGCC
TCCCCCTCAGCCTCTGCACCAGAAAGGCTCAGCTTCACACACTCCAAGTAT
GTTTTCTACAAGAACTACACTTTGTGGCTTTCTGACCCAAACATTTTTATA
CTAAATTACACACAACAAGTTGTAGCTCAGAGAGGGAACAAATGGCTTA
[C/T]TAGGCCACCATTTTCTTGAGCCATTATGATTTACACAGGGCTCCCT
TGGCCCTGTAAATTGGCAAGGATTCCATTATTCAACCCGCATACATGTACA
GAGACCCTGCTCTGGCCCAGATAGTATTCTGGGTACAGGCGGATAGAGCA
GGAAACAAAACAGCTACAGTGATGGACAGGTCAGCCTGCAGCAATGCC

FIG. 8.15

SG13S109

TTTTTATACTAAATTACACACAACAAAGTTGTAGCTCAGAGAGGGA
ACAAATGGCTTATTTAGGCCACCATTTTCTTGAGCCATTATGATTTACAC
AGGGCTCCCTTGGCCCTGTAAATTGGCAAGGATTCCATTATTCAACCCGCA
TACATGTACAGAGACCCTGCTCTGGCCCAGATAGTATTCTGGGTACAGGC[
A/G]GATAGAGCAGGAAACAAAACAGCTACAGTGATGGACAGGTCAGCCT
GCAGCAATGCCTGCAGTCTCTGCAAAGGTAGCTGTATGGGTGGGCAGGTG
GCTAGCACTTATTCAGCTCTGGAAGGATCTCCCCTCTGGCCTCTCCCCTGA
CACCCATCAATAAAACTGAGGAGCATCGGTGGACAGGGGACCTTGTGCCC
SG13S110

TTTCTTGAGCCATTATGATTTACACAGGGCTCCCTTGGCCCTGTA
AATTGGCAAGGATTCCATTATTC AACCCGCATACATGTACAGAGACCCTG
CTCTGGCCCAGATAGTATTCTGGGTACAGGCGGATAGAGCAGGAAACAAA
ACAGCTACAGTGATGGACAGGTCAGCCTGCAGCAATGCCTGCAGTCTCTG
C[A/G]AAGGTAGCTGTATGGGTGGGCAGGTGGCTAGCACTTATTCAGCTCT
GGAAGGATCTCCCCTCTGGCCTCTCCCCTGACACCCATCAATAAAACTGA
GGAGCATCGGTGGACAGGGGACCTTGTGCCCCCTCCCTGCCTGTGCAGTT
GGGGCTGAACCCAGCTACGAAGTTGAGCTCACTCTCTCCAGCTCCCTCTC
SG13S111

GACAGGTCAGCCTGCAGCAATGCCTGCAGTCTCTGCAAAGGTAGCT
GTATGGGTGGGCAGGTGGCTAGCACTTATTCAGCTCTGGAAGGATCTCCC
CTCTGGCCTCTCCCCTGACACCCATCAATAAAACTGAGGAGCATCGGTGG
ACAGGGGACCTTGTGCCCCCTCCCTGCCTGTGCAGTTGGGGCTGAACCCA
GC[C/T]ACGAAGTTTGAGCTCACTCTCTCCAGCTCCCTCTCAATTCAGAGCT
GAACTGTGGGAAGCTTCAGAGCTCTCTGTTTCAAGGACAGGTTCTCCTCAC
CTCTCCTAATGGAGGTGCACCAGGGAAGTGGCCCTGCTCTGCCCAGGGCT
TTCTCCTGGACTTTGCCATCATGGTCTAGCAAACCCTGTTCAGATTGAGG
SG13S112

CACTCTCTCCAGCTCCCTCTCAATTCAGAGCTGAACTGTGGGAAGC
TTCAGAGCTCTCTGTTTCAAGGACAGGTTCTCCTCACCTCTCCTAATGGAG
GTGCACCAGGGAAGTGGCCCTGCTCTGCCCAGGGCTTTCTCCTGGACTTTG
CCATCATGGTCTAGCAAACCCTGTTTCAGATTGAGGTGAGTGGTGAGATTT[
C/T]GAATTTCTTTTGGACAGATAGGATTAAGTCTTCTTCTGTGGGACAAGTG
GGAGGTAGAGGTAAGATTAAAGATGGCCAAATGTCTGAGTCCTGACAGCC
ACAATATGGAGATCTAGACTTTTTACAGACCACAGGGCACAGGGGCCTCA
CTAACAGAGTTCCCGGAAGTGATGAGTGTGCTGGGGGCTTCTTGTTGA
SG13S113

TAGGATTAAGTCTTCTTCTGTGGGACAAGTGGGAGGTAGAGGTAAG
ATTAAAGATGGCCAAATGTCTGAGTCCTGACAGCCACAATATGGAGATCT
AGACTTTTTACAGACCACAGGGCACAGGGGCCTCACTAACAGAGTTCCCG
GAAGTGATGAGTGTGCTGGGGGCTTCTTGTTGAAGAGACACTAGAATGG
AC[C/G]AGCTGGGAGCTAATTTTTTGGGCTGGAGTGTGATGGCCTGCACAT
CACTGCCTCTGTCCCTCCATTGTCACAGCTGCCCCTTAGGAGCCAGCTGAG
GCAATTTGTGGTCAGAGTGACTTTGCACAGTTGTCCTGCCTGTGTTTCAGGA
AGGGAGTTTCTGTGGTCCCTTTGAAACCACAGAAGAGCCCCCTCGTATAGC
SG13S114

AGTTGTCCTGCCTGTGTTTCAGGAAGGGAGTTTCTGTGGTCCCTTTGA
AACCACAGAAGAGCCCCTCGTATAGCTCTCAATGGAGGGGGCAAACATT
CAAATAACTCAGGAGATAACACAACCTATTTGTTTTTAAGTGTGAGTTTTTA
GGCAATCACAAAGATCCAGATGTATGTCCAAGCCTCTCTTTGCAATTCTA[

FIG. 8.16

A/T]TTAACCTCAATGTTGCAACCATAGACCTACCTTACAGAGTTCAAAAA
AATATGCAAAAACCCTGCCTTTCTTCTTCCTCATACCCCAAATGCCATT
TGAACATTTCTGTAGTTAAAAAAGATTTCCATGGTGTTACCAGGCACT
GTACACAGTCTGTGTCCCAAGACAAGGAGGTACAGTTCCACATGCGCC
SG13S115

AGGGGGCAAAACATTCAAATAACTCAGGAGATAACACAACCTATTT
GTTTTAACTGTGAGTTTTTAGGCAATCACAAAGATCCAGATGTATGTCCA
AGCCTCTCTTTGCAATTCTAATTAACCTCAATGTTGCAACCATAGACCTAC
CTTACAGAGTTCAAAAAAATATGCAAAAACCCTGCCTTTCTTCTTCCTCAT
[A/T]CCCCAAAATGCCATTCTGAACATTTCTGTAGTTAAAAAAGATTT
CCATGGTGTTACCAGGCACTGTACACAGTCTGTGTCCCAAGACAAGGAGG
TACAGTTCCACATGCGCCCATGACTGGGTTGGGCTCTGCACTCTCTCTATA
CTTTGAGAGCCTGATTTTCTGTGATTGGGCAGAGCTGGCCACCTGGTG
SG13S116

TCTGCACTCTCTCTATACTTTGAGAGCCTGATTTTCTGTGATTGGGC
AGAGCTGGCCACCTGGTGCAATGTCTCTCTGCCTTTCAAACATGTTTT
AGTCATCAAGATCTTCAAATTTGTAACCCTTTCCAGCTTGATCCAGCAGAA
TGCAGATTTGGAAAAACAGAACGAGTTTAAATACATGATTCTAAGAAA[
C/T]CTGGACCAGAACTATCAAACTTGGTTTCCCAGAGAATATAGCAAAT
GGGCTCATTGGCCAATACTATGACATTGGCTTTTGAGAAAAGAAAGGCTT
TATTGCAAGGCTGGCCAGCAAGGAGACAGGAGTTGGGCTCAAATCTGTCT
CCCCAGTTTGGGGCTTAGGGCAAGTTTAAATTACACAGACGCATTTCTTA
SG13S117

AACCCTTTCCAGCTTGATCCAGCAGAATGCAGATTTGGAAAAACAG
AACGAGTTTAAATACATGATTCTAAGAAACCTGGACCAGAACTATCAAA
ACTTGGTTTCCCAGAGAATATAGCAAATGGGCTCATTGGCCAATACTATG
ACATTGGCTTTTGAGAAAAGAAAGGCTTTATTGCAAGGCTGGCCAGCAAG
GA[A/G]ACAGGAGTTGGGCTCAAATCTGTCTCCCCAGTTTGGGGCTTAGGG
CAAGTTTAAATTACACAGACGCATTTCTTATGAGTAGCAGGCAGAGAGCC
TCCAACTTCTTCTGCCTAGGTACCAGCAGCTTAGACATGATGCAAACCTGG
GAAGCACATACTGTATTTGGAGAAAGTGATTGGGAAGAAATGTGAGCTGA
G

SG13S118

TACATGATTCTAAGAAACCTGGACCAGAACTATCAAACTTGGTTT
CCCAGAGAATATAGCAAATGGGCTCATTGGCCAATACTATGACATTGGCT
TTTGAGAAAAGAAAGGCTTTATTGCAAGGCTGGCCAGCAAGGAGACAGG
AGTTGGGCTCAAATCTGTCTCCCCAGTTTGGGGCTTAGGGCAAGTTTAAAT
TA[C/T]ACAGACGCATTTCTTATGAGTAGCAGGCAGAGAGCCTCCAACTTC
TTCTGCCTAGGTACCAGCAGCTTAGACATGATGCAAACCTGGGAAGCACA
TACTGTATTTGGAGAAAGTGATTGGGAAGAAATGTGAGCTGAGGGGAGG
GGCTCAGTGCCCCTGAGCTACACTTAGTGATGGCAGAGGAAGGATGTCCT
CCC

SG13S119

TGGGGCTTAGGGCAAGTTTTAATTACACAGACGCATTTCTTATGAG
TAGCAGGCAGAGAGCCTCCAACTTCTTCTGCCTAGGTACCAGCAGCTTAG
ACATGATGCAAACCTGGGAAGCACATACTGTATTTGGAGAAAGTGATTGG
GAAGAAATGTGAGCTGAGGGGAGGGGCTCAGTGCCCCTGAGCTACACTTA
GT[A/G]ATGGCAGAGGAAGGATGTCCTCCCGCAGGAGGCTGTTCCACATCT
GCTCTGGTTGTAGGGGGAGCTGGCAGGCATTAGCAGCGGCCTCTTTCCCC
CAAGAGAGGCAGCCTCCTCCAAGTTTTGGCGACATTATGGCCCTGCAATC

FIG. 8.17

ATAAGGGTTTGTGAGCATAGTGCTAAGGAGGGAAATGGAGCTGCTGTTAC
TA

SG13S120

CCTCCTGAGTAGCTAGGACTACAAGCATGTGCCACCACGCCCAGCT
AATTTTGTATTTTAGTAAGGACAGGGTTTCACCATGTTGGCCAGGTTGG
CCTCCAACCTCCTGACCTCAAGTCATCCTCCTGCCTCGACCTCCCAAAGTGC
TGGGATTACAGGCATGAAACCAGCCTAGAAATACATACTATTATTTATTC[
C/T]TGTTTTACAGATAAGCAAAGTGAGTCATGGAGAATTTGGTTGAAAGT
CCCAAGGTCAGGAGTCGTGAAGCTGGGATTAAACCTAATCATCTGACTT
TAGAGAGTAGACACTTGCTCCATGCATATTGCCTCCAATTCATTCAATCAA
GCACTCCCTGCTCAAGAAGTTCTTTCTTATGTTGAGCTGAAATCTGCAG

SG13S121

TCATCTGACTTTAGAGAGTAGACACTTGCTCCATGCATATTGCCTCC
AATTCATTCATTCAAGCACTCCCTGCTCAAGAAGTTCTTTCTTATGTTGAG
CTGAAATCTGCAGCCCTATGCGTTTTACCCAGCAGTCCTGGTGCTGTTCCC
TAAATCACTTAGACTGTGCCTGCTCTTTCTGTGTTTACAGTGTGAGCT[A/
G]TAATATCCCCCTCTTCGGCCTAACGTTTCTGAAGTCCCTTGCCACTGGGT
CTCCTCTCCTCTTCCTGTGTTCTTTCTAAGAACACCTATGCAGATAGGTGTC
TTCTGTACAGGGAAGCTGTTCCCTGAGATCCGGGCATCGACTCTGTTAGAAT
AATCTACGTATGAGTTATTTTTTTGAGAACTATGTGTCATTGCT

SG13S122

ATGTTGAGCTGAAATCTGCAGCCCTATGCGTTTTACCCAGCAGTCC
TGGTGCTGTTCCCTAAAATCACTTAGACTGTGCCTGCTCTTTCTGTGTTTAC
AGTGTGAGCTGTAATATCCCCCTCTTCGGCCTAACGTTTCTGAAGTCCCTT
GCCACTGGGTCTCCTCTCCTCTTCCTGTGTTCTTTCTAAGAACACCTAT[A/G
]CAGATAGGTGTCTTCTGTACAGGGAAGCTGTTCCCTGAGATCCGGGCATCG
ACTCTGTTAGAATAATCTACGTATGAGTTATTTTTTTGAGAACTATGTGTC
ATTGCTGACTCATATTAACCTCTGTGGTTAACTAAAATCTCAAGATCTCTTT
ATGTTTGTTGAGAACTTATTTAACTTCTCTGGCCCTCCGTTTCC

SG13S123

GTCTGCTGCTGTTCCCTAAAATCACTTAGACTGTGCCTGCTCTTTC
TGTGTTTACAGTGTGAGCTGTAATATCCCCCTCTTCGGCCTAACGTTTCTG
AAGTCCCTTGCCACTGGGTCTCCTCTCCTCTTCCTGTGTTCTTTCTAAGAAC
ACCTATGCAGATAGGTGTCTTCTGTACAGGGAAGCTGTTCCCTGAGATC[C/T
]GGGCATCGACTCTGTTAGAATAATCTACGTATGAGTTATTTTTTTGAGAA
CTATGTGTCATTGCTGACTCATATTAACCTCTGTGGTTAACTAAAATCTCAA
GATCTCTTTATGTTTGTTGAGAACTTATTTAACTTCTCTGGCCCTCCGTTT
CCTTCACTGAGCAGTGGAGTGATTGATAACCTCCACCTGTGGTT

SG13S43

CACCTATGCAGATAGGTGTCTTCTGTACAGGGAAGCTGTTCCCTGAG
ATCCGGGCATCGACTCTGTTAGAATAATCTACGTATGAGTTATTTTTTTGA
GAACTATGTGTCATTGCTGACTCATATTAACCTCTGTGGTTAACTAAAATCT
CAAGATCTCTTTATGTTTGTTGAGAACTTATTTAACTTCTCTGGCCCTC[A/
C]GTTTCCTTCACTGAGCAGTGGAGTGATTGATAACCTCCACCTGTGGTTG
CTGAAGGTCTTGACAAGATGATATAGTTAAAGTAGCTAGCAGTGCCAC
GTACGGCGGATGCCTCACAACGTTTGCAGCCATCTCTCTATCTGTGTCTT
TGTCTCTCTCACACTGGTTTTGGCTTACTGTTAGCAGCTAGCCGA

SG13S399

TCTGTGGTTAACTAAAATCTCAAGATCTCTTTATGTTTGTTGAGAAA
CTTATTTAACTTCTCTGGCCCTCCGTTTCCTTCACTGAGCAGTGGAGTGATT

GATAACCTCCACCTGTGGTTGCTGAAGGTCTTGCACAAGATGATATAGTT
AAAGTAGCTAGCAGTGCCACGTACGGCGGATGCCTCACAACGGTTTGC[
A/C]GCCATCTCTCTATCTGTGTCTTTGTCTCTCTCACACTGGTTTGGCT
TACTGTTAGCAGCTAGCCGAGATAAGTGTGTTTATGGTCTTTCATGTATT
GTTTCTGTAGCATACTGGAGGATTACAAGAGGTGGGGAGTGAGGGGGCG
GTGAGGAGTAGACAAAGGCAGCCAACCTCTTCCAAGTTTAGCTTAGAA
SG13S124

TTGATAACCTCCACCTGTGGTTGCTGAAGGTCTTGCACAAGATGAT
ATAGTTAAAGTAGCTAGCAGTGCCACGTACGGCGGATGCCTCACAACGG
TTTGCAGCCATCTCTCTATCTGTGTCTTTGTCTCTCTCACACTGGTTTGT
GCTTACTGTTAGCAGCTAGCCGAGATAAGTGTGTTTATGGTCTTTCATG[
C/T]ATTGTTTCTGTAGCATACTGGAGGATTACAAGAGGTGGGGAGTGAG
GGGGCGGTGAGGAGTAGACAAAGGCAGCCAACCTCTTCCAAGTTTAGCTTA
GAAGGAAGGAGCGGTAAACCTAGTTGAATGTTGGAAGTGAAGCAGGTTTG
TTTTTGTTTGTGTTAAAGGATAGGGAAGATCTGTGCGTGTTCCAGGATA
SG13S125

ACTTGAAGTCAGTGGCATGGACAGGGTCAAGATCACAGTTAGAGG
ATGCAGCCTTAGAGAAAAGGAAGGGGCTCGGTTCTCTGAGCAAGGAGGG
AAAGAAGAGAGGCAGATGCAGAGAAGTACGGCACATCGTGCTGCTGGTT
GTAGAAATAACCTCTGACTTTTAATAAAGTCATCCCTCGGTATCCCTGGGG
GATT[A/G]GTTCTATGACCTCCCTCGGATGCCAAAATTCGTGGATGCTCAA
GTCCCTGATATAAAATGGCATAGTATTTGCATTAAACCTACACACATCCTC
CATATCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTGAGATGGAGT
CTTGCTCTGTGCGCCTGGCTGGAGTACAGTGGCTCGATCTTGGCTCACT
SG13S400

AATACCTGATAGAATGTAAATGCTATGTAAACAGTTGTTATACTGT
ATTGTTAAAAGACAGTAACAAGAAAAAAATCTGTACATGTTCAAGTCCAG
ACAAATGGTTTTCTGTTTTTTTTTTTTTTTTTTTTAATATTTTGGTCAGTGGTT
GGTTGACTCCAGGAATGCAGAACCCGCAGATATAGAAGGTTGATTATGC[
A/G]TTCAGAGGCAGGGAATACCATCTTGGGTTCCAGAAAGAAAATGATCA
GCATTTTCTGTCATACTCTGGTAAAAACAGATCTTTTGAATGGACAGGTGT
ATTAAACCCTGTGGAGCTGGCTGGGCCTGGCGGCTCACGCCTGTAATCCC
AGCACTTTGGGAGGCTGAGGCAGGTGGATCACGAGGTCAGGAGTTCGAG
SG13S126

TGCCCCGCAGAGTTTGAAGTCCCGGCTGCACCTCTCCCCAGCAGCA
GGTTGACTCTGGAAAGTTGCAGCGTTCTTACCTACAGAGTGGGAACAGTA
CTACCCATTGCACAGAGTGGGTGCAAAGCTCTGTGACGGAATACATGGCA
AGTGCCCAACCATTCCTGGGATGAGGTGGGCCCTTCCTTTACGTAAGA
GA[A/G]CCCTACAGATACACTCAAAGTGGGCACATTCCTACAGAAGGAGT
GTTATTTGTGTAGAAAAGAAAAACATGAAAGGCTTTTATTCCTATACACA
ATAAAGCACCCCTTTAATGTCTTTTTGAGGAGGATAATATGAAATTGATGA
AAAGGAACCCTGTGGTTGGATCCCTGACAATCACATGTATCCCTTTTTTCA
C

SG13S127

TACAGATACACTCAAAGTGGGCACATTCCTACAGAAGGAGTGTTAT
TTGTGTAGAAAAGAAAAACATGAAAGGCTTTTATTCCTATACACAATAAA
GCACCCCTTTAATGTCTTTTTGAGGAGGATAATATGAAATTGATGAAAAG
GAACCCTGTGGTTGGATCCCTGACAATCACATGTATCCCTTTTTTCACTCT
T[A/G]AAAAAGGAGTAAAGGAATAAAATAGAAANNNNNNNNNNNNNNNNNN
NN

FIG. 8.19

NNATGTTTCAGTCA
CTGTATAATAACTAGCCAGATTTTTTGTTGTTGTTGTTTGGTTTTGTTTTG
TTTT

SG13S128

ACATTCTGAACCACAGACAGTTCTTTACCCTGAACCTTTGCATATTT
TGTTCTCTTAGCTTAGAGCGGCCCTCTCCCTCCGTCTGCTTGGCTAATTC
TACTTGTTCTTCAGATTTTATCTTAGATGTCAATCCCTCAAGGAATCCTTCT
GTGACTCAACATGGAATTAAGTTGCCTCCTTTGACCCTGAAAGCACC[A/G]
TGTACTCAATCTCATCTTGGCATGACTCACTTTGCTGTGTGGAATGTCTGC
TTTCCTTGTTTGTCTATTCCCTTLAGACTGTAAGATCCTAGAAAGTGGGGGC
CGTGCCCTTGCTCATGACTGTGTTTCTAACACCAAACACAGTGTTTCAGTAGA
GAGCAGCTGCTGAGTACGTTTCTGCTAAATGACAGTTGATGGAG

SG13S129

AATCCTTCTGTGACTCAACATGGAATTAAGTTGCCTCCTTTGACCCT
GAAAGCACCATGTACTCAATCTCATCTTGGCATGACTCACTTTGCTGTGTG
GAATGTCTGCTTTCCCTTGTTTGTCTATTCCCTTAGACTGTAAGATCCTAGAA
AGTGGGGGGCCGTGCCTTGCTCATGACTGTGTTTCTAACACCAAACACA[A/
G]TGTTCAGTAGAGAGCAGCTGCTGAGTACGTTTCTGCTAAATGACAGTTG
ATGGAGGACATTTAGGGTTGCTTGGAGGTCAAGTCAAGGAGGCATTTAAC
ATTCTAGTAAAACAAGGAAGTAACAGGCTCCTGAACATGCCACAATGAA
CCAGATGCAAACCTTTTCCCTTGGCAGGATTCTTTGCCCATAAAGTGG

SG13S130

AAAGCACCATGTA CTCAATCTCATCTTGGCATGACTCACTTTGCTGT
GTGGAATGTCTGCTTTCCTTGTTTGTCTATTCCTTTAGACTGTAAGATCCTA
GAAAGTGGGGGCCGTGCCTTGCTCATGACTGTGTTTCTAACACCAAACAC
AGTGTTCAGTAGAGAGCAGCTGCTGAGTACGTTTCTGCTAAATGACAGT[G
/T]GATGGAGGACATTTAGGGTTGCTTGGAGGTCAAGTCAAGGAGGCATTT
AACATTCTAGTAAAACAAGGAAGTAACAGGCTCCTGAACATGCCACAAT
GAACCAGATGCAAACCTTTTCCCTTGGCAGGATTCTTTGCCCATAAAGTGG
AGCACGAAAGCAGGACCCAGAATGGGAGGAGCTTCCAGAGGACCGGAA

SG13S190

TTCTGCTAAATGACAGTTGATGGAGGACATTTAGGGTTGCTTGGAG
GTCAAGTCAAGGAGGCATTTAACAATTCTAGTAAAAACAAGGAAGTAACAG
GCTCCTGAACATGCCACAATGAACCAGATGCAAACCTTTTCCCTTGGCA
GGATTCTTTGCCATAAAGTGGAGCACGAAAGCAGGACCCAGAATGGGA
GGAG[C/T]TTCCAGAGGACCGGAACACTTGCCTTTGAGCGGGTCTACACTG
CCAAGTGAGTCCTAACCCTGATGTTGCTAATAAGTGGGGGCATGGGCAGG
GGGGCCTCCTTCTAGGAGTGATGACCACCCTTAATACCACATGTCTGTCTG
AGCCAAGTTTCTGAGCGCCAGGGAGGTGAGGAAGGTTGGACTTCACCAGA
GAG

SG13S192

GGCATTTAACATTCTAGTAAAACAAGGAAGTAACAGGCTCCTGAA
CATGCCACAATGAACCAGATGCAAACCTTTTCCCTTGGCAGGATTCTTTG
CCCATAAAGTGAGACGACGAAAGCAGGACCCAGAATGGGAGGAGCTTCCA
GAGGACCGGAACACTTGCCTTTGAGCGGGTCTACACTGCCAAGTGAGTCC
TAA[A/C]CCTGATGTTGCTAATAAGTGCGGGCATGGGCAGGGGGGCCTCCT
TCTAGGAGTGATGACCACCCTTAATACCACATGTCTGTCTGAGCCAAGTTT
CTGAGCGCCAGGGAGGTGAGGAAGGTTGGACTTCACCAGAGAGGCTTTGT
GGACACCCTTTATCATCTTAGTGAGTGCTAGTGTCAAAACAAAGGGAGTG
GG

FIG. 8.20

SG13S193

GCTCCTGAACATGCCCACAATGAACCAGATGCAAACCTTTTCCCTT
GGCAGGATTCTTTGCCCATAAAGTGGAGCACGAAAGCAGGACCCAGAAT
GGGAGGAGCTTCCAGAGGACCGGAACACTTGCCTTTGAGCGGGTCTACAC
TGCCAAGTGAGTCCTAACCCCTGATGTTGCTAATAAGTGGGGGCATGGGCA
GGG[A/G]GGCCTCCTTCTAGGAGTGATGACCACCCTTAATACCACATGTCT
GTCTGAGCCAAGTTTCTGAGCGCCAGGGAGGTGAGGAAGGTTGGACTTCA
CCAGAGAGGCTTTGTGGACACCCTTTATCATCTTAGTGAGTGCTAGTGTC
AAACAAAGGGAGTGGGGATATGGGGGCACATTGGTGGAGGGAGGTGTGAT
CTC

SG13S88

TTGCCCATAAAGTGGAGCACGAAAGCAGGACCCAGAATGGGAGGA
GCTTCCAGAGGACCGGAACACTTGCCTTTGAGCGGGTCTACACTGCCAAG
TGAGTCCTAACCCCTGATGTTGCTAATAAGTGGGGGCATGGGCAGGGGGGC
CTCCTTCTAGGAGTGATGACCACCCTTAATACCACATGTCTGTCTGAGCCA
AG[C/T]TTCTGAGCGCCAGGGAGGTGAGGAAGGTTGGACTTCACCAGAGA
GGCTTTGTGGACACCCTTTATCATCTTAGTGAGTGCTAGTGTCAAAACAAA
GGGAGTGGGGATATGGGGGCACATTGGTGGAGGGAGGTGTGATCTCTGCAG
CTTCAGAAAGATCTGAAAGAGTCATTTGGTTAGAGAAGTTGACCTATTTCC
T

SG13S131

AAACAAAGGGAGTGGGGATATGGGGGCACATTGGTGGAGGGAGGTG
TGATCTCTGCAGCTTCAGAAAGATCTGAAAGAGTCATTTGGTTAGAGAAG
TTGACCTATTTCTGTGGGGTTAGACCAGGGTTGCTACTGTGAACACCAGC
CATGACTCACCAGTCACCTTCAGAAGCCACAGGCAGGACATGCTGACGAC
AG[C/T]CTTCAACTCACCCACCCCTTGCTCCCCTGCGGGTGGAAGTCTGGA
GGTGACACCACTGCATTTTCTAACACGGGGGCTCCTTGAGCAACTAGAAC
AAGAACAGAAAGAATGGGGACATTAGCAGGTGCTTTCCCCCTCTCTCATT
CTTTTCTTTGAATAAAAAGGTTGTTTGAACACCTGAGCGGCTCCTAAAG
A

SG13S132

CTCCTCTCTTCTTTATGCAGAGTGTAATTTCAAGGCTCAGCCAGTGGC
AGGCATGCTGGGGACTATGGACTACGGACTAGGGGCCTGTCACAGAGGA
AGGCCTCATGCTAGAGAGCTAAGGGAGGAGCTGGCCTTCAGTTCCATCCC
AGGAGCAACTTTGATGTTCCCAGAGATCCTTCCAAAGGGGGAGTCATGGT
CA[A/C]CCAAGAAAAATGTATTCAGAATGCCAAGAATGGTGCAAACCTCAG
GACAAAGATTACACTGCAGGGTTGGAGTCCCTGGGCTTGCTGCTGGCAC
CATGGGAGGGAGGGTCCCCTTCAGGGGTACCGTTGGTTTCCTGTGAATTA
AACTGGCTTCAAGGGATCTCGACTGAACAGGCCTATATCACACTCACTGA
TAT

SG13S133

TTCCTCATCTAGGTATTTTAAATTGTTTCAGTGAGGTGTAGGCATG
AGGGGATTGGAGGGGGCATCTCCTCCATTGCAGTTTTTTCATTGGCTGCTTT
GCTCCCTCAGCTCCGAAATCGCTGGGGCACTCTCGAACGCATTAGTACGG
TAGTCACAGGTTGATTGCCTGGCCCCCTTGCCCTCTGTGGGCATTTTCCCT[C
/T]TCAGACAGCCCCTGAGTACTCACAGTGCTGCTACAGTGGGGCACCTAG
ATCTCCCTCTTTCTCCATGCTCCACGTGCTCTGGGCTCCACTCCCTTCTCC
CAAGCACTTCTGTCCAGGGCTATTCCAGCAGTCTGACCTCAAGGAAATCC
TTTGCTAAACTGATTATAGAGAGGTTTCTATTTTAACATTTAGGTCT

FIG. 8.21

SG13S38

ATCTAGGTATTTTAAATTGTTTCAGTGAGGTGTAGGCATGAGGGGA
TTGGAGGGGGGCATCTCCTCCATTGCAGTTTTTCATTGGCTGCTTTGCTCCCT
CAGCTCCGAAATCGCTGGGCCACTCTCGAACGCATTAGTACGGTAGTCAC
AGGTTGATTGCCTGGCCCCCTTGCCCTCTGTGGGCATTTTCCCTTTCAGAC[A
/T]GCCCCCTGAGTACTCACAGTGCTGCTACAGTGGGCCACCTAGATCTCCCT
CTTTCTCCATGCTCCCACGTGCTCTGGGCTCCACTCCCTTCTCCCAAGCACT
TCTGTCCAGGGCTATTCCAGCAGTCTGACCTCAAGGAAATCCTTTGCTAAA
CTGATTATAGAGAGGTTTCTATTTTAAACATTTAGGTCTTCCATGT

SG13S134

AGGTGTAGGCATGAGGGGATTGGAGGGGGGCATCTCCTCCATTGCA
GTTTTTCATTGGCTGCTTTGCTCCCTCAGCTCCGAAATCGCTGGGCCACTC
TCGAACGCATTAGTACGGTAGTCACAGGTTGATTGCCTGGCCCCCTTGCCCT
CTGTGGGCATTTTCCCTTTCAGACAGCCCCCTGAGTACTCACAGTGCTGCTA
[C/T]AGTGGGCCACCTAGATCTCCCTCTTTCTCCATGCTCCCACGTGCTCTG
GGCTCCACTCCCTTCTCCCAAGCACTTCTGTCCAGGGCTATTCCAGCAGTC
TGACCTCAAGGAAATCCTTTGCTAAACTGATTATAGAGAGGTTTCTATTTT
AACATTTAGGTCTTCCATGTATTAATTCTCAGAATCAATTTAAGATG

SG13S135

CCTTTCAGACAGCCCCCTGAGTACTCACAGTGCTGCTACAGTGGGCC
ACCTAGATCTCCCTCTTTCTCCATGCTCCCACGTGCTCTGGGCTCCACTCCC
TTCTCCCAAGCACTTCTGTCCAGGGCTATTCCAGCAGTCTGACCTCAAGGA
AATCCTTTGCTAAACTGATTATAGAGAGGTTTCTATTTTAAACATTTAGG[C/
T]CTTCCATGTATTAATTCTCAGAATCAATTTAAGATGTTTAAAGGTGTGAT
TTAAGACATTTTAAAACCATTTGGAGGAGAGTACAGAAATTATGTCACTT
GCTGTCAGCCTCTTTGCACCATCTGCAGAGAAAGATACTAGAGTCCCGCC
TTGGACACATCCACATGCAAGAGGTGCAAAGAAGGTGTCTTTGATGA

SG13S136

TTCTCAGAATCAATTTAAGATGTTTAAAGGTGTGATTTAAGACATTT
TAAAACCATTTGGAGGAGAGTACAGAAATTATGTCACTTGCTGTCAGCCT
CTTTGCACCATCTGCAGAGAAAGATACTAGAGTCCCGCCTTGGACACATC
CACATGCAAGAGGTGCAAAGAAGGTGTCTTTGATGAGGCAAGGTCAAAA
CT[C/T]CTCCCCAGACGAAATCCAAAGAAAGCATTCTACTATGCTATATC
AGTTTGGAAGAAAAAATCTTCTGCCAGGTGACTGCATTCTCACTGGTCACA
TTGTGTTTCTATGGACTCCTCAGCTCAACCAATTTGGAGAAGTTATGGTGC
AATTTACCATATCTGGTTAGAAGTTAAGTTTCCAATTTGCTGGCAATGAA

SG13S137

AAGAAGGTGTCTTTGATGAGGCAAGGTCAAAACTTCTCCCCAGACG
AAATCCAAAGAAAGCATTCTACTATGCTATATCAGTTTGGAAAGAAAAA
CTTCTGCCAGGTGACTGCATTCTCACTGGTCACATTGTGTTTCTATGGACT
CCTCAGCTCAACCAATTTGGAGAAGTTATGGTGCAATTTACCATATCTGG
[C/T]TAGAAGTTAAGTTTCCAATTTGCTGGCAATGAAGAAGAAATGGAGCA
GGCCAGGCTGTGTAGTTTCTGCCACGTGCCCCCGGGAGTGAACAGCTCTG
TTTGTAAGAAGCCATGGTGCTTAGACCTGGGCTCGCTAGTTGCCAGCCTCC
AAATTGCAGAAGTGCCCTTTGGTTGGTGGCTATGCTGTGTCACTTGGGA

SG13S86

GCAACATATCTGTGTGCCTGTCTGGGTTGTAAAAAGGGTCAAAGAT
CAATGCAGCAGGCAGCTACATGCTGGCAAAGGCCAGAGGCAGCTGGTCT
GTTTGCTGTGCCAGGAAACCACTGGGAATGGGGTTGTGTGTTATTCTAGG
AGAAAGTCGTCCCAGCAGCAGCTTCTCCAGGGGCATCCAAGAGCACTGAA

FIG. 8.22

AA[A/G]GGTTGCAAGATGACCCATGAGGCTGCAGGAAGAAAAGAACATGC
ATTTAACTTTGCTATCTGAAAAGTAAGACATGAAGCTTTCCTCATTTTTAA
TATACACATGGACAGTAGTATGTGTATATAGTTTATATGCAAATATACTTG
TTATAAGGTTGCATGCTCAAAATTTTGGTTCATGGGGTGTGGGATCATAA
SG13S87

CAGCTACATGCTGGCAAAAGCCAGAGGCAGCTGGTCTGTTTGCCTG
TGCCAGGAAACCACTGGGAATGGGGTTGTGTGTTATTCTAGGAGAAAGTC
GTCCCAGCAGCAGCTTCTCCAGGGGCATCCAAGAGCACTGAAAAGGGTTG
CAAGATGACCCATGAGGCTGCAGGAAGAAAAGAACATGCATTTAATCTTG
CT[A/G]TCTGAAAAGTAAGACATGAAGCTTTCCTCATTTTTAATATACACA
TGGACAGTAGTATGTGTATATAGTTTATATGCAAATATACTTGTATAAGG
TTGCATGCTCAAAATTTTGGTTCATGGGGTGTGGGATCATAAATGTTTAG
GGACCATGGCTATCAAGGAAAAACAGCATGAAGGATAAATGATACTGGT
G

SG13S138

CTATCTGAAAAGTAAGACATGAAGCTTTCCTCATTTTTAATATACA
CATGGACAGTAGTATGTGTATATAGTTTATATGCAAATATACTTGTATAA
GGTTGCATGCTCAAAATTTTGGTTCATGGGGTGTGGGATCATAAATGTTT
AGGGACCATGGCTATCAAGGAAAAACAGCATGAAGGATAAATGATACTG
G[C/T]GGATTAAAAAGACAGATGCATGTATTTTAGCATAAAACACAACCTG
CTGACTGATACAGATAGCTCAAGATTCTGGGGCAGCTGCTGAACAGATAC
ACTAGCCAGTGTGGCTCATCGGCTCAGACTTGGCCTTAATTAATGGGCTGT
CCCTCCACCCATCTCCCATGAGGGCAGAGCTGAGCCAGGGTTTGAGAGCT
SG13S139

AGTTTATATGCAAATATACTTGTATAAGGTTGCATGCTCAAAATTT
TTGGTTCATGGGGTGTGGGATCATAAATGTTTAGGGACCATGGCTATCAA
GGAAAAACAGCATGAAGGATAAATGATACTGGTGGATTAAAAAGACAGA
TGCATGTATTTTAGCATAAAACACAACCTGCTGACTGATACAGATAGCTC
AA[C/G]ATTCTGGGGCAGCTGCTGAACAGATACACTAGCCAGTGTGGCTCA
TCGGCTCAGACTTGGCCTTAATTAATGGGCTGTCCCTCCACCCATCTCCCA
TGAGGGCAGAGCTGAGCCAGGGTTTGAGAGCTAAAAGGAATTGGACCTG
GACTCTGTTACAGTGTATATTTAATTCTAATTAATTCATTCTTTGAAAGA
SG13S140

GTATTTTLAGCATAAAACACAACCTGCTGACTGATACAGATAGCTCA
AGATTCTGGGGCAGCTGCTGAACAGATACACTAGCCAGTGTGGCTCATCG
GCTCAGACTTGGCCTTAATTAATGGGCTGTCCCTCCACCCATCTCCCATGA
GGGCAGAGCTGAGCCAGGGTTTGAGAGCTAAAAGGAATTGGACCTGGAC
TC[A/G/T]GTTACGTGTATATTTAATTCTAATTAATTCATTCTTTGAAAG
ACAGAGTCACACTCTGTTGCCTAGGCTGGAGTGCAGTGGCACGATCTTGG
CTCACTGCAACCTCGGCCTCCAGGTTCAAGTTATTCTCCTGCTTCAGCCT
CCTGAGTAGCTGGGATTATAGGCACATGCCCCCATGCCTGACTAATTTT
SG13S141

GCTAAAAGGAATTGGACCTGGACTCTGTTACGTGTATATTTAAT
TCTAATTAATTCATTCTTTTGAAGACAGAGTCACACTCTGTTGCCTAGGC
TGGAGTGCAGTGGCACGATCTTGGCTCACTGCAACCTCGGCCTCCAGGT
TCAAGTTATTCTCCTGCTTCAGCCTCCTGAGTAGCTGGGATTATAGGCACA
[C/T]GCCCCCATGCCTGACTAATTTTGTATTTTLAGTAGAGACGGGGTTTC
ACCATGTCAGGCTGGTCTTGAACCTCCTGACCTCAGGTTATCCACCCGCCTT
GGCCCCCTCAAAGTGTTGGAATTACAGGTGTGAGCCACCGTGCCTGGCCTG
TTCACATGTATAAAACACAGTTTAATGTCCTATTCCCAGCCAATGAGC

FIG. 8.23

SG13S39

TCAGGTTATCCACCCGCCTTGGCCCCCTCAAAGTGTTGGAATTACAG
GTGTGAGCCACCGTGCCTGGCCTGTTACATGTATAAAACACAGTTTAAT
GTCCTATTCCCAGCCAATGAGCATGGCTAGAGCAGCCTTGGTCAAAGTTT
GGTTTTTGGAGAAAAATCCTTGTTAGCTGACCTAAGATTCTTCTTTGTGAG
T[G/T]TAAGTAAGCACAGGTTGCAGAGAGGAGAAGGGTCTCTGGAGAGGT
GTAATTTTCTAAATGGATTACAAGTTCATGGACTTTTAACAGGTGTTACAG
GGGATAACAAGTTCTTTATAGACAGACTTTTGAGGACGTTTAAGGGTATTC
TGATTCTTGGTTTTCTAAGAGGGGAATGTATTATTAACTACAGACACCC

SG13S142

AAAATCCAGAATAATAATAATTTGTCAATAGGAAAGACATTTCCAC
TGGGGGTAAAGAAGGAAGACATTGGAACAATGATAGCCACCACTTATTGA
ATGCTTACTGTGAGCCAGGTGGCACTTCACCTTGTTTCATTCTCACAACAG
TCTAGGGAAGTAATTACTAATGTCTCCATCCACCTCTTGTAGATGAGCAAA
[C/T]TGAGGCTCATTGAGGCTAGGAAATGCACCCACACTCACATAGCCCAT
AAGAGGCAGCCATGGCATTGGGCCCAGACCATGTGAACTTCAAAGACTAC
ACGAGCAGCCACTGGGCAGCTGTCATGGCTAAAGCCACTTGAATTCAGCC
CAGCAGCAACCCCTCTCCAGGAGGGGCACATAAGCTTGCAGCTTTGGGT

SG13S143

ATAATAATAATTTGTCAATAGGAAAGACATTTCCACTGGGGGTAA
GAAGGAAGACATTGGAACAATGATAGCCACCACTTATTGAATGCTTACTG
TGAGCCAGGTGGCACTTCACCTTGTTTCATTCTCACAACAGTCTAGGGAAG
TAATTACTAATGTCTCCATCCACCTCTTGTAGATGAGCAAAGTGAAGGCTCA
[C/T]TGAGGCTAGGAAATGCACCCACACTCACATAGCCCATAGAGGCAG
CCATGGCATTGGGCCCAGACCATGTGAACTTCAAAGACTACACGAGCAGC
CACTGGGCAGCTGTCATGGCTAAAGCCACTTGAATTCAGCCAGCAGCAA
CCCCCTCTCCAGGAGGGGCACATAAGCTTGCAGCTTTGGGTAGAAGCTGC
A

SG13S144

GCACTTGAAGTCCTGGATGGCGAGAGGGACTGGCTTGAGCCAGAG
CCAGGAACAAGGCTCTGAGAATATTCTGGAAATCCACAGGAGGAACCCAT
TTTCTTACAGCTGGGAGAATTTCACTCAACTCCAGGCTGACCATGTTTTAT
TAGGAACGAAGGTGACTTGAACATAAGTCAGGAATGGTTGAATACGGAC
CC[A/G]ATGTCAAATCACTAGGCAGTTCACATTTCTAATGAGCAAATCCCT
TAGACAATTAAGAATTTTTTCTTTTGCATAACCCAGACAAAATCGCTAC
TTAAAAACAAACCAAAGACCCGAAACATGAGAAAGAGAAGGAAGCAGG
GGAAATCTTTGGTACTAATAAGTTTTTAAACAATAAGAGCACCAGATATTT
TA

SG13S145

ATGAGCAAATCCCTTAGACAATTAAGAATTTTTTCTTTTGCATAA
CCCAGACAAAATCGCTACTTAAAAACAAACCAAAGACCCGAAACATGAG
AAAGAGAAGGAAGCAGGGGAAATCTTTGGTACTAATAAGTTTTTAAACAA
TAAGAGCACCAGATATTTTACCCCATCAGACACAGAATGTTATTCTGAATA
AC[C/G]AAAAAAGGAATTTTTTCTCTAAGTTTCTTGAAGTGGAAAATGAAT
CATATTTTCTCAGTCCTGAGGCTGCAATTTTGTGCCTCTAGTAACATATAA
GAATAGATGTGATGCCAGTGCCAGTAGCTGCTGCAATTGTTACTTGGGG
ACCTGTTTATTCTACTAAGCACTTCACCCAGTGATAAATTTGTAGGGGCCT

SG13S146

CCGTGTCCATTAGATCAGTGGAATTCTGGGATTCAGAGCACTTTG
CAAGGTCAGCAGGGGTCTGCTCTTTCTGTCCTGTTCTGGTTTTTGGTTGTG

CCTGGATTCCAGGGTAGGTTTCTCATCTGTTACCTTCATAGACTTCTCCAG
AAAAGGATCTTTTGACCATCAGAGGACCACGAAGATTCCATTGGTGAGG[
C/T]GCAGATAACCTGATCTCTCTGGGTTCTCTGCAGGGCACAGATGAAGG
GCTGGCCATTCCCAAGTTCTCAGTGGTACCACTGAGGCATGAGACCCTAA
TGGTTTGCATGAGCAGTTTGAAAATTGCATCTTTGTTTTTACCTATATAATC
ACATGAAACCCGTGGTTCTCAAACGTCAGCAGGCATCAGCATCACATG
SG13S26

TCAGTGGTACCACTGAGGCATGAGACCCTAATGGTTTGCATGAGCA
GTTTGAAAATTGCATCTTTGTTTTTACCTATATAATCACATGAAACCCGTG
GTTCTCAAACGTCAGCAGGCATCAGCATCACATGGAGGGCTTGTTAAAC
AGATTTCTGGGCCCCAACACAGAGTTTAAATTCTGAAGGCCTGAGGTGG
G[C/T]GTGAACATTTGCATTTCTAACATGTTCTCGATGCTGCTGCCGCCTCT
GGTCCCGAGAGCATGCCTGGAGAACTGCCACCTTCGACCATGGACTGTGA
GAATTCACATGGACCTCAGAATTATAATCAGTCTCTCAGTTTTACAGATAA
GGAACTAAATCCAGAGAGATTGTTTTGCCAATGGTGAACAGCTGGTTA
SG13S27

ATGGTTTGCATGAGCAGTTTGAAAATTGCATCTTTGTTTTTACCTAT
ATAATCACATGAAACCCGTGGTTCTCAAACGTCAGCAGGCATCAGCATCA
CATGGAGGGCTTGTTAAACAGATTTCTGGGCCCCAACACAGAGTTTAA
ATTCTGAAGGCCTGAGGTGGGTGTGAACATTTGCATTTCTAACATGTTCTC
[A/G]ATGCTGCTGCCGCCTCTGGTCCCGAGAGCATGCCTGGAGAACTGCCA
CCTTCGACCATGGACTGTGAGAATTCACATGGACCTCAGAATTATAATCA
GTCTCTCAGTTTTACAGATAAGGAACTAAATCCAGAGAGATTGTTTTGCC
AATGGTGAACAGCTGGTTAAAGTCAGGATGGAGACTTTAATCCTAGTCA
SG13S147

GAGCAGTTTGAAAATTGCATCTTTGTTTTTACCTATATAATCACATG
AAACCCGTGGTTCTCAAACGTCAGCAGGCATCAGCATCACATGGAGGGCT
TGTTAAACAGATTTCTGGGCCCCAACACAGAGTTTAAATTCTGAAGGC
CTGAGGTGGGTGTGAACATTTGCATTTCTAACATGTTCTCGATGCTGCTGC[
C/T]GCCTCTGGTCCCGAGAGCATGCCTGGAGAACTGCCACCTTCGACCAT
GGACTGTGAGAATTCACATGGACCTCAGAATTATAATCAGTCTCTCAGTTT
TACAGATAAGGAACTAAATCCAGAGAGATTGTTTTGCCAATGGTGAACA
GCTGGTTAAAGTCAGGATGGAGACTTTAATCCTAGTCAAGTGACCTTTC
SG13S28

AGTTTGAAAATTGCATCTTTGTTTTTACCTATATAATCACATGAAAC
CCGTGGTTCTCAAACGTCAGCAGGCATCAGCATCACATGGAGGGCTTGTT
AAAACAGATTTCTGGGCCCCAACACAGAGTTTAAATTCTGAAGGCCTGA
GGTGGGTGTGAACATTTGCATTTCTAACATGTTCTCGATGCTGCTGCCGCC
[G/T]CTGGTCCCGAGAGCATGCCTGGAGAACTGCCACCTTCGACCATGGAC
TGTGAGAATTCACATGGACCTCAGAATTATAATCAGTCTCTCAGTTTTACA
GATAAGGAACTAAATCCAGAGAGATTGTTTTGCCAATGGTGAACAGCTG
GTAAAGTCAGGATGGAGACTTTAATCCTAGTCAAGTGACCTTTCCTCT
SG13S148

CATCTTTGTTTTTACCTATATAATCACATGAAACCCGTGGTTCTCAA
ACGTCAGCAGGCATCAGCATCACATGGAGGGCTTGTTAAACAGATTTCT
GGGCCCCAACACAGAGTTTAAATTCTGAAGGCCTGAGGTGGGTGTGAAC
ATTTGCATTTCTAACATGTTCTCGATGCTGCTGCCGCCTCTGGTCCCGAGA[
G/T]CATGCCTGGAGAACTGCCACCTTCGACCATGGACTGTGAGAATTCAC
ATGGACCTCAGAATTATAATCAGTCTCTCAGTTTTACAGATAAGGAACT

FIG. 8.25

AAATCCAGAGAGATTGTTTTGCCAATGGTGAACAGCTGGTTAAAGTCAGG
ATGGAGACTTTAATCCTAGTCAAGTGACCTTTCCTCTGTATTTATTTCCC
SG13S98

ATTTCTGACATCCTGAACCATAGTAAAAGGGTGTTTTTTGTTTTTTT
GAGACAGAGTCTTGCTCTGTTGCCTGGGCTGGAGTGCAGTGGTGTGATCTT
GGCTCGCTGCAACCTCCGCCTCCCAGGTTCAAGTGATTCTCCTGCCTCAGC
CTCCTGAGTAGCTGGGATTACAGGTGCTTGCCACCACACCTGGCTATTT[G/
T]TTGTGTTTTTAGTAGAGACAGGGTTTACCATTGTTGGCCAGGCTGGTCTT
GAACTCCTGACCTTGTGATCTGCCTGCCTCAGCCTCCCAAATTGCTGGGAT
TACAAGGCGTGTTGTTTTAAGCCACTCAGTTTGTGGCCACTTGTACAGCA
GCAAGAGGAACTCATACAGTTATCATGTGAACTCACAGGAATAT
SG13S149

GATCTGCCTGCCTCAGCCTCCCAAATTGCTGGGATTACAAGGCGTG
TTGTTTTAAGCCACTCAGTTTGTGGCCACTTGTTACAGCAGCAAGAGGAA
ACTCATACAGTTATCATGTGAACTCACAGGAATATGGTGAGTTAAAAAGA
GAGGAAGGGTGCAAAACATCCACGGTAGAGTGAGAACTCTCCAGGGAGT
GAG[A/G]ACTGTGCCCAGCATACAGTGATCACCTCTTAGTAAGCTAAGTT
TCTGAGCACCAGCTTTTTTGAGTTGACTTTGTTGTCTTTAACATTTGAAGAT
CACCTTCTTTGCTCAGCCTGGCTTGCAGACCTGGGCTGATTTGTGGATCT
GATAGAAAAGTTTCCTTAGTTGGGCTCTTCTCCCCGACCACCCCCATGCC
SG13S29

TGCCTCAGCCTCCCAAATTGCTGGGATTACAAGGCGTGTTGTTTTA
AGCCACTCAGTTTGTGGCCACTTGTTACAGCAGCAAGAGGAACTCATAC
AGTTATCATGTGAACTCACAGGAATATGGTGAGTTAAAAAGAGAGGAAG
GGTGCAAAACATCCACGGTAGAGTGAGAACTCTCCAGGGAGTGAGGACT
GTGC[A/C]CAGCATACAGTGATCACCTCTTAGTAAGCTAAGTTTCTGAGC
ACCAGCTTTTTTGAGTTGACTTTGTTGTCTTTAACATTTGAAGATCACCTT
CTTTGCTCAGCCTGGCTTGCAGACCTGGGCTGATTTGTGGATCTGATAGAA
AAGTTTCCTTAGTTGGGCTCTTCTCCCCGACCACCCCCATGCCAGTGTGGC
SG13S89

GCTACTTTGCAGCCAAGGTAACCTCAGACTTCCCTTTGTTCAATTCTCC
TTCTATAAAGTGCATCTCAAGGAGGTTCAAAGGGCAGGCTTTTTGTTGAA
AGGACTTTGCCTGACCTCTGGCTCCCATCTGTGAAGCCCTGGAGAGGTGA
GAGCCCTCGGGAGGCCGTGTTTCAGGCATGCTCTGCACCCGTGCAGAGCG
C[A/G]TGTGATAATGCATTGCTAATGCTTGCTCCCTGGTGGCTGGCTGAGA
GCTGCTGTGCTGACAAGGGTGGTTTAAAGGCTAAATGTGACTCAGAATCCT
TAAGCAGTGTTAGTTCAGATACAAGGGCATTATAAATGAGAGTGCCTGAG
GGATCTATTTTGGGACCGCTGTCACTTGGCTCTTCTGCTAATAAGCTTCCA
SG13S96

ACAGTTATCAGCAGCCCACAGGCTTGACTTGAGCAAGTTGGAAAG
ACAAATCAACTTCCAGAGTTGATTTAACATTGAGTGGAAATCAGTCATAC
TTTTGGTCCCCTTTCGGGGCCACGCCTGGCACTGTGCCTGGTGGCAGATCG
GCATGAACTGGCCAGCTTCTGTGGCCCTGGAGGGCACAGGCAGAAAGGCC
AC[A/G]CTCAGTCCCATGATGAACTGTTTAAAGACTTATTGTTGTCTCCCCGC
TCTGTAAAGTAGATAGAGTGGATTTTATGTCCCTTATTACCTTTCAGGATA
CTTTGACTCAGGGAGATAAAGTAACTTGGGTACAGCTACTCAGCTGGTGA
AGAACACAGGCAGAATGAGTGCCTGGGTCTTTTGACTIONAAAATTCTGGAT
SG13S150

CTGTGCCTGGTGGCAGATCGGCATGAACTGGCCAGCTTCTGTGGCC
CTGGAGGGCACAGGCAGAAAGGCCACACTCAGTCCCATGATGAACTGTTT

AAGACTTATTGTTGTCTCCCCGCTCTGTAAAGTAGATAGAGTGGATTTTAT
GTCCCTTATTACCTTTCAGGATACTTTGACTCAGGGAGATAAAGTAACTTG
[C/G]GTACAGCTACTCAGCTGGTGAAGAACACAGGCAGAATGAGTGCCTG
GGTCTTTTGACTTAAAATTCTGGATTTTTCACAAAGATCCTCTTACTTTATT
CATTTACATAATAAATATATATTGAAGAGCTACTCTGTGCCAAGCCCTGTG
CCTAGATATACAGTGATAAATAAAGAGTAGCTTCTAGAGGGTCACCTGG
SG13S401

AAGTTCAGTGATAGAGAGCAGAGGTGAGGCGGCAGCAGAAACCAC
TTAAGGGACACCACGTGGCACTCCTTCTGTGCTGAGAAGGCTGTCAGTAA
GCTCACCATTTATTTTCTATTTTCTCTCCTGAGTTAAATAGGAAACATGTCT
CGCATTACTTGAAAAATCAAGTCAAACATGCTCTTACTAGGAGTTATGGT
[C/T]CTTTTTATGTCTTAGATGATGCTTGATCTAGATGAATGCCGACTTGCT
GTAGCTAGATAAATACAATGGGAGTTTGAAGGTGTTTCGTAGCCCTGGAA
ATAGGTATTTTCTGTCAAAACAAGCTTTGTTCATTGCCAGCAGACAAAAGC
ATCAGTAACCTTGGTTGATAATCGTCATTTCTTAGGAATAAAGTAGACT
SG13S151

GTATTTTCTGTCAAAACAAGCTTTGTTCATTGCCAGCAGACAAAAGC
ATCAGTAACCTTGGTTGATAATCGTCATTTCTTAGGAATAAAGTAGACTGT
AGAATTTTTTTTAGCAGAAAGGAAACCCAAAGATAATTCTAGTGCAAATC
CCTCACTTTATAGAGCAGAAGCTCAAGTCCCAGAGGAACAAGTGGCTTGA
A[C/T]GAACATCAGAATTTTAGGGGCTGGATTTGTACCCTCCTGGTGCCAG
CAGCCCACTTCCCTGCAGGAGGCACCTTCCTTGACAGGGGGTATGA
GTGTGGCCATTTTCCACCCATAATCTCTGTAGCTCATGTTCAATTGGGT
CCCATTGAAAGAAAAATGGACCAGTAAGTTGGAGCAGAATCATTGAGATG
SG13S30

AGCTTTGTTCATTGCCAGCAGACAAAAGCATCAGTAACCTTGGTTGA
TAATCGTCATTTCTTAGGAATAAAGTAGACTGTAGAATTTTTTTTAGCAGA
AAGGAAACCCAAAGATAATTCTAGTGCAAATCCCTCACTTTATAGAGCAG
AAGCTCAAGTCCCAGAGGAACAAGTGGCTTGAACGAACATCAGAATTTTA
G[G/T]GGCTGGATTTGTACCCTCCTGGTGCCAGCAGCCCACTTCCCTGCAG
GAGGCACTCACCTTCCTTGACAGGGGGTATGAGTGTGGCCATTTTCCACCC
ATAATCTCTGTAGCTCATGTTCAATTGGGTTCCTTGAAGAAAAAATGG
ACCAGTAAGTTGGAGCAGAATCATTGAGATGGTATAACATAAGGAAAAA
SG13S31

TGTTTAAATTGCTTTTATATCTGTAGCTCTAGATAACACTAGTTCCA
GCTTAGTTAACTCCCAGCTCCAAGCCTTCAGGACTTCATAGAGTTATTGGG
GTGCTGCTCTTGGCAGTTTCCCAAAAAGCTAGAATGCAGAGGGAATCTCC
TTCCCAAAAAGCTAGAATGCAGAGGGAATCTCCTTCCCAAAAAGGCTAGAA
[C/T]GCAGAGGGAATCTCCTTCCCAAAAAGCTAGAATGCAGAGGGAATCT
CCTTCCCAAAAAGGCTAGAACGCAGAGGGAATCTCCTTCCCAAAAAGGCTAG
AACGCAGAGGGAATCTCCTTCCCAAAAAGGCTAGAATGCAGAGGGAATGT
CCTTCTCTTCTAAATGGTAGCTGTTAGTTCAAGAAAGGTTAAACATTGTGC
T

SG13S152

GCTGCGTTTGCTGGACTGATGTACTTGTTTGTGAGGCAAAAGTACT
TTGTGCGTTACCTAGGAGAGAGAACGCAGAGGTAGGTAACCTGGGACTACT
AAAGAAGTGTGGAGCGATTCTGATTTTTGAGCAGGAAGAGTGACAATTC
AAAACAGTATTTGACTAGATTCACGGCTCCGTAGCATCCCCTTGGGTGGG
AG[C/G]GGGAAGGCTGACTAGGACCTCTGATTCTTCTTCCCTGAGCTTGT
AAGGCTCTGAAAATACAGCTGGGGGGACTTGCCAGTTTTCTTATTAAGC

FIG. 8.27

AATTCCTCCGCATGGTGCTGGCTTTCAAAGGGTGCTTCAGTGCTGTTTGCT
GCACGTGCCTTGCAGCCCCACACCCTGCACTCCCGCCCTGCAGAGTCTGG
C

SG13S402

GAGGCCAAAAGTACTTTGTTCGGTTACCTAGGAGAGAGAACGCAGAG
GTAGGTAACCTGGGACTACTAAAGAACTGTGGAGCGATTCTGATTTTGA
GCAGGAAGAGTGACAATTCAAAACAGTATTTGACTAGATTACGGCTCCG
TAGCATCCCCCTTGGGTGGGAGGGGGAAGGCTGACTAGGACCTCTGATTCT
TCT[C/T]TCCCTGAGCTTTGAAGGCTCTGAAAATACAGCTGGGGGGACTTG
CCCAGTTTTCTTATTAAGCAATTCCTCCGCATGGTGCTGGCTTTCAAAGGG
TGCTTCAGTGCTGTTTGCTGCACGTGCCTTGCAGCCCCACACCCTGCACTC
CCGCCCTGCAGAGTCTGGCGCTGGAATGACATTTTAGGTCTGGGTTCCCA
G

SG13S403

TATCTTTTCAGGGACCAGAAGAAAGAATGTTGGGAAAATAAGATGC
AGTAAGATGCAGACATGACAGCAGGGTGACGCGGCTCACGCCTATAATCC
CAGCACTTTGGGAGGCTGAGGTGGGTGGATCACCTGAGGTCAGGAGTTTG
AGACCAGCCTGGCCAACATGGTGAAACCCCGTCTCTACTAAAAAATATAC
AAA[A/G]CATTAGCCAGGCATGGTGGTGGGCGCCTGTAATCCCAGCTACTC
CATAGGCTGAGGCTGGAGAATCGCTTGAACCCAGGAGGCAGAGGTTGCA
GTGAGCCGAGATTGCGCCACTGCACTCCAGCCTGGGCAACAAAAGCAAA
ACTCCATCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAGATGCAGACACG
AGACTG

SG13S153

TGGGCGCCTGTAATCCCAGCTACTCCATAGGCTGAGGCTGGAGAAT
CGCTTGAACCCAGGAGGCAGAGGTTGCAGTGAGCCGAGATTGCGCCACTG
CACTCCAGCCTGGGCAACAAAAGCAAACTCCATCTCAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAGATGCAGACACGAGACTGTGAACTGACTAGCAT
CACC[A/T]TTGCATTGTTTATAGATGTTGCCAGACAGAAAGCCCCAAAGCA
GCACAGTACCTTCCTGACATCTGGACTAGGAAATCTAGATTTTAGTAAAA
TACATGCTAATACTTACAGAAGAAATGTCGGCGTTAGAGTATGCCGTCAG
TTCCTTAGAGATTGCAATTCCTAATGCACTAGTATGGTTTCAGGTGCCAGG
AAC

SG13S97

ACTCCATCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAGATGCAG
ACACGAGACTGTGAACTGACTAGCATCACCATTGCATTGTTTATAGATG
TTGCCAGACAGAAAGCCCCAAAGCAGCACAGTACCTTCCTGACATCTGGA
CTAGGAAATCTAGATTTTAGTAAAATACATGCTAATACTTACAGAAGAAA
TGTC[A/G]GCGTTAGAGTATGCCGTCAGTTCCTTAGAGATTGCAATTCCTA
ATGCACTAGTATGGTTTCAGGTGCCAGGAACACGTTCTGTGAGGCTGCTG
CCCCAGGTGCTGACCCAGCCTTCCACACCATTTTCCTTCCTTGTGTTTAC
AGCCGCTCTGTCTTTTACAATAGCACCCCTCTCTAGTGGCTAATGGGCTCT
AT

SG13S154

AAAAAAAAAAAAAAAAAAAAAAAAAAGATGCAGACACGAGACTGTGAA
ACTGACTAGCATCACCATTGCATTGTTTATAGATGTTGCCAGACAGAAAG
CCCCAAAGCAGCACAGTACCTTCCTGACATCTGGACTAGGAAATCTAGAT
TTTAGTAAAATACATGCTAATACTTACAGAAGAAATGTCGGCGTTAGAGT
ATGC[C/T]GTCAGTTCCTTAGAGATTGCAATTCCTAATGCACTAGTATGGTT
TCAGGTGCCAGGAACACGTTCTGTGAGGCTGCTGCCCCAGGTGCTGACCC

CAGCCTTCCACACCATTTTCCTTCCTTGTGTTACAGCCGCTCTGTCTTTTA
CAATAGCACCCCTCTCTAGTGGCTAATGGGCTCTATGATTAGATAGCATCC
SG13S40

TTTCAGGTGCCAGGAACACGTTCTGTGAGGCTGCTGCCCCAGGTGC
TGACCCCAGCCTTCCACACCATTTTCCTTCCTTGTGTTACAGCCGCTCTGT
CTTTTACAATAGCACCCCTCTCTAGTGGCTAATGGGCTCTATGATTAGATA
GCATCCTTCAGTAGTGATAAAGGCAGTGACATCCTAGGGAGGTCAGCGG[
G/T]TGAAAGCGCTATATCTGGAAAACCTGAGAGCCTGTGAAGCTCAAGGA
CTTGACGGGGTTAGACCGTGAGCCGGGCTGCAGCTGGAAAAAGAATGACT
GTTCTTTCAGCAGATCCTTCCCTGTGCCATCTCTTCTTCATTCTCTCTAG
TGGCATTCTTATTTATCCTCTAAAACCACAATTCCATTATCTCTCTA
SG13S155

GAGGGTCTTCTCTTTTGCCTGGCTCCCTATGCAGCCCTATCTTACCC
CCTGCAAAGTCCCAGGGATGTGGCTCAGTCACTGCTCCTCTCTTCATCTGT
CACCATTGCTTGAGATCCTACAGCTGCTTTAATTCCGAGACCATCTGCAG
AACATGACAAAATTTGTCCACCTACCCACATGTCTTTTAACTTTAAAG[A/
G]CTTTACTAACTGATTCTTATTAGGGAATGAACAGAGGTGGCAAAAATAA
ACAATAGGAGATTGATTTACAAGAAATCTTTAAAATAGTAGATTTCTTCG
GACCTCATTGAAATATAAATGGCCTGCCTTCTTGTGTCCCTCCCTGGTCTC
CCTCTTTAGGTGATAAGAAGAAGATCCTGCCAGCCCCATAACCCGCC
SG13S156

TTAAAATAGTAGATTTCTTCGGACCTCATTGAAATATAAATGGCCT
GCCTTCTTGTGTCCCTCCCTGGTCTCCCTCTTTAGGTGATAAGAAGAAGAT
CCTGCCAGCCCCATAACCCGCCATCTGCGCGGGTTCTAGACCCCCTTCTCC
TCCCCTCTGGCCGTGGTAGGCATTACTGATGAATCATGGTGCTCTTTCTT[A
/C]CAGAGACCAAACCTGGCCTCGGAATCCTTCTTAACACAGATACTGCTT
AACACAACCACTCTGAGCAGCTGTCATAAGTAGAAGTAATAGATACTAGA
AGAAATGTCTAAGCCTAATCTAGACCAAATAACGGCCTGATATAGATGCA
AGCCAGAGGGGCTTTATGGTTAAATGCAAGGAGATTTTCAACCCTGCCG
SG13S157

CTGGTCTCCCTCTTTAGGTGATAAGAAGAAGATCCTGCCAGCCCCA
TAACCCGCCATCTGCGCGGGTTCTAGACCCCCTTCTCCTCCCCTCTGGCCG
TGGTAGGCATTACTGATGAATCATGGTGCTCTTTCTTCCAGAGACCAAACC
TGGCCTCGGAATCCTTCTTAACACAGATACTGCTTAACACAACCACTCTG[
A/G]GCAGCTGTCATAAGTAGAAGTAATAGATACTAGAAGAAATGTCTAAG
CCTAATCTAGACCAAATAACGGCCTGATATAGATGCAAGCCAGAGGGGCT
TTATGGTTAAATGCAAGGAGATTTTCAACCCTGCCGTCTAGAAGCTACTTG
CTGAGATCTTCTTCAGTTGGGCCCATCTCCTCCCCAGGCCTCTCTTCTG
SG13S158

CCATAACCCGCCATCTGCGCGGGTTCTAGACCCCCTTCTCCTCCCCT
CTGGCCGTGGTAGGCATTACTGATGAATCATGGTGCTCTTTCTTCCAGAGA
CCAAACCTGGCCTCGGAATCCTTCTTAACACAGATACTGCTTAACACAAC
CACTCTGAGCAGCTGTCATAAGTAGAAGTAATAGATACTAGAAGAAATGT
[A/C]TAAGCCTAATCTAGACCAAATAACGGCCTGATATAGATGCAAGCCA
GAGGGGCTTTATGGTTAAATGCAAGGAGATTTTCAACCCTGCCGTCTAGA
AGCTACTTGCTGAGATCTTCTTCAGTTGGGCCCATCTCCTCCCCAGGCCTC
TCTTCTGTTCCCTGGGCTATGTCACACTTGGACTCTGCAGACACCTAATGC
SG13S159

TGGTAGGCATTACTGATGAATCATGGTGCTCTTTCTTCCAGAGACC
AAACCTGGCCTCGGAATCCTTCTTAACACAGATACTGCTTAACACAACCA

CTCTGAGCAGCTGTCATAAGTAGAAGTAATAGATACTAGAAGAAATGTCT
AAGCCTAATCTAGACCAAAATACGGCCTGATATAGATGCAAGCCAGAGG
GGC[G/T]TTATGGTTAAATGCAAGGAGATTTTCAACCCTGCCGTCTAGAAG
CTACTTGCTGAGATCTTCTTCAGTTGGGCCCCATCTCCTCCCCAGGCCTCTCT
TCTGTTCCCTGGGCTATGTCACACTTGGACTCTGCAGACACCTAATGCTCTT
GGGACCTGCTTTAGTTCTTGACCTCACCAACCGAGGAGGAATTGCTAGAT
SG13S160

CAGAGACCAAACCTGGCCTCGGAATCCTTCTTAACACAGATACTGC
TTAACACAACCACTCTGAGCAGCTGTCATAAGTAGAAGTAATAGATACTA
GAAGAAATGTCTAAGCCTAATCTAGACCAAAATACGGCCTGATATAGATG
CAAGCCAGAGGGGCTTTATGGTTAAATGCAAGGAGATTTTCAACCCTGCC
GT[C/T]TAGAAGCTACTTGCTGAGATCTTCTTCAGTTGGGCCCCATCTCCTCC
CCAGGCCTCTCTTCTGTTCCCTGGGCTATGTCACACTTGGACTCTGCAGACA
CCTAATGCTCTTGGGACCTGCTTTAGTTCTTGACCTCACCAACCGAGGAGG
AATTGCTAGATGAGATCCTTCCCCCGGAATTTCTCTCTTGAACCCCA
SG13S32

GGGCTTTATGGTTAAATGCAAGGAGATTTTCAACCCTGCCGTCTAG
AAGCTACTTGCTGAGATCTTCTTCAGTTGGGCCCCATCTCCTCCCCAGGCCT
CTCTTCTGTTCCCTGGGCTATGTCACACTTGGACTCTGCAGACACCTAATGC
TCTTGGGACCTGCTTTAGTTCTTGACCTCACCAACCGAGGAGGAATTGCT[
A/C]GATGAGATCCTTCCCCCGGAATTTCTCTCTTGAACCCCAAGATGGTCCG
TTGCCCTTTCCAGAAGTTGCTCCAGCCCTGTCCGCTTAGGAAGTTCAGTG
TCATCCTTGATCCAGTGGGTAGGGAAGACATTCCATAATGAATGCCCCAG
TCTGAGCTTCTTCCCTTCAGGCTTCAGGCTGCCCTGCGAGGATTTTGCA
SG13S161

GTAGCTGAGACTACAGGTGTGCACTACCACACCCAGCTAATTTTTT
GTATTTTTAGTAGAGATAGGGTTTAGCTATGTTGGCCAGGCTGGTCTCGAA
CTGCTGAACTCAAGCAATCTGCCATCCCCGGCCTCCCAAAGTACTGGGAG
TATAGGCATAAGCCACCCATGATGCCAGCCTGAATCTTGGTTTCTTCCCC
[A/G]TTCATTTAAGCTATTACCTGGGCCTGAACTCAATGGCACCTGGCACC
AACTGGCAACTGACTCTTGGTCTTTTATTACCTACCTTCCCTAGCAGGCAC
TGGGTTGCTCCCTCTTCCCTATCCCATGGAGTCCCTGTCCTCTGTTGGGGCTCC
TACTGATCCTCTTGGCAATATGAAGTTCTCAGCTCAATGGTGGGTGG
SG13S162

CCCGGCCTCCCAAAGTACTGGGAGTATAGGCATAAGCCACCCATG
ATGCCAGCCTGAATCTTGGTTTCTTCCCCATTCAITTAAGCTATTACCTG
GGCCTGAACTCAATGGCACCTGGCACCAACTGGCAACTGACTCTTGGTCT
TTTATTACCTACCTTCCCTAGCAGGCACTGGGTTGCTCCCTCTTCCCTATCCC
[A/G]TGGAGTCCTGTCCTCTGTTGGGGCTCCTACTGATCCTCTTGGCAATAT
GAAGTTCTCAGCTCAATGGTGGGTGGGCAATGACTGCCAACTCTTGAGGC
CAATGAACTCAGGTTACCCCACTCCTCCTCCTGAGTTGCTCACTCACT
CCTCATTCACTCAACATTGATTCAGTAGATATTTGCTACCTGCTCTGT
SG13S163

CCGGCCTCCCAAAGTACTGGGAGTATAGGCATAAGCCACCCATGAT
GCCAGCCTGAATCTTGGTTTCTTCCCCATTCAITTAAGCTATTACCTGGG
CCTGAACTCAATGGCACCTGGCACCAACTGGCAACTGACTCTTGGTCTTTT
ATTACCTACCTTCCCTAGCAGGCACTGGGTTGCTCCCTCTTCCCTATCCCA[C
/T]GGAGTCCTGTCCTCTGTTGGGGCTCCTACTGATCCTCTTGGCAATATGA
AGTTCTCAGCTCAATGGTGGGTGGGCAATGACTGCCAACTCTTGAGGCCA

FIG. 8.30

ATGAACTCAGGTTACCCCACTCCTCCTCCTCCTGAGTTGCTCACTCACTCC
TCATTCACTCAACATTGATTAGTAGATATTTGCTACCTGCTCTGTG
SG13S164

GGCATAAGCCACCCATGATGCCAGCCTGAATCTTGGTTTCTTCCC
CATTCAATTAAGCTATTACCTGGGCCTGAACTCAATGGCACCTGGCACCAA
CTGGCAACTGACTCTTGGTCTTTTATTACCTACCTTCCCTAGCAGGCACTG
GGTTGCTCCCTCTTCCTATCCCATGGAGTCCTGTCCTCTGTTGGGGCTCC[C/
T]ACTGATCCTCTTGGCAATATGAAGTTCTCAGCTCAATGGTGGGTGGGCA
ATGACTGCCAACTCTTGAGGCCAATGAACTCAGGTTACCCCACTCCTCCTC
CTCCTGAGTTGCTCACTCACTCCTCATTCACTCAACATTGATTAGTAGAT
ATTTGCTACCTGCTCTGTGCCAGGTACCAGGTCAGTTGCTGAAGGA
SG13S165

CCTGGCACCAACTGGCAACTGACTCTTGGTCTTTTATTACCTACCTT
CCCTAGCAGGCACTGGGTTGCTCCCTCTTCCTATCCCATGGAGTCCTGTCC
TCTGTTGGGGCTCCTACTGATCCTCTTGGCAATATGAAGTTCTCAGCTCAA
TGGTGGGTGGGCAATGACTGCCAACTCTTGAGGCCAATGAACTCAGGTT[A/
T]CCCCACTCCTCCTCCTCCTGAGTTGCTCACTCACTCCTCATTCACTCAAC
ATTGATTAGTAGATATTTGCTACCTGCTCTGTGCCAGGTACCAGGTCAGT
TGCTGAAGGAGTAACAGTGAACATGACGGAGTCTTTGTCCCCAAGGAGAC
CCAAGGTGTCTCCTAGAGCCAGGGGCACATTGCAAGACCAAATATA
SG13S166

CTGGCAACTGACTCTTGGTCTTTTATTACCTACCTTCCCTAGCAGGC
ACTGGGTTGCTCCCTCTTCCTATCCCATGGAGTCCTGTCCTCTGTTGGGGC
TCCTACTGATCCTCTTGGCAATATGAAGTTCTCAGCTCAATGGTGGGTGGG
CAATGACTGCCAACTCTTGAGGCCAATGAACTCAGGTTACCCCACTCCT[C/
T]CTCCTCCTGAGTTGCTCACTCACTCCTCATTCACTCAACATTGATTAGT
AGATATTTGCTACCTGCTCTGTGCCAGGTACCAGGTCAGTTGCTGAAGGA
GTAACAGTGAACATGACGGAGTCTTTGTCCCCAAGGAGACCCAAGGTGTC
TCCTAGAGCCAGGGGCACATTGCAAGACCAAATATATTCAACTTACC
SG13S167

CCATGGAGTCCTGTCCTCTGTTGGGGCTCCTACTGATCCTCTTGGCA
ATATGAAGTTCTCAGCTCAATGGTGGGTGGGCAATGACTGCCAACTCTTG
AGGCCAATGAACTCAGGTTACCCCACTCCTCCTCCTCCTGAGTTGCTCACT
CACTCCTCATTCACTCAACATTGATTAGTAGATATTTGCTACCTGCTCT[A/
G]TGCCAGGTACCAGGTCAGTTGCTGAAGGAGTAACAGTGAACATGACGG
AGTCTTTGTCCCCAAGGAGACCCAAGGTGTCCTAGAGCCAGGGGCACA
TTGCAAGACCAAATATATTCAACTTACCAAATAATCATAGACCTAGTTCT
CAAAAAGCAAGAAGACTGATTCTCGTTGTCATTTCTCCTCCTCAGCA
SG13S168

TTAGAGTCTGTGGGCCCCCTCCAAGTGTGGAGTATGGTGTACTTCA
CCAGAGTTTGAGGAGAAACATTCTTCTTTTGGGAAGGCCGGGGAGCATAGA
TGGATATCAAGGCTGCTGTTTCTAAAAGCGAAACCCACCAAACAACAGTA
TTAGAATCATCTGTGGTGCTTATTAAAGATACAGATTCCTGGGCCCCATCC
C[A/C]GACTTATGAATCAGAATCTCTGCCAGAGGAAGCCTGAGAATTTGCA
TTCTCAGATGATTCTGCATTCTCAGATAACACATTCTTTAGGTGATTCTTAC
ACACACTGGAGTTTGGGAATCGCTGAAGGCTGTTCACTTCTCTTTTCTGAG
AAATGATTCAATTCATTTCAGAAATATTTGCAGAGGTCCTTATTTATTG
SG13S33

TGGCCTCATTCGTGTGATAAATCTGAGCCACCACGATATTTGACTTT
TCACAATTTAATTTATCTGAACCTCTATTCTCTGGCTAAAAAATATCCCT

FIG. 8.31

TACTTGGACTTCTTTATTTTATTTTCAATTCCTTACCAGCACTAGCAGGGG
ACTCTGTACTCATCTGCTGGCGCTGCCATAACAAAGCACTGCAGCCTG[G/T
]GGGGCTCAAACCACAGAATTTATTCTCTCACAGTCCTAGAGGCTAGAAGT
CCAAGATCAAAGTGTGGGCAGGGTCGGTTTCTCCTGCAGCCTCTCTCCTTG
GCTTATAGAGTGCCACCTTCTACCTGTGTCTTCACATCATCACCTCACTGA
GCATGTCTGTGTCCAAATCTCCCTTCTTATAAGACCCCAGTCAT
SG13S41

TCTCCTTGGCTTATAGAGTGCCACCTTCTACCTGTGTCTTCACATCA
TCACCTCACTGAGCATGTCTGTGTCCAAATCTCCCTTCTTATAAGACCCC
AGTCATACTGGATGAGGATCCACCCATATGAGTTCATTTTACCTTAATTAT
CTCTTTAAACACCCTGTCTCCAAATACAGTCCCATTCTGAGGAACTGAG[A/
G]GTAAAGATTCAACATATGAATTTTGGAAAGGGACCTAATTCAGCCCACA
ACACCCTCTTTTGGGATGTTTATTTTCCCCCTTAAGGAGCTAGTTAGGATG
TCTTATCTCATGAACATGACTGTGAACAGGAAAACAGGGAGAGAATGAA
GCTGGCCAAGGAACAGGGCTGGTGTGCTAGCTAGCAGTGCTTTTCTGATGT
SG13S169

CATTTTACCTTAATTATCTCTTTAAACACCCTGTCTCCAAATACAGT
CCCATTCTGAGGAACTGAGAGTAAAGATTCAACATATGAATTTTGGAAAGG
GACCTAATTCAGCCCACAACACCCTCTTTTGGGATGTTTATTTTCCCCCTT
AAGGAGCTAGTTAGGATGTCTTATCTCATGAACATGACTGTGAACAGGAA[
A/G]ACAGGGAGAGAATGAAGCTGGCCAAGGAACAGGGCTGGTGTGCTAGCT
AGCAGTGCTTTTCTGATGTGAGTGGGTCCACAGGGAGCTTGTTAAAATG
CAGATTCTGATTCAATTAGGTTCCAGAGGGACCTGAGATTTCCCATTTCTGA
CAAGTTTCCAGTGTGGGGGCTGATGCTGCTGGTCCACGGACCATACTTTG
SG13S404

GGGAGAGAATGAAGCTGGCCAAGGAACAGGGCTGGTGTGCTAGCTAG
CAGTGCTTTTCTGATGTGAGTGGGTCCACAGGGAGCTTGTTAAAATGCA
GATTCTGATTCAATTAGGTTCCAGAGGGACCTGAGATTTCCCATTTCTGACA
AGTTTCCAGTGTGGGGGCTGATGCTGCTGGTCCACGGACCATACTTTGAGT
A[G/T]CAAGGAGCTTGATACATAATGGCTGAGTGACTTTCAGACTCCTGCT
GTAGAAAAATTATGAGTTGGCTGGGCGTGGTGGCTCACGCCTGTAATCCC
AGCACTTTGGGAGGCCGAGGTGGGCAGATCACCTGAGGTCAGGAGTTCTGA
GACCAGCCTGGCCAACATGGTGAAACACCATCTCTACCAAAAATACAAAA
A
SG13S170

ACTTAAGCCCAGAAGACTGAGGTTGCAGTGAGCCGAGATTGCACC
ACTGCACTCCAGCTTGGGCTACAGAGTGAGACTCTATCTCAAAAACAAAG
AAACAACAACAACAATAACAACAAAAACCAAGTCTCTCCCTCCACTCAA
AAATGCAAGGGCCTGTCTCCCATTTGCTGGGTGCCCAGGTCTCATGAATGT
AGA[C/T]ATGAATTATTCAGTCAGCCTCAGGAGAATAGAATGAGCCCTCA
GATGCCGAAGCACCTTTCAGATTCCACCGGTTTTATCGGCTCATTTAACCT
TCACTTCTAACACAGTCCTGCATTACACACGTGTCTGTGCTTATGGGCAGC
TGCAGAGAGGGTCTTAATGGTCCTAATGCTCAGTGAGGATGCCCAATGGT
C
SG13S171

CTCAAAAACAAAGAAACAACAACAACAATAACAACAAAAACCA
AGTCTCTCCCTCCACTCAAAAATGCAAGGGCCTGTCTCCCATTTGCTGGGTG
CCCAGGTCTCATGAATGTAGATATGAATTATTCAGTCAGCCTCAGGAGA
ATAGAATGAGCCCTCAGATGCCGAAGCACCTTTCAGATTCCACCGGTTTT
ATC[A/G]GCTCATTTAACTTCACTTCTAACACAGTCCTGCATTACACACGT

FIG. 8.32

GTCTGTCGTTATGGGCAGCTGCAGAGAGGGTCTTAATGGTCCTAATGCTC
AGTGAGGATGCCCAATGGTCAACAGAACCTGCCATCTTCAGGCCATCAAG
GAGCTCTGGAGTTAAGGAAATCATGAGAGCACAGAGGGGCGGGTACAGC
AGA

SG13S172

TGTAGATATGAATTATTCCAGTCAGCCTCAGGAGAATAGAATGAGC
CCTCAGATGCCGAAGCACCTTTCAGATTCCACCGGTTTTATCGGCTCATT
AACTTCACTTCTAACACAGTCCTGCATTACACACGTGTCTGTCGTTATGG
GCAGCTGCAGAGAGGGTCTTAATGGTCCTAATGCTCAGTGAGGATGCCCA
[A/G]TGGTCAACAGAACCTGCCATCTTCAGGCCATCAAGGAGCTCTGGAGT
TAAGGAAATCATGAGAGCACAGAGGGGCGGGTACAGCAGAGCCCTCGTG
GTAATGGGTTTTGAGGTCTAGGCTCTCTTCACTTGGGTTTGAAATAAGTTC
AATGACTAGTAATAGCTGAGACACTTCTACCCTTCAAATGAAGTAAATGG
SG13S173

AGCACCTTTCAGATTCCACCGGTTTTATCGGCTCATTTAACTTCAC
TTCTAACACAGTCCTGCATTACACACGTGTCTGTCGTTATGGGCAGCTGCA
GAGAGGGTCTTAATGGTCCTAATGCTCAGTGAGGATGCCCAATGGTCAAC
AGAACCTGCCATCTTCAGGCCATCAAGGAGCTCTGGAGTTAAGGAAATCA
[A/T]GAGAGCACAGAGGGGCGGGTACAGCAGAGCCCTCGTGGTAATGGGT
TTTGAGGTCTAGGCTCTCTTCACTTGGGTTTGAAATAAGTTCAATGACTAG
TAATAGCTGAGACACTTCTACCCTTCAAATGAAGTAAATGGGAAAATGGA
GCATTGTTGAGTCCAGGGAGCTATAATTTAAACCCCATATATCTAAAAGG
SG13S42

CACACGTGTCTGTCGTTATGGGCAGCTGCAGAGAGGGTCTTAATGG
TCCTAATGCTCAGTGAGGATGCCCAATGGTCAACAGAACCTGCCATCTTC
AGGCCATCAAGGAGCTCTGGAGTTAAGGAAATCATGAGAGCACAGAGGG
GCGGGTACAGCAGAGCCCTCGTGGTAATGGGTTTTGAGGTCTAGGCTCTC
TTC[A/G]CTTGGGTTTGAAATAAGTTCAATGACTAGTAATAGCTGAGACAC
TTCTACCCTTCAAATGAAGTAAATGGGAAAATGGAGCATTGTTGAGTCCA
GGGAGCTATAATTTAAACCCCATATATCTAAAAGGGGTAACATTTTTGTGT
GTGTGAAATTGGTGTCATTTCGCACTGCATCTACAGTTTCTTTTCTCTCTC
SG13S194

ACATATTTGGGAAACGCATCATACTCTTCCTGTTCCCTCATGTCCGTT
GCTGGCATATTCAACTATTACCTCATCTTCTTTTTTCGGAAGTGACTTTGAA
AACTACATAAAGACGATCTCCACCACCATCTCCCCTCTACTTCTCATTCCC
TA ACTCTCTGCTGAATATGGGGTTGGTGTTCTCATCTAATCAATACCTA[C/
T]AAGTCATCATAATTCAGCTCTTGAGAGCATTCTGCTCTTCTTTAGATGGC
TGTAATCTATTGGCCATCTGGGCTTCACAGCTTGAGTTAACCTTGCTTTT
CCGGGAACAAAATGATGTCATGTCAGCTCCGCCCTTGAACATGACCGTG
GCCCCAAATTTGCTATTCCCATGCATTTTGTTTGTTTCTTCACTTA
SG13S195

TGGTGTTCTCATCTAATCAATACCTACAAGTCATCATAATTCAGCTC
TTGAGAGCATTCTGCTCTTCTTTAGATGGCTGTAAATCTATTGGCCATCTG
GGCTTCACAGCTTGAGTTAACCTTGCTTTTTCCGGGAACAAAATGATGTCAT
GTCAGCTCCGCCCTTGAACATGACCGTGGCCCCAAATTTGCTATTCCC[A/
G]TGCAATTTTGTTTGTTTCTTCACTTATCCTGTTCTCTGAAGATGTTTTGTGA
CCAGGTTTGTTGTTTTCTTAAAATAAAATGCAGAGACATGTTTTAAGCTGAT
AGTTGAGGGGTTTTGTTAATGGCTTTTGGGGGATTTATCTCTATACCCACA
AACGACTAGTTTGTTTTCCTCAAACCTAAATGATAATATTAATAA

FIG. 8.33

SG13S174

TTATCTCTATACCCACAAACGACTAGTTTGTTCCTCAAACCTAAAT
GATAATATTAATAACACATCCTGGCCAGGTGTGGTGGCTCATACCTGT
AATCCCAGCACTTTGGGAGGCCGAGGCAGGTGGATCACTTGAGGTCAGGA
ATTAAGACCAGCCTGGCCAATATGGTGAAAGCCTGTCTGTACTAAAAATA
C[A/G]AAAATTAGCCAGGTATGCTGGTGGATGCTTATAATCCCAGCTACTT
GGGAGGTTGAGGCAGGAGAATTGCTTGAACCCGGGAGGTTAGAGGTTGCA
GTGAGCCAAGATCATGCCACTGCACTCCAGCTTGGGCAACAGAGTGAGAC
TCCATCTCAAATTAATAAATAACACATCTGGCTTCTGGAAAAATTACTT
GA

SG13S34

GATCATGCCACTGCACTCCAGCTTGGGCAACAGAGTGAGACTCCAT
CTCAAATTAATAAATAACACATCTGGCTTCTGGAAAAATTACTTGAAGA
TCTTTTATGACATCCATCCCTCTTCACACAGCCATGTGAATTAGGTTGGTA
TCTTCATATACTAGCATCGTGCCAGCACTTCCATGTTATACAGTTTAAAA[
G/T]GTTCTGTAATTCCTGTGGGAACCTAAGATAATGCGAGGACCGTCAT
ACGTGCCCCCAAATATTGGCAAACCAATGAATAAATGAATGAATGAGTTT
ATGAATCGCTAACTGGCTGTATTTAATGAAGTATGTGTGTTGAGCCATTTT
CCACAGTGTGGACAGATTTGTCCACAATATGGGCCTCTTCCCAAAGGC
SG13S175

AATTAATAAATAACACATCTGGCTTCTGGAAAAATTACTTGAAGA
TCTTTTATGACATCCATCCCTCTTCACACAGCCATGTGAATTAGGTTGGTA
TCTTCATATACTAGCATCGTGCCAGCACTTCCATGTTATACAGTTTAAAA
TGTTCTGTAATTCCTGTGGGAACCTAAGATAATGCGAGGACCGTCATAC[
A/G]TGCCCCCAAATATTGGCAAACCAATGAATAAATGAATGAATGAGTTT
ATGAATCGCTAACTGGCTGTATTTAATGAAGTATGTGTGTTGAGCCATTTT
CCACAGTGTGGACAGATTTGTCCACAATATGGGCCTCTTCCCAAAGGCC
CTACCACCTAATGCCATCACACTGGGGATTGATTTCACATGTGAATT
SG13S176

AGTTCATAGTGACAGTGATCCAGCCACTGTCATGACAGGTGCCACT
TGGCAGAAACAGCACAGCTTGGGAAGATGGCGGGGTGTAGTCAAGATTCC
AGGATCCCCAACAGAGAAGCCAGCTCTTATAGGGGAGCCATTCATCAGGA
TTGAACTCTCAATCGAGCTGGACAGTAATAGGTGGGTCTGTGTTATCCCC
AG[A/G]TGAGTATCATGACAGTCACAATCCTAGGAAGGATGTGAAGCCTC
CCCCAGCTCTCCTCCAGTTGCCTGCTTGGGCAGCAGAGATGATGGAATGT
GGAGTCTGGCGTGGTCTGAGGCCTGAATCCATGTGCCTCATGTATGATGCT
CAGGCAAGAGGATCTCTCAATTCAAGGGAGAGGGCCTGAATGAGCCTTGC
TT

SG13S177

CTTGGCAGAAACAGCACAGCTTGGGAAGATGGCGGGGTGTAGTCAA
GATTCCAGGATCCCCAACAGAGAAGCCAGCTCTTATAGGGGAGCCATTCA
TCAGGATTGAACTCTCAATCGAGCTGGACAGTAATAGGTGGGTCTGTGTT
ATTCCCCAGATGAGTATCATGACAGTCACAATCCTAGGAAGGATGTGAAG
CCT[C/T]CCCCAGCTCTCCTCCAGTTGCCTGCTTGGGCAGCAGAGATGATG
GAATGTGGAGTCTGGCGTGGTCTGAGGCCTGAATCCATGTGCCTCATGTA
TGATGCTCAGGCAAGAGGATCTCTCAATTCAAGGGAGAGGGCCTGAATGA
GCCTTGCTTCCAGGCCTGTCTGATGGTCCAGGCTGAAGCCCCCTCCTGGCT
TG

SG13S178

CTGGCGTGGTCTGAGGCCTGAATCCATGTGCCTCATGTATGATGCT

FIG. 8.34

CAGGCAAGAGGATCTCTCAATTCAAGGGAGAGGGCCTGAATGAGCCTTGC
TTTCCAGGCCTGTCTGATGGTCCAGGCTGAAGCCCCTCCTGGCTTGCACTG
CCAGACCTCATCCAGCAGGAGCTCCTTGGCATTGACTGCTTCAGGATAGTT
[C/G]CTTCTGCTCTGAGTGCTCTCTAAAGAGCAGTGCTCTACCATCCAAGC
TGGGCTTTTCTTTTCTTCTTGCTGATAGGGAAGGCATGGGACATTGCAGGA
TGGAAGTGGCCCCCAGGCCCTTCTCATGCCTGGGCTTGGTTTGGAAGGTGG
TCAGGTGATCAATAATCCTGATTGGCCTGGCATTGAGGAGTTTTCCTGG
SG13S35

TGCTCTCTAAAGAGCAGTGCTCTACCATCCAAGCTGGGCTTTTCTTT
TCTTCTTGCTGATAGGGAAGGCATGGGACATTGCAGGATGGAAGTGGCCC
CCAGGCCTTCTCATGCCTGGGCTTGGTTTGGAAGGTGGTCAGGTGATCAAT
AATCCTGATTGGCCTGGCATTGAGGAGTTTTCCTGGGATGTGGTCCTTTC[A
/G]GTTTTTTAAAAATTATTTTTATTGATACACATATTTGTAGGTATTTGTGG
GGTGCATGTGATACTTTATTATGTGTGTGGATTGTGTAATGATGAAGTCAG
GGCATTTAGGGTCTTCATCACCTTGATTATCATTCTATGTGTTGAGAACAA
TTTCAAGTTCTCAGTTCCAGCTATTTTGAAATAGACAGTCCATTT
SG13S179

GATACTTTATTATGTGTGTGGATTGTGTAATGATGAAGTCAGGGCA
TTTAGGGTCTTCATCACCTTGATTATCATTCTATGTGTTGAGAACATTTCA
AGTTCTCAGTTCCAGCTATTTTGAAATAGACAGTCCATTTTGTAGCTACA
GTCACCCAACCCGGCTGTCAGACATTGGAACCTTACTCCTATTGAACTGT[A/
G]TATTTGTACCCATTACCAAACCTCTCTTTGGGCTTTCAGTTTACAACCTG
GGATGATCCTGGGAAAACCTAAAGTAAATCAGACACCCGACGTGTGAGCTA
GGTTATAATATGCCCAGTGGACCCTGGGGACATCTTAGCTTTCAGAGGTC
ATGCTGTCCAAGCTGACTGTGGGGCTTCCAGAAGGTGGGGAGAGGAA
SG13S180

TATGTGTGTGGATTGTGTAATGATGAAGTCAGGGCATTTAGGGTCT
TCATCACCTTGATTATCATTCTATGTGTTGAGAACATTTCAAGTTCTCAGT
TCCAGCTATTTTGAAATAGACAGTCCATTTTGTAGCTACAGTCACCCAAC
CCGGCTGTCAGACATTGGAACCTTACTCCTATTGAACTGTGTATTTGTAC[C/
T]CATTCACCAAACCTCTCTTTGGGCTTTCAGTTTACAACCTGGGATGATCCT
GGGAAAACCTAAAGTAAATCAGACACCCGACGTGTGAGCTAGGTTATAATA
TGCCCAGTGGACCCTGGGGACATCTTAGCTTTCAGAGGTCATGCTGTCCA
AGCTGACTGTGGGGCTTCCAGAAGGTGGGGAGAGGAAATGATGCAAT
SG13S181

TGGGAAAACCTAAAGTAAATCAGACACCCGACGTGTGAGCTAGGTT
ATAATATGCCCAGTGGACCCTGGGGACATCTTAGCTTTCAGAGGTCATGC
TGTCCAAGCTGACTGTGGGGCTTCCAGAAGGTGGGGAGAGGAAATGATGC
AATGGCCCATCAGAGGCACTACTTGGGGCCTGGGGCCAGAGTGCATGTCT
AAG[C/G]CATTAAGGGGAGGGGAGAGCAGCCTTCATAATTATGAAGAGGA
GTCTCAGGTGCACAGCTTCTGATGAGGGACAGCTTCTAATTGAAGACAGC
ATTGTGTAATGCTCAAACCTCCCTGTCTTCAGAGTGCCTGCTGTATCCCACC
ATCAGTTCTGTGACTTCTCCCTAAGCCTCAATTTTGCATGTGTTACATTGG
GA
SG13S182

CCTGCATAGCAAATTCTTGCAAATGTAGGGACTCAAAACAATATAA
ATTTATTATCTGACAGTTTTTCTGGGTCAGAGGTCTTACTAGGCTGTAATC
AGAGGGCAACCAAAGCTGTGATCTCAGCTGAAGCTCAGGATTCTCTTCCA
AGCTCACTGGTTGTTGGCAGAAATTCAGTTCTTTCCAGTTGGAAGACTAAAG
[C/T]CTACAGTCTTCAGTCTCTAGAAGCCTTTTCTCTGGCACAGGTTTCTCT

FIG. 8.35

ACAACATGGCCATTTATGTCTTTAAGGCCAATAGGAGAACATGATTAGCA
TATTTTTTTTAAAGTGAACCTTTAGACCCTTTTTTAAAGGCCTATCTGATTAGG
CCAGGCCCAAGTGAGCTTTAAGTCAACTGATTAGAGATCTTAATTAC
SG13S183

CTGAAGCTCAGGATTCTCTTCCAAGCTCACTGGTTGTTGGCAGAAT
TCAGTTCTTTCCAGTTGGAAGACTAAAGCCTACAGTCTTCAGTCTCTAGAA
GCCTTTTCTCTGGCACAGGTTTCTCTACAACATGGCCATTTATGTCTTTAA
GGCCAATAGGAGAACATGATTAGCATATTTTTTTTAAAGTGAACCTTAGAC[
C/T]CTTTTTTAAAGGCCTATCTGATTAGGCCAGGCCCAAGTGAGCTTTAAG
TCAACTGATTAGAGATCTTAATTACATCTGCAAAGTCCCTTCATGTTTACC
GTATAACATAACTTAGTGAAAGGAGTGAAATTGCAACCAGGTTCTGCCTG
CACTCCACGGAAGGGGATTCTGCAGAAGTGTGGGTACGGGGGGGGTTA
SG13S184

AGAACATGATTAGCATATTTTTTTTAAAGTGAACCTTAGACCCTTTTT
TAAAGGCCTATCTGATTAGGCCAGGCCCAAGTGAGCTTTAAGTCAACTGA
TTAGAGATCTTAATTACATCTGCAAAGTCCCTTCATGTTTACCGTATAACA
TAAGTGTGAAAGGAGTGAAATTGCAACCAGGTTCTGCCTGCACTCCAC[
A/G]GAAGGGGATTCTGCAGAAGTGTGGGTACGGGGGGGGTTATTTTGGGA
TTCTGCCTACGTCACTGAGTCAAAAGAAGCTGAATGGTTGTGATGCTGAG
GTTTTTGGGCAGCAGCAGTGTGTGTGTGTGAGTGAATTCATACGTATGACC
ACCTGGGAAGAAAGGAGGCTGTGGTTTCTCCACCTCCTGGCAGACAGA
SG13S185

GGGATTACAGACACACACTGCCACGCCTGGCTAATTTTTGTATTTTT
AGTAGAGACGAGGTTTTGCCATGTTGGCCAGGCTGGTCTTGAACCTCCTGA
CCTCAAGTGATCCGCCACCTCAGCCTCCCAAAGTGCTGGGATTACAGAC
GTGAGCCACCATTAAACCATTTTTCTATCTCCTGTGGGAAAGGGGCACAGTG
A[A/G]AGAACAGATGAAGCTGAGACATACAAGTGAACCTCCTCCCTCCTCTC
CATTTAGACTAAAATAGGATTATTCATACTGAGATTCTCCCTGGTTGCAA
GAGATAATCTGTGCAACTGGGTTTTTACAATTATCCCTACCCTATGCTTTC
CTCATCTGTCTTCCTCGTAGTCAGCTCAGGCTGCTATAACAAAACACCA
SG13S405

GGCAGATTCGGTGTCTAATGAGGTCCTGCTTTCCAGTTTATAGACA
GTGCCCTTATCGCTACCGCCTTACACAGTGGAAGGAGAGGACGAGAAGCTC
CTTGGGCTTTTTTTTGTCTTTCTTTCTCTCTCTCTCTTTTTTTTTTTTT
AATAAGGTCATCTTAGTCCATTTTGTGTTGCTAAAAGGAACATCT[A/G
]AGGTTGAGTAATTTATTTTATTTTAAAAAGTGGCCAGGCATGGAGGCTTA
TCCTGTAACCCTAATCCTTTAGGAGGCCAAAACAGCAGGATTGTTTGAGG
CCAGGAGTTCAAGACCAGCCTAGGCAAGATAGTGAGACCCCATCTACCCC
ATCTCTACTAAAATTTTAAAAAATTAGCTGTGTGTGTGTAAAGTGTGC
SG13S91

AATTTATTTTATTTTAAAAAGTGGCCAGGCATGGAGGCTTATCCTGT
AACCTAATCCTTTAGGAGGCCAAAACAGCAGGATTGTTTGAGGCCAGGA
GTTCAAGACCAGCCTAGGCAAGATAGTGAGACCCCATCTACCCCATCTCT
ACTAAAATTTTAAAAAATTAGCTGTGTGTTGTAAAGTGTGCTTGTAGTCCC
[A/G]GCCACTTGAGAGGCTGAGGTGGGTGGAGTTCAAGGCTGCAGTGAGT
TATGATTGAGCCACTGCACTCCAACCCGGGTAAACGGGGCAAGACCTTGTC
TCTATTTAAAAAATCTTTATGTGGCTCACTATTCTGGGTGGCTGG
AAAGTTCAAGATTGGGCATCTGCATCTGGTGACAGCCTCATGTGCTTCC
SG13S186

TAACCCTAATCCTTTAGGAGGCCAAAACAGCAGGATTGTTTGAGGC

FIG. 8.36

CAGGAGTTCAAGACCAGCCTAGGCAAGATAGTGAGACCCCATCTACCCCA
TCTCTACTAAAATTTTAAAAAATTAGCTGTGTGTTGTAAAGTGTGCTTGTA
GTCCCGGCCACTTGAGAGGCTGAGGTGGGTGGAGTTCAAGGCTGCAGTGA
G[A/T]TATGATTGAGCCACTGCACTCCAACCCGGGTAACGGGGCAAGACCT
TGTCTCTATTTAAAAAATAATCTTTATGTGGCTCACTATTCTGGGTGG
CTGGAAAGTTCAAGATTGGGCATCTGCATCTGGTGACAGCCTCATGTCGC
TTCCAGTCATGGGGGAAGACGAAGGAGAGCTGGCACGTGCAGATATCAC
G

SG13S187

ATCCTTTAGGAGGCCAAAACAGCAGGATTGTTTGAGGCCAGGAGTT
CAAGACCAGCCTAGGCAAGATAGTGAGACCCCATCTACCCCATCTCTACT
AAAATTTTAAAAAATTAGCTGTGTGTTGTAAAGTGTGCTTGTAAGTCCCGGC
CACTTGAGAGGCTGAGGTGGGTGGAGTTCAAGGCTGCAGTGAGTTATGAT
T[A/G]AGCCACTGCACTCCAACCCGGGTAACGGGGCAAGACCTTGTCTCTA
TTTAAAAAATAATCTTTATGTGGCTCACTATTCTGGGTGGCTGGAAA
GTTCAAGATTGGGCATCTGCATCTGGTGACAGCCTCATGTCGCTTCCAGTC
ATGGGGGAAGACGAAGGAGAGCTGGCACGTGCAGATATCACGTGTTGAG
G

SG13S188

TTAAAAAATTAGCTGTGTGTTGTAAAGTGTGCTTGTAAGTCCCGGCC
ACTTGAGAGGCTGAGGTGGGTGGAGTTCAAGGCTGCAGTGAGTTATGATT
GAGCCACTGCACTCCAACCCGGGTAACGGGGCAAGACCTTGTCTCTATTT
AAAAAATAATCTTTATGTGGCTCACTATTCTGGGTGGCTGGAAAGTT
CA[A/G]GATTGGGCATCTGCATCTGGTGACAGCCTCATGTCGCTTCCAGTC
ATGGGGGAAGACGAAGGAGAGCTGGCACGTGCAGATATCACGTGTTGAG
GGCAGAAGCGAGAGAGAGAGGGGAGAGATGCCAGGCTCTTTTAAACAAC
CAGCACTGGGGAACTAATAGAGTGAGAGCTCACTGACTCCTGAGGGAG
GACAT

SG13S406

ATGGGGGAAGACGAAGGAGAGCTGGCACGTGCAGATATCACGTGT
TGAGGGGCAGAAGCGAGAGAGAGAGGGGAGAGATGCCAGGCTCTTTTAA
CAACCAGCACTGGGGAACTAATAGAGTGAGAGCTCACTGACTCCTGAGG
GAGGACATTAATCTATTGATGAGCGACCTGCCTCCATGACCCAAACACCT
CCAA[C/T]GATACCCACCTCCAACACTGCCACACTAGGGATTAACCTTCA
ACTTGAGATTTAGAGGGGGGAACTTACAACTATCGCAGGCACTAATAC
CACTCATGAGGGCTCCACCTTCATGACCTAATCACTTCCTAAAGGCCTTAC
CTCTTAATCTCATCACATTGAGGATTCGATTTCAACTTGAATTTTGGGGGG
AC

SG13S92

CTCGCTGCCACCTGAAATTAGATCATTTATTTACCCCTTTATTTGTT
CAGTTTGCCTTGTCGTTAGAATATAAGCTTCCAAAGGGCAGGAGCTTTGC
CTATATTGTTAGGCCGGGCATACAATGAGCACTCAAAAAAATATTTGATG
AGTGTATGAAAGAACAGACTGGGTTATGTAATTGTGCCTACTTACCTATA[
C/T]GACCGTGTGGTGGGGTTTATGGTGGGTGTGGTGGTGATGGCTATAGG
GCTATAAGCAAATTTGGGACAGGGAGTCTAAGAAATGTTCTTAAATTTTA
GTAAGCAAAGCATCCTCTACAGAACCTGTCTTAAACATGAAAGTTCCTT
AGTGCTACCCCCAGAGGTATGATTTGGTAGGTCAAGGATAGGGCCTGGAA

SG13S93

TGCCACCTGAAATTAGATCATTTATTTACCCCTTTATTTGTTTCAGTT
TGCTTGTCCGTTAGAATATAAGCTTCCAAAGGGCAGGAGCTTTGCCTATA

FIG. 8.37

TTGTTAGGCCCGGCATACAATGAGCACTCAAAAAAATATTTGATGAGTGT
ATGAAAGAACAGACTGGGTATGTAATTGTGCCTACTTACCTATATGACC[
A/G]TGTGGTGGGGTTTATGGTGGGTGTGGTGGTGATGGCTATAGGGCTAT
AAGCAAATTTGGGACAGGGAGTCTAAGAAATGTTCTTAAATTTTAGTAAG
CAAAGCATCCTCTACAGAACCTGTCTTAAACATGAAAGTTCCTTAGTGCT
ACCCCCAGAGGTATGATTTGGTAGGTCAAGGATAGGGCCTGGAAATCA
SG13S36

CCTGTCTTAAACATGAAAGTTCCTTAGTGCTACCCCCAGAGGTAT
GATTTGGTAGGTCAAGGATAGGGCCTGGAAATTCACATTCTTGTTAAGAT
GTTCTTCATCCGGGGTTTGTGACCACCTTTTCAGAAGATTTTGTCTCTGTA
GCTGTACTACCCAATGCAGTAGTTCGTAGTCAGTGTGGCTCCTGAGCCCT[
C/T]GAAGTGTAGCTCCTCTGAACTGAGACGTGCTGTAAATGTAAATTGCA
CACCGGAGTTTGAAGAGTTAATACAAAGAAAAAGGAATGCAAAACATCT
CATTAATAATGCTTTACACTGATTACATATTGAAATGGTAATCTTGTAGAT
ATAGTGC GTTAAATAAAATATACTGTTAGGCTTAATTTACAGTCTTTATA
SG13S407

TCAGCCAATCAACAAGAGGGCAAAAGAACAACATTTGATGTGTA
ATTACTTAATTTAGTGCATATGCATTTGGGTCCCTCAATGTCAGCACTATGG
CAACCAGAACATGGCCACAATAACTGTCTGGAAATGTCTATTCTTACCTG
GACCCAGCAGGCCATGCCCCACTGATTATATAATCTCCCTCTCTCCTTGTT
A[C/T]GGTCTGAATGCTTGCATCCCTCAAAAATTCATGTGTTGAAATCCTA
ACCCCCAAGGTGATGATATTAGGAGGTCTGGCCTTTTGAGAGGTAATTAGG
TCATGAAGACAGCATCCTCATGAATGGGATTAGTGTCTTATAAAATAGG
CCCAAGGGAGCTCATTCACTTTGTCCACCATGTGAGAACACAGCGAGAGG
G

SG13S408

CCTTGTTACGGTCTGAATGCTTGCATCCCTCAAAAATTCATGTGTTG
AAATCCTAACCCCCAAGGTGATGATATTAGGAGGTCTGGCCTTTTGAGAGG
TAATTAGGTCATGAAGACAGCATCCTCATGAATGGGATTAGTGTCTTATA
AAATAGGCCCAAGGGAGCTCATTCACTTTGTCCACCATGTGAGAACACAG
[C/T]GAGAGGGCACCATTTATGCACCAGGAAATGGGCCTTTTCCAGACAAT
CTGTCTGGTGCCTGGATCTTGGACTTCACAGCCTCTAGAACTGTGAGAAAT
AATTTGTTTTTTTATAAGCCACCAAATCTATGGTTTTTTTTTATAGAAACCGT
ATGGACTAAAACACTCCCTAATTATTTAACTTATCAGTGCCTG

SG13S7

CTAACCCCCAAGGTGATGATATTAGGAGGTCTGGCCTTTTGAGAGGT
AATTAGGTCATGAAGACAGCATCCTCATGAATGGGATTAGTGTCTTATA
AAATAGGCCCAAGGGAGCTCATTCACTTTGTCCACCATGTGAGAACACAG
CGAGAGGGCACCATTTATGCACCAGGAAATGGGCCTTTTCCAGACAATCT
GT[C/T]GGTGCCTGGATCTTGGACTTCACAGCCTCTAGAACTGTGAGAAAT
TAATTTGTTTTTTTATAAGCCACCAAATCTATGGTTTTTTTTTATAGAAACCGT
AATGGACTAAAACACTCCCTAATTATTTAACTTATCAGTGCCTGGGC
AGTGACATATTAAGAAGATGCTGGCCAACGTAATTGACACCATAAGGCT

SG13S37

TCATCTCATTTTAACCTTTTGTTCACAAAGCCTCTCTTTTCATGACTTC
CCCGCCTTCATTTTCCCATATGGTGGGGTTATTATTAAGACATTAAATGA
GAGTGGACAGGTAGGCAAAGGAGGTGGGTGTCAGGGGAGTTGAGGGTTG
CCTGTGTACTTTTCTAGACTGTTCCACTTCACATCAGTGAAATATCCCA[A
/G]TTGATACTATCATGAAACAAAGCAAATGAAATGCTGAGCACGGAGCTT
CGTCTTGATGAAATGCTGAAAGAAAAGAAAGGAAAAATAAAGTAGCCAT

FIG. 8.38

TATTTTTGCCCTTCCTCCCACCCCATGTTTACTACTCTTATTTCTCTTTTGT
ATTGTTGTGTTGGAAGCACAGCATCAGAAAACTCCCAGTTTGTGAGA
SG13S409

ACAGGTAGGCAAAGGAGGTGGGTTGCAGGGGAGTTGAGGGTTGCC
TGTGTACTTTTCTAGACTGTTCCACTTCACATCAGTGAAATATTCCCAATT
GATACTATCATGAAACAAAGCAAATGAAATGCTGAGCACGGAGCTTCGTC
TTGATGAAATGCTGAAAGAAAAGAAAGGAAAAATAAAGTAGCCATTATTT
TT[A/G]CCCTTCCTCCCACCCCATGTTTACTACTCTTATTTCTCTTTTGTAT
TGTTGTGTTGGAAGCACAGCATCAGAAAACTCCCAGTTTGTGAGAGATAA
CTCAGTGTTTAGTTCACTTAAACCTGAGAAAGGAGAAGAGGATGCCACCG
TGAGGTCCAGGACGTAAAGAGGAAAAAAACAGACAAAAAAATCCATATG
A

SG13S8

CAGGTAGGCAAAGGAGGTGGGTTGCAGGGGAGTTGAGGGTTGCCT
GTGTACTTTTCTAGACTGTTCCACTTCACATCAGTGAAATATTCCCAATTG
ATACTATCATGAAACAAAGCAAATGAAATGCTGAGCACGGAGCTTCGTCT
TGATGAAATGCTGAAAGAAAAGAAAGGAAAAATAAAGTAGCCATTATTTT
TG[A/C]CCTTCCTCCCACCCCATGTTTACTACTCTTATTTCTCTTTTGTATT
GTTGTGTTGGAAGCACAGCATCAGAAAACTCCCAGTTTGTGAGAGATAAC
TCAGTGTTTAGTTCACTTAAACCTGAGAAAGGAGAAGAGGATGCCACCGT
GAGGTCCAGGACGTAAAGAGGAAAAAAACAGACAAAAAAATCCATATGA
A

SG13S410

TTCGTCTTGATGAAATGCTGAAAGAAAAGAAAGGAAAAATAAAGT
AGCCATTATTTTTGCCCTTCCTCCCACCCCATGTTTACTACTCTTATTTCT
CTTTTGTATTGTTGTGTTGGAAGCACAGCATCAGAAAACTCCCAGTTTGT
AGAGATAACTCAGTGTTTAGTTCACTTAAACCTGAGAAAGGAGAAGAGGA
[C/T]GCCACCGTGAGGTCCAGGACGTAAAGAGGAAAAAAACAGACAAAA
AAATCCATATGAAATGAAATGTGAAAGAGGCGCTTTCGAGCAGATGAGT
GTTGTAGATTACAGTGTTGAGAGCTGTTTGTGTCCAGAGCTGCTTGCTGCA
CCTGGCGGGATAAACACTGGTCTAACAGAGGATCCTTGTTTCAAGGAGGC
T

SG13S411

AAGAAAAGAAAGGAAAAATAAAGTAGCCATTATTTTTGCCCTTCCT
CCCACCCCATGTTTACTACTCTTATTTCTCTTTTGTATTGTTGTGTTGGA
GCACAGCATCAGAAAACTCCCAGTTTGTGAGAGATAACTCAGTGTTTAGT
TCACTTAAACCTGAGAAAGGAGAAGAGGATGCCACCGTGAGGTCCAGGA
C[A/G]TAAAGAGGAAAAAAACAGACAAAAAAATCCATATGAAATGAAAA
TGTGAAAGAGGCGCTTTCGAGCAGATGAGTGTTGTAGATTACAGTGTTGA
GAGCTGTTTGTGTCCAGAGCTGCTTGCTGCACCTGGCGGGATAAACACTG
GTCTAACAGAGGATCCTTGTTTCAAGGAGGCTGCCTTTTATTTGGGGGGAC
AA

SG13S9

ATTATTTTTGCCCTTCCTCCCACCCCATGTTTACTACTCTTATTTCT
CTTTTGTATTGTTGTGTTGGAAGCACAGCATCAGAAAACTCCCAGTTTGT
AGAGATAACTCAGTGTTTAGTTCACTTAAACCTGAGAAAGGAGAAGAGGA
TGCCACCGTGAGGTCCAGGACGTAAAGAGGAAAAAAACAGACAAAAAA
[C/T]CCATATGAAATGAAATGTGAAAGAGGCGCTTTCGAGCAGATGAGT
GTTGTAGATTACAGTGTTGAGAGCTGTTTGTGTCCAGAGCTGCTTGCTGCA

FIG. 8.39

CCTGGCGGGATAAACTGGTCTAACAGAGGATCCTTGTTTCAAGGAGGC
TGCCTTTTATTTGGGGGGACAAAATTGTTCTTGAAAGCTGCTCAGTGGTT
SG13S412

TTTGTATTGTTGTGTTGGAAGCACAGCATCAGAAAACTCCCAGTT
TTGAGAGATAACTCAGTGTTTAGTTCACTTAAACCTGAGAAAGGAGAAGA
GGATGCCACCGTGAGGTCCAGGACGTAAAGAGGAAAAAACAGACAAAA
AAATCCATATGAAATGAAAATGTGAAAGAGGCGCTTTCGAGCAGATGAGT
GTT[A/G]TAGATTACAGTGTTGAGAGCTGTTTGTGTCCAGAGCTGCTTGCT
GCACCTGGCGGGATAAACTGGTCTAACAGAGGATCCTTGTTTCAAGGA
GGCTGCCTTTTATTTGGGGGGACAAAATTGTTCTTGAAAGCTGCTCAGTGG
TTCAAGCTACAGCATGGTGGACTAGCAGAATGGACTCCAGGGCCTCCGAG
GA

SG13S413

TTTTGAGAGATAACTCAGTGTTTAGTTCACTTAAACCTGAGAAAGG
AGAAGAGGATGCCACCGTGAGGTCCAGGACGTAAAGAGGAAAAAACAG
ACAAAAAATCCATATGAAATGAAAATGTGAAAGAGGCGCTTTCGAGCA
GATGAGTGTTGTAGATTACAGTGTTGAGAGCTGTTTGTGTCCAGAGCTGCT
TGC[C/T]GCACCTGGCGGGATAAACTGGTCTAACAGAGGATCCTTGTTT
CAAGGAGGCTGCCTTTTATTTGGGGGGACAAAATTGTTCTTGAAAGCTGCT
CAGTGGTTCAAGCTACAGCATGGTGGACTAGCAGAATGGACTCCAGGGCC
TCCGAGGAGACAGTGACTGCTGCCAGAAATAGTCAAGGATAGAAAGGAA
GGA

FIG. 8.40

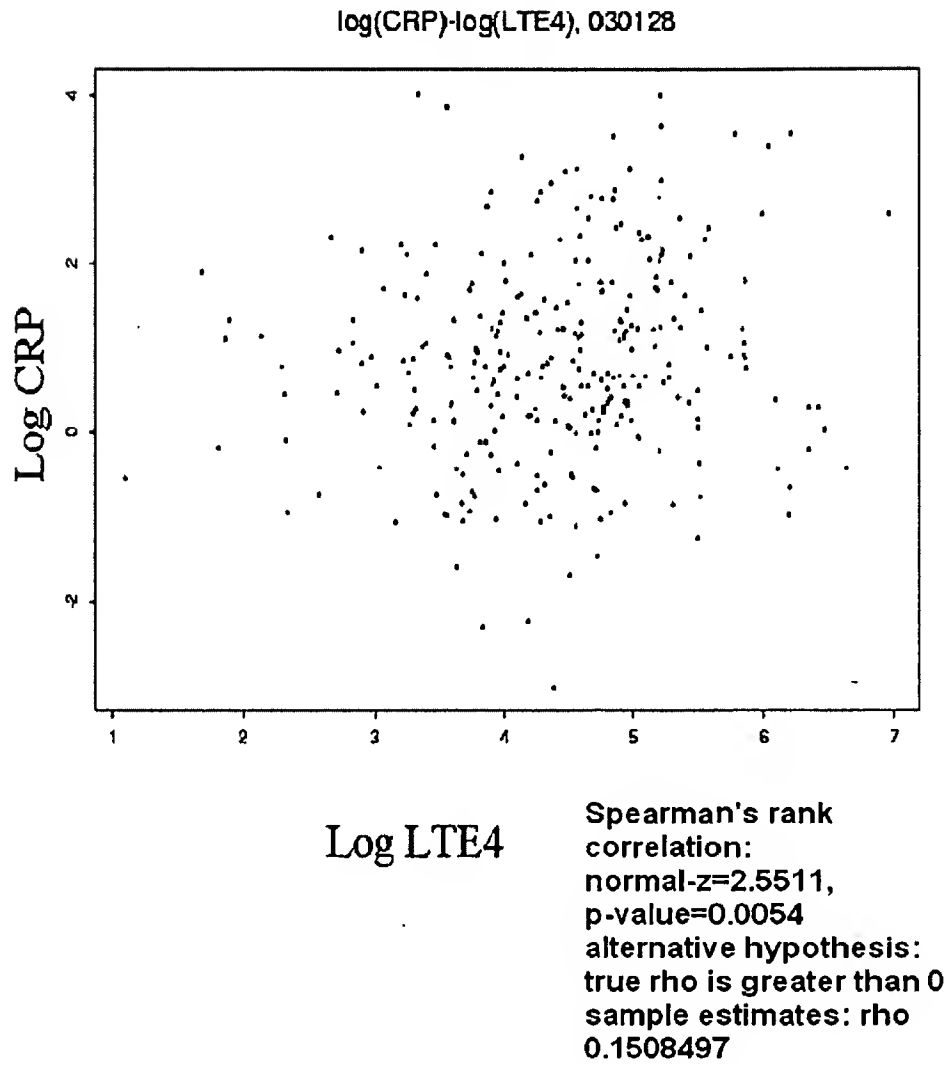


FIG. 9

Figure 10

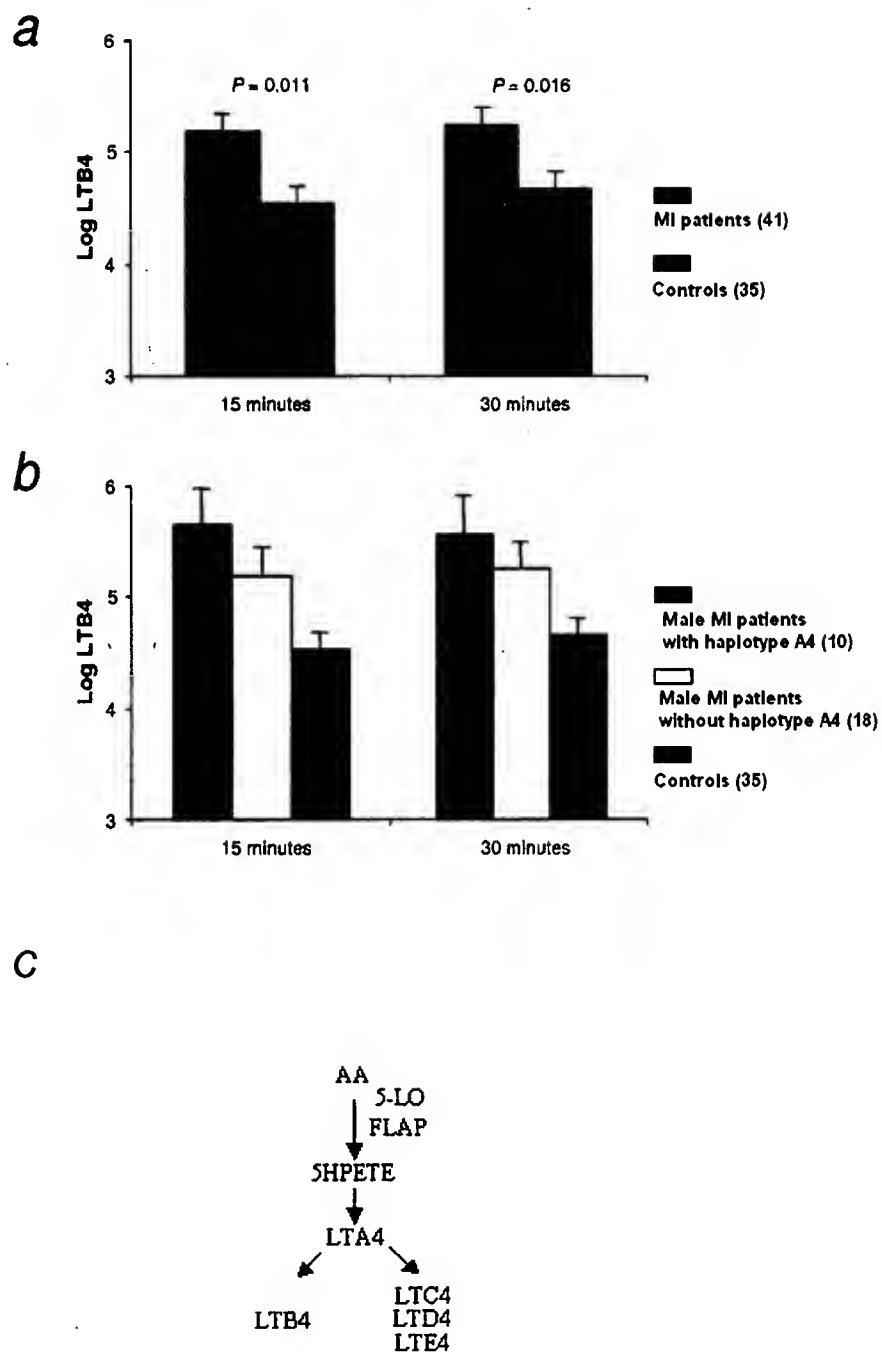


FIG. 10

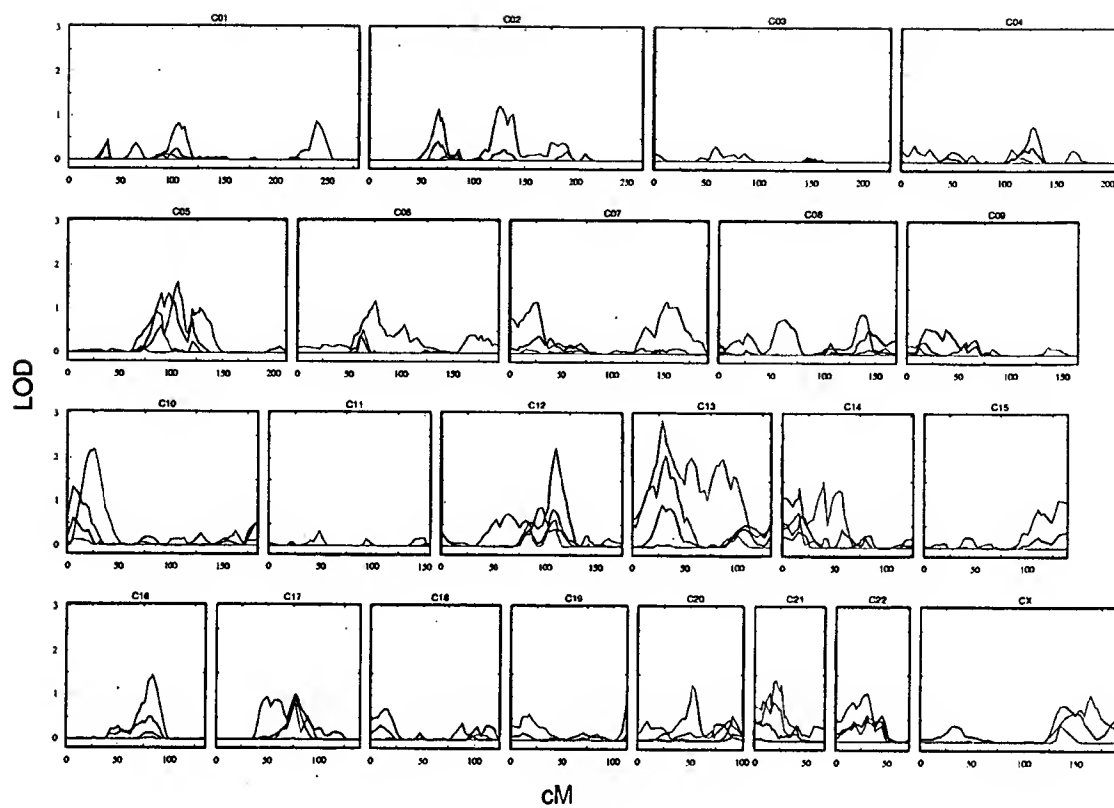


FIG. 11

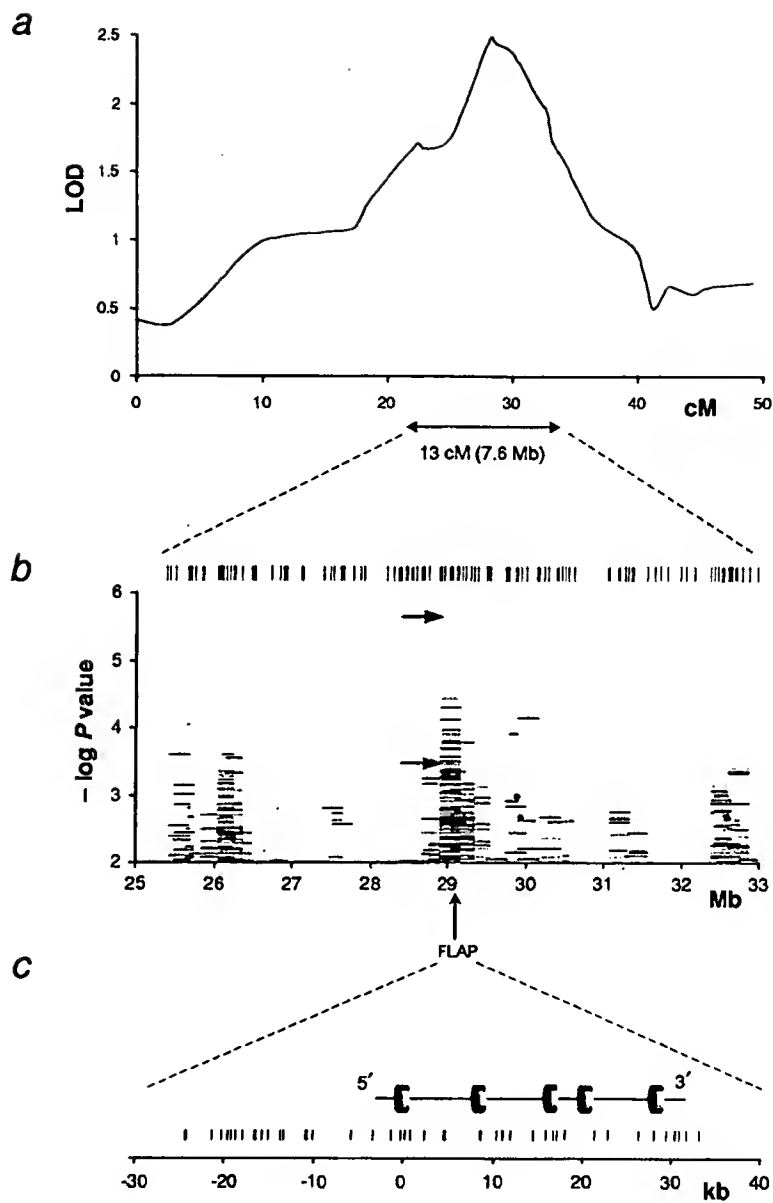


FIG. 12

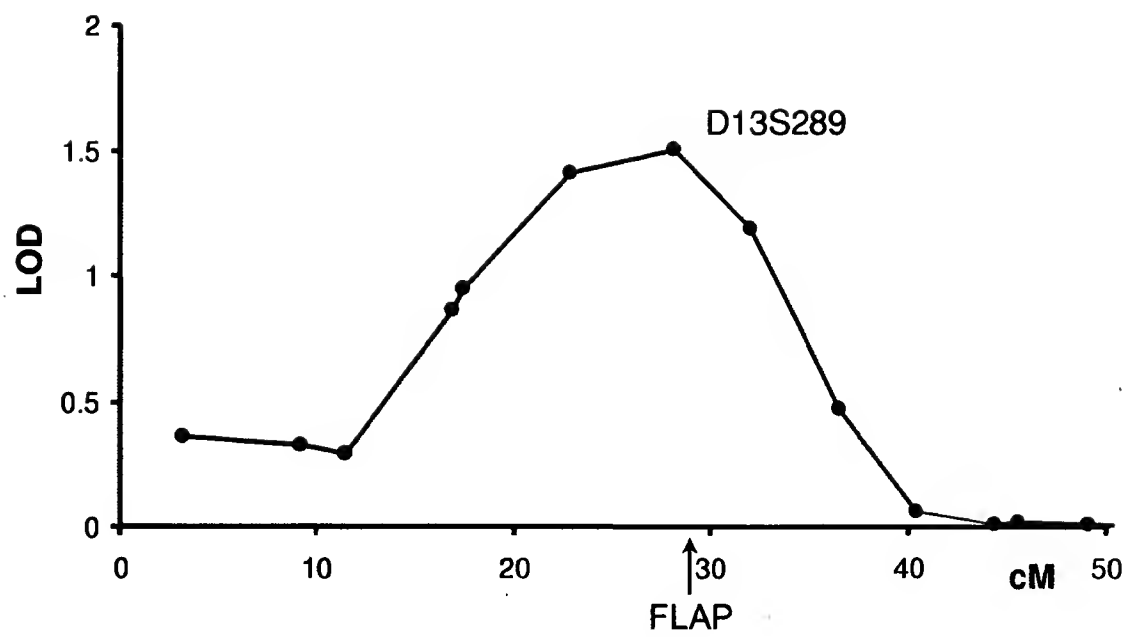


FIG. 13

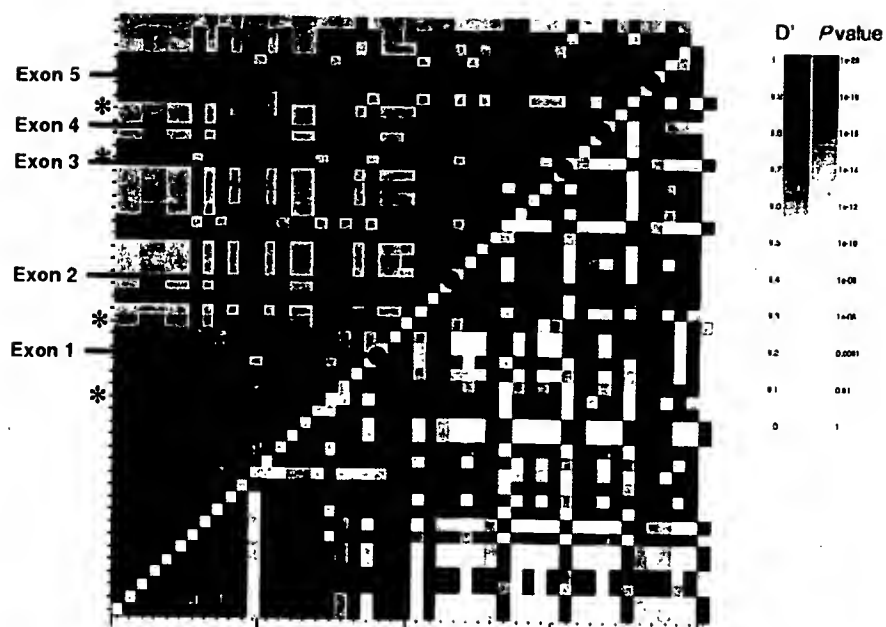


FIG. 14



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Legal Date: 01-30-2004

No.	Doccode	Number of pages
1	TRNA	1
2	SPEC	23
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12	FRPR	37

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013004

UTILITY PATENT APPLICATION TRANSMITTAL <small>(Only for new nonprovisional applications under 37 C.F.R. 1.53(b))</small>	Attorney Docket No.	2345.2051-004
	First Named Inventor or Application Identifier	Anna Helgadottir
	Express Mail Label No.	EV 052030864 US

Title of Invention	SUSCEPTIBILITY GENE FOR MYOCARDIAL INFARCTION, STROKE, AND PAOD; METHODS OF TREATMENT
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APPLICATION ELEMENTS See MPEP chapter 600 concerning utility patent application contents.	ADDRESS TO: Mail Stop Patent Application Commissioner for Patents P.O. Box 1450 Alexandria, VA 22313-1450
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| <input checked="" type="checkbox"/> Assignee - deCODE Genetics ehf. Reykjavik, ICELAND | |
| 8. <input type="checkbox"/> Power of Attorney | <input type="checkbox"/> 37 C.F.R. 3.73(b) Statement |
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☐ Continuation ☐ Divisional ☒ Continuation-in-part (CIP) of prior application No.: PCT/US03/32556

Prior application information: Examiner: Group Art Unit:

The entire disclosure of the prior application is considered a part of the disclosure of the accompanying application and is hereby incorporated by reference.
(Add standard Related Applications section with incorporation by reference to specification or update same)

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